

ADVANCES IN GENOMIC APPROACHES FOR DEVELOPING CLIMATE-RESILIENT VEGETABLE CROPS

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ABSTRACT

In this era of climate change, the agricultural sector is facing numerous challenges. To overcome these challenges, we must utilize the latest and most advanced genomic approaches and genetic engineering technologies. Innumerable improvements can be made in crop breeding through genetic engineering, including enhanced tolerance to abiotic and biotic stresses, as well as improved yield quality. Over the last two decades, numerous genetically modified horticultural crops have been developed, with a few more in the pipeline. This study provides a comprehensive outline that will assist researchers in better understanding the improvements in genetic modification and their impact on abiotic and biotic stress tolerance, as well as the enhanced traits related to plant genetic modification, such as quality, shelf life, and texture, in various crop varieties. Some of these noteworthy approaches, including gene mutation, epigenome editing, repression, activation, and precise genome editing technologies, such as CRISPR/Cas9, have been effectively used in potatoes and brinjal, among others. Prospects were also discussed that primarily emphasize the development of products to advance fields such as medicine, agriculture, and health, thereby raising living standards worldwide.

Keywords: Genetic engineering, Biotic and Abiotic stresses, Improvements, Technologies

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1. INTRODUCTION

A statistically significant change in the climate and weather patterns over the past three decades was observed (Corwin, 2021). Human activity is the primary factor contributing to the rising atmospheric CO₂ concentrations and excessive use of nitrogen fertilizer is one of the main causative agent of global warming (Piao et al., 2020). Climate change resulting from higher CO₂ levels may result in pest and disease outbreaks that are typically overlooked in advanced study (Skendžić et al., 2021; Zafar et al., 2021; Bhatti et al., 2023). This process is normally followed by variations in rainfall and temperature that may then result in severe weather conditions/fluctuations (Munaweera et al., 2022; Zafar et al., 2022). Climate-resilient vegetable crops are heterogeneous and enhance the tolerance towards biotic and abiotic stresses (Giordano et al., 2021). Developments in climate-resilient vegetable crops through genomic approaches and genetic engineering technologies could be made (Khar et al., 2020). Standard methods practiced for crop development, quality association, and crop protection (Wang et al., 2021) and enhancing other horticultural features now have considerable scope and promise to improve and advance biotechnology (Parmar et al., 2017). Creating desired genotypes for specific breeding objectives, cultivating disease-free and healthy crop plants, enhancing yield and quality, lengthening shelf life, making bio-pesticides and bio-fertilizers available, among other aspects, widens the promising prospects for enhancing fruit yield (Gurjar, 2022; Zafar et al., 2023). In certain crop varieties, genetic engineering has made it possible to incorporate desirable characters into the crop genome (Kumar et al., 2020). Additionally, for a novel function in a plant, genetic engineering involves isolating a desired gene, joining it to an appropriate vector to make a recombinant-DNA molecule and then inserting the resulting gene into the targeted plant's genome (Sedek et al., 2019; Zafar et al., 2024). Unlike closely associated plant species, resistance genes are not limited to close relatives, making transgenic technology the most contemporary/advanced technology in agriculture today. (Osmond and Colombo, 2019). The keystone and core of sustainable agriculture is the

management of numerous biotic and abiotic stresses (Venkatramanan & Shah, 2019). Although marker-assisted breeding and traditional genetics are being utilized to develop more valuable genotypes, however, due to lengthy sexual generation times (Maji et al., 2023) (Shrestha et al., 2020), such methods/ techniques are not practical for biennial or perennial horticultural crops, especially fruit trees (Simko et al., 2021). Transgenic technology enables the modification of plant genetic architecture using any organism, including bacteria and plants (Samal & Rout, 2018). Transforming genes into elite backgrounds requires high frequency and effectiveness of genetic transformation and plant regeneration methods (Gheysen et al., 2022). The development of appropriate regeneration procedures/methods and genetic transformation protocols for a variety of horticulture species, including apples, have been studied extensively in the past (Parmar et al., 2017). In terms of genetically modified (GM) horticultural crops, GM papaya is reported to have a resistance against the papaya ring spot virus and has been since grown worldwide (Lobato-Gómez et al., 2021). Most GM horticultural crops exhibit insecticide resistance, viral resistance, and herbicide tolerance (Mercado et al., 2015; Niraula & Fondong, 2021).

The genetically modified FlavrSavr tomato, which was authorized for distribution in the USA in 1994, is the first prominent example of a genetically engineered cultivated plant (Baranski et al., 2019). Adaptation to herbicide tolerance is a major adaptation for growing areas that have already achieved commercial success, while virus resistance, male sterility, and other innovations are also being researched. (Munaweera et al., 2022). In terms of genetically modified (GM) ornamental crops, GM papaya, which is resistant to the Papaya ring virus, accounts for about 53% of all GM ornamental crops grown worldwide (Kour et al., 2022). The most common GM ornamental crop trait is herbicide tolerance, preceded by pest, disease and viral resistance characteristics (Liu et al., 2022).

Additionally, the availability of stable transgene expression and RNA interference (RNAi) technology has been increasingly popular in recent years in the fields of system biology and plant genetics (Rajput et al., 2021; Haroon et al., 2023; Kamal et al., 2024). Despite coat protein genes, the RNAi approach has shown great potential in creating viral resistance in horticultural crops (Liu et al., 2020). Abiotic stresses such as drought, salinity and heat hinder crop productivity and production (Oshunsanya et al., 2019). Genes associated with heat shock proteins, mannitol, and glycine betaine, as well as transcription factors such as WRKY, DREB1, and MAPK, are crucial for abiotic stress tolerance (Parmar et al., 2017; Firdous et al., 2024). The uses of this technique have a broad range of applications from drought, heat, insect resistance, viral and disease resistance, and salinity tolerance (Fig. 1) (Mall et al., 2018). The tomato has received the most attention so far, but other horticultural crops, like fruits and vegetables, are being studied as well (Krishna et al., 2019). This review paper summaries and discusses widespread research that includes genes for different abiotic and biotic stress resistance, increasing shelf-life, adjustment of plant architecture, and color-shape modification traits in several horticultural crops due to advancements in regeneration and genetic transformation protocols.

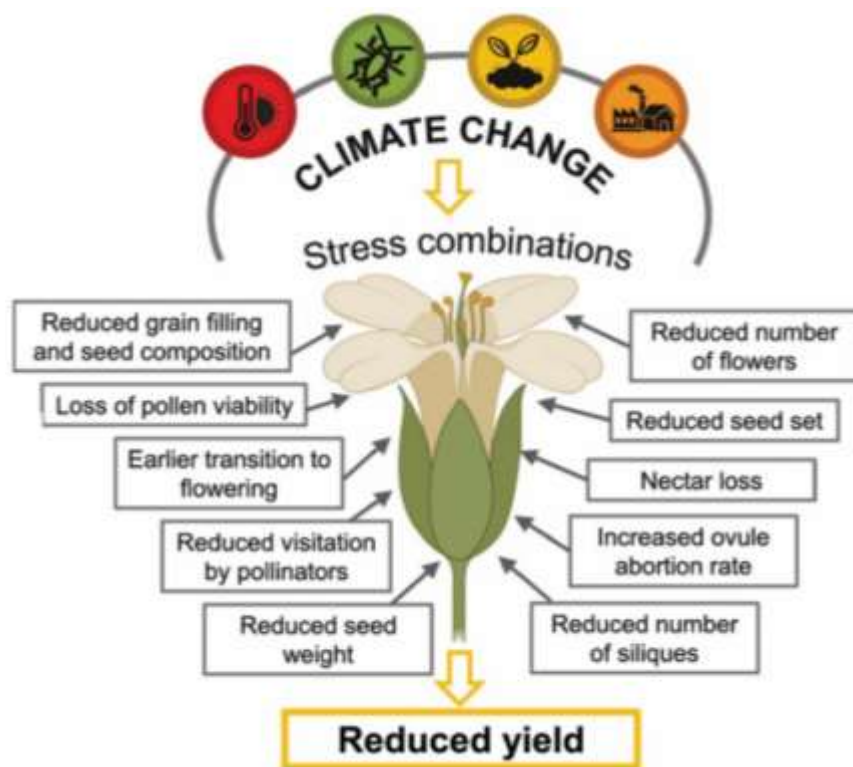


Fig. 1: Effects of climate change on plants and ultimately a reduction in yield.

2. EFFECT OF CLIMATE CHANGE

2.1. Effect of Climate Change on Plants

Global warming and drought stress is causing a reduction in agricultural output and undermining food security worldwide (Dong et al., 2019; Zafar et al., 2025). Malnutrition is a significant issue in many countries, particularly those with limited resources (Calicioglu et al., 2019). To fulfill the world's increasing population's food demand, food security is of immense importance (Haddad et al., 2016). Food with nutrients, minerals, analgesics, and health supplements that are essential for treating maladies (Saravanakumar et al., 2020). A variety of agro-climatic factors can influence vegetable growth and development; thus, any climatic fluctuation brought on by climate change might put this group of plants under unprecedented stress and even cause the crop to fail in a breeder's field. (Parajuli et al., 2019). Abrupt climatic changes impact agricultural productivity, disease and pest occurrence, innate immune responses, soil microbiota, and insect activity (War et al., 2016). Climate change's ultimate result is lower productivity and production due to the development of genetically compromised seeds, which could lead to a future food shortage. Because of the development of genetically modified seeds, climate change ultimately results in decreased productivity and production, which could cause a future food scarcity** (Fig. 1) (Raza et al., 2019).

2.2. Effect of Climate Change on Vegetable Production

In the majority of plants, fertilization is significantly affected by increasing temperatures at higher altitudes (Reed et al., 2022). Similar to pepper plants, the development of its fruits can be affected by significant temperature changes due to the plant's sensitivity to high temperatures during pollination (Hirpo & Gebeyehu, 2019). However, low temperatures can cause chilling and freezing, which in turn affect the cell membrane and inner structure of the plant (Manasa et al., 2022). It has been observed that low temperatures can significantly impact the germination rate of plants, e.g., in tomatoes and watermelons (Bhattacharya, 2022). Crops with shallow roots are more vulnerable to flooding. As plant roots require a steady oxygen supply, flooding causes a cut-off in soil respiration, resulting in suffocation of plant roots (Ponting et al., 2021). Due to reduced oxygen levels, the production of low ethylene and 1-aminocyclopropane-1-carboxylic acid (ACC) increases (Borbely et al., 2020). Regarding this, Fig. 2 provides a comprehensive list outlining how climate change affects plant growth and soil.



Fig. 2: Effect of climatic changes on plant and soil growth.

2.2.1. Improvement of Vegetable Crops for Stress Resistance: Plants can thrive in a few different conditions. These stresses, which are both biotic and abiotic, prevent plants from growing or may even kill them if certain conditions are not met effectively (Gull et al., 2019). Over the past forty years, genetic recombination has significantly improved postharvest quality and resilience to biotic and abiotic stresses (Yerasu et al., 2022). However, the constraints of genetic recombination, can only be overcome by advancements in modern biology (Atkins & Voytas, 2020). Over the past ten years, one trait that has been effectively bred into vegetable crops is tolerance to biotic and abiotic stresses (Gonzalez Guzman et al., 2022). Fig. 3 shows the list of biotic and abiotic factors that affect plant growth.

3. BIOTIC STRESS

3.1. Insect-pests

Currently, many crop plants lack sufficient resistance to insect pests (Tyagi et al., 2020; Zafar et al., 2020). The chemicals used to combat insect pests are not only hazardous to human health but also have adverse effects on the environment, including reduced soil fertility, pollution, and financial losses to farmers (Kumar et al., 2022; Zafar et al., 2022). Farmers cannot afford chemicals as they are expensive. Genetic advancements that result in cheaper pesticides would be beneficial for farmers (Anderson et al., 2019). These issues have a significant impact on crop production, which could be eradicated/minimized by the Bt (Cry) gene (Tokel et al., 2022). Fig. 4 is an illustration of the mode of action of Bt on insects. First, the Bt gene has been used to detect insect resistance in tomatoes. (Gu et al., 2021). Numerous genes, including lectins, protease inhibitors, trypsin inhibitors etc. have been employed to induce insect-pest resistance in several field crops (Malik, 2022). In plant bio-assays, Snow Lady, Beauty Lady, and Known You Early no. 2 all express the trypsin in indicating that the transgenic plants showed resistance to *Spodopteralitura* and *Plutellaxyllostella* (Appugol et al., 2022). The resistance gene was acquired from a nearby sweet potato (Ding et al., 1998). Sea Anemone Equistatin (SAE), a protease inhibitor, has three features that can block either cysteine or aspartic proteases (Parmar et al., 2017). According to another study, the transgenic chrysanthemum plants had a high expression of *Chrysanthemum morifolium* WRKY48 (CmWRKY48) transcription factor, which prevented aphid population growth (Li et al., 2015; Thakur et al., 2018).

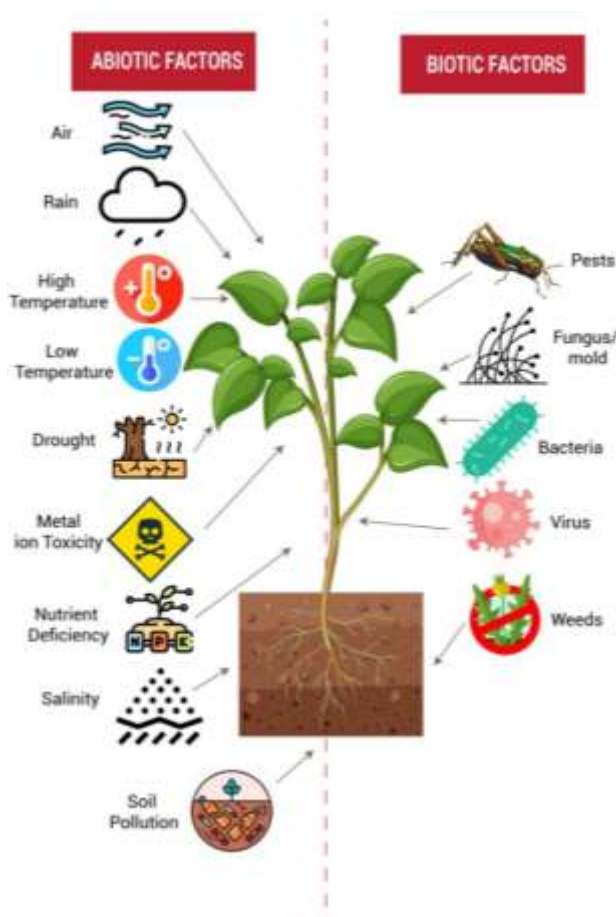


Fig. 3: The illustration for list of abiotic and biotic factors that affect plants.

(CMVP0-CP) were developed (Rajam et al., 2021). Three distinct transgenic events exhibited this tolerance despite of previously showing a high level of CMVP1 pathogen tolerance (Lee et al., 2009). Two of the viruses, namely Zucchini yellow mosaic virus (ZYMV) and papaya ring spot virus type W (PRSV W), are reported to have substantial adverse effects on watermelon (*Citrullus lanatus*) production and productivity worldwide (Ahsan et al., 2023). Three watermelon cultivars, namely Quality, 'Feeling', and 'China rose', were engineered using an *Agrobacterium tumefaciens* gene modification technique with transgenic constructs carrying shortened ZYMV coat protein (CP) and PRSV W CP genes to develop resistance against these viruses (Pandey, 2021). In

3.2. Nematodes

In most horticultural crops, plant pests such as root-knot nematodes (*Meloidogyne incognita*) cause significant yield losses (Sikandar et al., 2020). The most effective method to avoid such yield losses is by inducing genetic modifications in several proteinase inhibitors derived/obtained from respective crops (Van Esse et al., 2020). A molecule named "cystatin" is involved in the digestion of root-knot nematodes, and collisions with cystatins cause proteolytic digestion, thus destroying their mode of action (Yadav et al., 2013). For enhanced resistance against the root-knot nematode (RKN), a modified rice cystatin gene (OC-I-D86) was expressed in transgenic brinjal plants via the action of the root-specific promoter TUB- (Parmar et al., 2017). The transgenic plants' gene integration and appearance were assessed via ELISA, PCR, Southern blotting, Western blotting, and qPCR techniques (Papolu et al., 2016). Transgenic potato roots expressing the identical gene showed a partial resistance (67%) to *M. incognita* (Mejias et al., 2022). In the USA, especially, the lily (*Lilium longiflorum*) cv. "Nellie white" has significant commercial value as cut flowers and is a home to one of the most valuable species, Root lesion nematode (RLN), *Pratylenchus penetrans*, which's main pest (Vieira et al., 2015).

3.3. Viruses

To develop resistance against various viral infections in cultivated plants, the coat protein-mediated method of virus induction has been employed (Guria & Pandi, 2019). Engineered plants containing the coat protein gene for chili peppers

greenhouse experiments, two completely immune transgenic lines of the 'Feeling' cultivar were developed (Aduse, 2021). These two transgenic lines exhibited complete resistance to ZYMV and PRSV W viruses, and upon Western blot analysis, no trace of the viruses was detected (Yu et al., 2011). Without attempting to prevent local infection, the marketer of these products represented an identity hairpin similar to RNA that is controlled by the demand for these products, which decreased the propagation of the plum pox virus and systemic disease (Makeshkumar et al., 2021). Development of transgenic plants in various crops to induce tolerance against biotic stresses (Shekhawat et al., 2012). The transgenic horticultural crops having resistance to biotic stress are represented in Table 1.

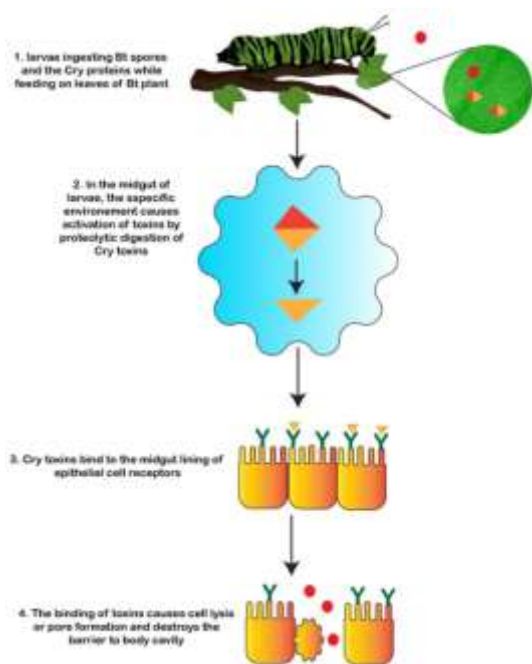


Fig. 4: Illustration of mode of action of Bt gene on insect. The insect ingests the Bt spores while feeding on the leaves. The Cry protoxin becomes lysed and activated in the alkaline environment of midgut of insect. The activated Cr toxins binds to the receptors on the midgut of epithelial cells. And binding results in pore formation or cell lysis.

peroxidase to recycle peroxide ions (H_2O_2) (Zafar et al., 2023). As a catalyst for neutralizing oxidative stress under heat stress in plants, Cu/Zn SOD works as an antioxidant for ROS. (Bhattacharjee, 2019). In comparison to non-transgenic plants, transgenic plants showed improved resistance to heat stress. Furthermore, transgenic plants were only damaged by heat stress about 25% of the time (Do et al., 2023).

Cold stress is a significant element affecting agricultural output and sustainability (Ritonga and Chen, 2020), it affects metabolism, cellular components, and overall plant physiology. (Atayee & Noori, 2020). Elevated temperatures are expected to accelerate crop maturation, resulting in earlier phenological stages and shortened growth cycles for certain crops (Ding et al., 2019). However, this faster pace, coupled with increased susceptibility to extreme events during crucial growth phases, may challenge yield and quality (Yadav et al., 2020). Customized assessments of crop-environment interactions are recommended for adaptable strategies (Liu et al., 2019). Temperature role in flower initiation and molecular aspects of flowering during climate changes, revealing the intricate landscape of plant stress responses (Borghi et al., 2019).

4.2. Drought

Transgenic lines tested for resistance against drought (polyethylene glycol in medium), salt and salinity (sodium chloride in medium) showed greater resistance to abiotic stresses than non-transformed plants (Njeru, 2019). To develop tolerance for a variety of abiotic stresses, StnsLTP1 (the potato-derived gene) was transferred into potato using agrobacterium tumefaciens-regulated genetic transformation. Under stress, transgenic potato lines showed improved cell membrane integrity by comparatively reducing membrane lipid peroxidation activity and H_2O_2 concentration. Moreover, the transgenic potato plants exhibited higher ascorbate deposition, as well as enhanced and overexpression of several genes, including StAPX, StCAT, and StSOD (Gangadhar et al., 2016; Zhang et al., 2019).

4. ABIOTIC STRESS

Abiotic stresses such as heat, cold, drought and salinity are the major environmental factors that affect the production of nearly all the horticultural crops (Oshunsanya et al., 2019). As far as abiotic stress is concerned, plant breeding hasn't been very effective until now (Islam et al.). Perhaps this is because several genes control traits at a specific locus (Tibbs Cortes et al., 2021). As a result of abiotic stresses, plants' cellular machinery often undergoes physiological, metabolic, and structural modifications (Ahmad et al., 2021).

4.1. Temperature

Heat stress impacts the physiological growth of plants by generating a range of reactive oxygen species (ROS), including superoxide and hydrogen peroxide (H_2O_2) (Sachdev et al., 2021; Zafar et al., 2023). ROS damages plant cells in many ways, including the denaturation of enzymes and cellular elements (Argosubekti, 2020). Plant tolerance to heat stress is directly linked with its ability to absorb ROS (Liu et al., 2021). To sustain the regular growth of plants, the filtration of ROS is a very crucial step (Hasanuzzaman et al., 2020). A variety of enzymatic systems have developed in plants to resist ROS, including glutathione reductase (GR), superoxide dismutase (SOD) for removal of superoxide ions, and

Table 1: Transgenic vegetable crops for biotic stress resistance improvement

Sr.#	Vegetable Crop	Target Gene(s)	Transformation method	Targeted Trait	Remarks	Reference
Disease Resistance						
1	Tomato(<i>Solanum lycopersicum</i>)	ANT1	Agrobacterium-mediated-transformation	Resistance against pathogenic bacteria	Resistance against <i>Pseudomonas syringae</i> pv. Tomato	(Paula de Toledo Thomazella et al., 2016)
2	Tomato(<i>Solanum lycopersicum</i>)	MIO1	Agrobacterium-mediated Cotyledon transformation	Resistance against fungus	Resistance against <i>Oidium neolyopersici</i>	(Nekrasov et al., 2017)
Nematode Resistance						
1	Brinjal (<i>Solanum melongena</i> L.)	OC- IAD86	Agrobacterium tumefaciens-mediated transformation	Root knot nematode resistance	Significant resistance observed against nematode; <i>Meloidogyne incognita</i>	(Papolu et al., 2016)
Virus Resistance						
1	Cucumber (<i>Cucumis sativus</i> L.)	eIF4E	Agrobacterium-mediated Cotyledon transformation	Virus Resistance	Resistance observed against Cucumber vein yellowing virus, Zucchini yellow mosaic virus, Papaya ring spot mosaic virus-W	(Chandrasekaran et al., 2016)
Salt Tolerance						
1	Pumpkin (<i>Cucurbita</i>)	RBOHD	Agrobacterium mediated transformation	Hydrogen peroxide and potassium ion production	Significant decrease in Hydrogen peroxide and potassium ion production	(Huang et al., 2019)
Herbicide Resistance						
1	Tomato (<i>Solanum lycopersicum</i>)	CCD8	Agrobacterium strain EHA105 mediated transformation	Herbicide resistance	Resistance against <i>Phelipanche aegyptiacas</i> observed	(Dubey et al., 2017)
2	Potato (<i>Solanum tuberosum</i> L.)	StALS1	Agrobacterium tumefaciens-mediated transformation	Herbicide resistance	Significant resistance against herbicide was observed	(Butler et al., 2015)
Quality Improvement						
1	Camelina sativa	FDA2	Agrobacterium tumefaciens-mediated transformation	Oleic acid production	10 to 60% increased oleic acid production was achieved	(Morineau et al., 2017)
2	Tomato (<i>Solanum lycopersicum</i>)	SI- ALMT9	Agrobacterium strain C58 mediated electroporation method	Malate production	Significant increase in malate production was observed	(Ye et al., 2017)
3	Sweet potato (<i>Ipomoea batatas</i>)	GBSSI, SBEII	Agrobacterium strain LB4404 mediated transformation	Amylose and amylopectin production	Decrease in amylose and amylopectin production	(Wang et al., 2019)

4.3. Salinity

Salinity or salt stress is a major abiotic factor that adversely affects many crops is (Majeed & Muhammad, 2019). Approximately 20% of the world's agricultural land is affected by salinity. Salt tolerance is regulated by a complex mechanism involving multiple genes (Hernández, 2019; Zafar et al., 2022). In response to the abiotic stress, Plants release cytokinin proteins to mitigate the effects of stress (Yildiz et al., 2020). Plants produce osmotin, one of the key pathogenesis-related proteins, to combat various biotic and abiotic stresses (Islam et al., 2023). Tomatoes are considered one of the most important vegetable crops grown worldwide, due to it's high commercial value (Panno et al., 2021). By inducing the pea-derived cytosolic ascorbate peroxidase (*cAPX*) gene (*Pisum sativum* L.), *transgenic tomato plants exhibit resistance to salt and chilling stress* (Gantait et al., 2019). Ascorbate peroxidase neutralizes hydrogen peroxide (H₂O₂) in plant cells, preventing the cells from damage caused by cold and salt stress (Chen et al., 2022). The transgenic plants exhibited a higher seed germination rate (26-37%) compared to the native variety (3%) when seeds were stored at 9 °C for 5 weeks. The APX rate of the transgenic plants was found to be 10-25 times higher under salt stress (200-250 mM), with little to no leaf damage (Gambhir et al., 2023).

5. GENOMIC APPROACHES IN VEGETABLE BREEDING

Agronomic traits such as disease resistance, fruit flavor, fruit shape, and plant architecture should be prioritized during the breeding of vegetable crops (Natalini et al., 2021). Next-generation sequencing technology has accelerated the sequencing and re-sequencing of the vegetable crop genomes, enabling researchers to identify specific genes and apply the knowledge for molecular marker-assisted selection breeding (Hao et al., 2020).

Many genome re-sequencing methods have led to the development of numerous molecular markers. Reference genomes are the fundamental building blocks of the re-sequencing technology, which are used to analyze sequence

diversity at the genome level (Yu et al., 2021). For whole-genome re-sequencing, bulked segregant analysis (BSA) is the most effective technique (Zsögön et al., 2017). BSA is generated from the techniques, such as QTL-seq and MutiMap, which are applied to different (Wang et al., 2018). By using QTL-seq to produce extreme phenotypes in the F₂ progeny, it is possible to obtain the SNP-index of two extreme pools and align them to the reference genome. This considerably reduces the uncertainty of other genes and phenotypes (Li & Xu, 2022).

The *Solanaceae* family contains many important vegetable crops including the tomato (*Solanum lycopersicum*), pepper (*Capsicum spp.*), potato (*Solanum tuberosum*) and aubergine (*Solanum melongena*). The genome sequences of these vegetable crops have been assembled and made accessible (Hao et al., 2020). The cultivated tomato variety "Heinz 1706" has a high-quality genome sequence (approximately 900 Mb) resulting from the combination of Sanger and NGS technologies (Tripodi, 2022). By comparing the genome sequence with that of the larger genome (739 Mb) of its nearest wild relative, the nucleotide divergence between the cultivated and wild tomato genomes was identified (Tomato Genome Consortium, 2012). However, the wild tomato is more resilient to stress than the cultivated variety. This discovery implies that a few essential wild tomato genes respond to and tolerate stress. The genomes of two of the pepper varieties, i.e. cultivated *C. annuum* (3.26 Gb) and its wild ancestor *C. annuum* var. *glabriusculum* (3.07 Gb), were sequenced and assembled (de novo) from scratch. Thus contributing towards a high-quality pepper genome. Because of long-term selection breeding, some cultivated pepper accessions exhibit less variation in their complete genome than the wild type (Qin et al., 2014). The genetic diversity in landraces can lead to crop improvement. The global germplasm banks provide an essential service in maintaining and preserving the genetic resources gathered over many generations of crops (Panis et al., 2020).

5.1. Utilization of Advanced Technologies of Genetic Engineering

Plant researchers can alter crop genomes more precisely and accurately using CRISPR technology (Pramanik et al., 2021). The possibility of a CRISPR/Cas framework of altering organelles like chloroplasts and mitochondria has not yet been investigated, due to the absence of transport vectors that can access these organelles (Razzaq et al., 2019). Cell-based modifications will soon be possible by focusing on mitochondria and chloroplasts with different guide RNAs (gRNAs) (Breeze et al., 2020). Furthermore, additional advancements are still required, such as a solution to the CRISPR/Cas machinery/construct transport problem, which is the primary obstacle in genome editing (Karkute et al., 2017).

To identify the stressors that are expected to have the most tremendous impact on agricultural crop yield and production under a particular climate change scenario, an ag genomic-based breeding technique for new cultivars should be used (Dwivedi et al., 2020). Specific solutions may be required, as the effects of climate change vary across different crops and ecosystems (Bakala et al., 2020). Data from multi-environment testing enables modeling of the effects of stress on crops and target populations (Rotili et al., 2020). To increase crop resilience to such climate fluctuations, plant breeders, crop physiologists, and gene bank curators will look for morphological and physiological traits in the available germplasm. Crop physiology might be able to identify the objectives that must be met to promote this kind of adaptation (Nguyen & Norton, 2020). Genome editing under speed-rearing conditions will provide a well-organized framework to speed up crop reproduction cycles at low cost and a mechanical advancement in obtaining non-transgenic plants devoid of tissue culture. It will be labelled as non-GMO, increasing public awareness and enabling it to avoid strict regulatory measures. Research in plant science is reaching new heights, thanks to the fascinating AI-inspired phenotyping tools, such as robots and their integration with other OMICS data (Sharma, 2021; Han et al., 2024). We urgently require next-generation approaches in data fusion, swarm intelligence, hybrid intelligence and deep learning to develop large scale data handling techniques with phonemics knowledge across multi-scale and multi-domain (Kumar & Prakash, 2020). The incorporation of pipelines for advanced breeding to enhance crop yield is illustrated in Fig. 5.

Plant research could overcome its current obstacles and multidisciplinary approaches from genomics to phonemics should be used very carefully. Future yield rearing can develop irreversible progress to guarantee food safety and will fulfill the food requirements of a rapidly increasing population for a long time to drop by using coordinated cutting-edge draws (Nandini et al., 2022).

5.2. Bioinformatics Resources for Crop Breeding Analysis

Bioinformatics is a powerful tool for developing stress resistance and improving the breeding of crop plants. (Mu et al., 2022). The use of bioinformatic tools for crops can help to improve yield and quality (Mu et al., 2022). Crops can be further improved by doing the bioinformatics analysis of the genes related to seed germination, seedling growth, reproductive yield, and also by artificially interfering with the relevant genes for example, the main focus of genetic improvement is regarding the adaptability, yield, and quality of rapeseed (*Brassica napus*) by using advanced breeding approaches (Mu et al., 2022). Additionally, by elucidating the function of the desired gene, agriculture can benefit from using bioinformatics tools to search the genomes of plants and crops.

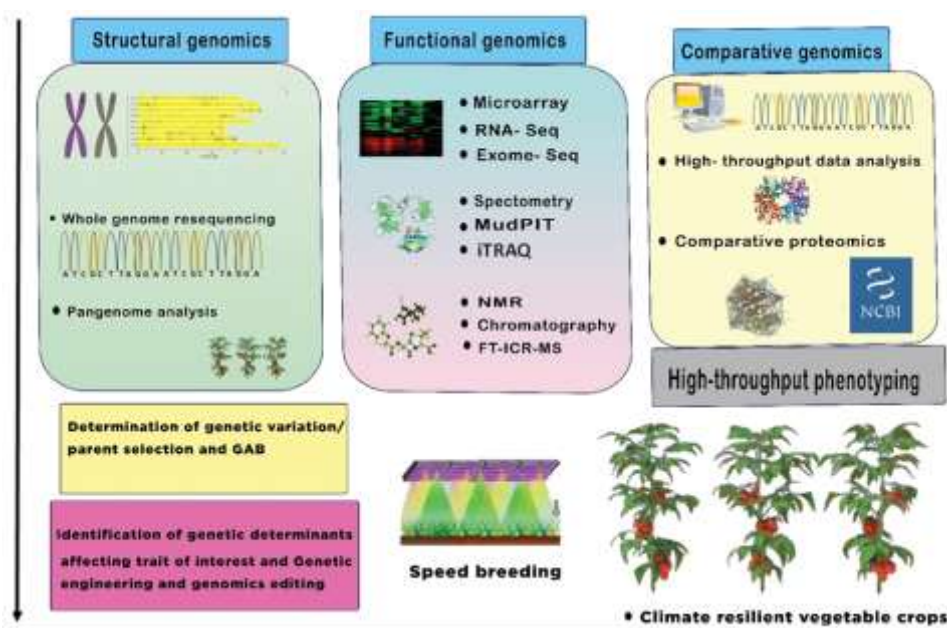


Fig. 5: Incorporating pipelines for advanced genomics approaches for developing climate resilient vegetable crops.

Several bioinformatics tools and databases are available and utilized for plant breeding and genomics. Some of these resources include the European Bioinformatics Institute Ensemble plants, the European Molecular Biology Laboratory (EMBL); nucleotide sequence database (Flicek et al., 2010), GenBank, GrainGenes, and Gramene. These databases are crucial for storing and analyzing vast and complex plant genome sequences (Lai et al., 2012).

5.3. Social Acceptance and Regulations Regarding Genetic Engineering

In terms of bio-defense, the traits of transgenic plants and the methods employed are significant (Gheysen et al., 2022). Because the transgenic organisms developed from toxigenic organisms barely express any outputs, they pose a lower risk (Anderson et al., 2019). According to the reports, a highly contagious genome analysis approach of gene regulation is especially effective in controlling the relevant viruses (Zhang et al., 2022). Since humans and animals often consume food from infected plants without causing harm, GM crops containing a small portion of the viral DNA are unlikely to raise serious biological safety concerns (Kumar et al., 2020). The antisense approach preserves the plant's natural metabolism by slowing down particular metabolic processes during ripening (Liscombe et al., 2022). Selection markers are greatly employed for the creation of transgenic agricultural crop varieties (Miller et al., 2022). The constitutive expression of these flag genes has detrimental effects on plant metabolism and is not beneficial for crop growth. However, certain methods can be employed to eliminate these flag genes from transgenic plants (Yali, 2022). Biosafety concerns could be minimized by taking appropriate measures throughout the transgenic variety development phase (Araki & Ishii, 2015).

6. FUTURE PROSPECTIVE

By using genetic engineering technology, we can manipulate the genetic material/ genome of an organism. With the help of this technology, a number of different products have been developed/produced, thus revolutionizing the fields of Health, Medicine, and Agriculture globally (Sharma et al., 2022). The aim to uplift living standards worldwide is disturbed by yield losses due to diseases. Pathogens, such as microbes, reduce crop yields by about 15%, whereas a 3% reduction in crop yield is attributed to viruses. In some vegetable crops, microbial diseases lead to a 30% yield loss. (Rao and Reddy, 2020). Genetic engineering, which modifies an organism's genetic makeup through the application of biotechnology, offers numerous benefits over conventional breeding. Firstly, it facilitates the insertion, removal, and modification of specific genes of interest, resulting in a smooth flow of information across the crop genome (Yali, 2022). Consequently, compared to crossbreeding, crops with desired seed yield could be achieved in fewer generations. Secondly, genetic engineering enables the transfer of genetic material between species. As a result, the raw genetic resources available for this process are not limited to the gene findings within the species (Dong and Ronald, 2019).

7. CONCLUSION

Due to climate change, crop production and food security are facing enormous consequences, especially in developing countries. To understand how plants react to abiotic stresses like salinity and drought at the molecular

level, crop productivity needs to be enhanced. Conventional breeding techniques are less beneficial in increasing agricultural productivity amidst these stresses. To better understand how rapidly diverse crop types can respond to abiotic stresses such as drought and salinity, this study primarily employed advanced molecular genomics techniques that target plant genes. Furthermore, we summarized the latest findings on plant genes, identified differences between them according to their response to abiotic stresses, and detailed recent advancements in these stress-response pathways. In conclusion, any two or all three genomic technologies would be coupled to produce crops that are resistant to drought and salinity.

DECLARATIONS

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Data Availability: All datasets generated and analyzed for this study are included in the article.

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