Chapter 13
Improvement of Vegetables Through Molecular Breeding in Changing Climate Scenario

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Abstract Vegetable crops have been cultivated since they were domesticated. These are the principal source of nutrients required in the growth and development of human beings. Rapid advances in the methods of next-generation sequencing technology and high throughput genotyping protocols have resulted in the collection and publication of reference genomes of major vegetable species. The large-scale genetic resource reorganization strategy has revealed the process of vegetable crops domestication and improvement of the essential traits through breeding procedures. The utilization of genetic mapping strategies and identification of quantitative trait locus has resulted in the exploration of significant molecular markers linked to essential traits in vegetables. Furthermore, the genome-based breeding approach is employed in most important vegetable crops families, such as Solanaceae and Brassicaceae, and allowing molecular selection at the single-base level. As a result, genome-wide molecular markers are extensively used for efficient genotyping in most vegetable crops. Molecular breeding has emerged as a key method for vegetables. Besides this, genome editing technology can dramatically increase vegetable breeding efficiency. This chapter examines the current scenario of genome-based molecular breeding tactics and genome editing approaches employed in

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significant vegetable crops to give insights into next-generation molecular breeding for a growing global population.

Keywords Molecular breeding · Vegetable crops · Genome editing · Climate change

13.1 Introduction

Abiotic stresses such as extremely low or high temperature, increase in soil salinity status, drought, and floods have an impact on vegetable production. Climate change significantly impacts various developmental stages of vegetables such as vegetative growth, flowering, and fruiting (Spaldon et al. 2015; Khar et al. 2022). The effects of high temperature and unpredictable rainfall can impede average plant growth and development, affecting crop yields. Environmental stress has a significant impact on soil organic matter decomposition, the nutrient cycle, and plant nutrients as well as water availability. The intensity and duration of the extreme environment, on the other hand, determines the crop growth cycle, biomass accumulation, and ultimately the range of economic benefits. Vegetable crops yields in Asia are expected to fall by 2510 per cent between 2020 and 2050, with South and Central Asia experiencing the steepest declines (Cruz et al. 2007; Ashraf et al. 2022). Several initiatives have been launched to reduce the potential impact of climate change on vegetable production. Advanced molecular breeding approaches have been used to improve the yields and quality of important vegetable crops and combat the abiotic stresses of climate change.

NGS (next-generation sequencing) technology has considerably accelerated vegetable crops genomic sequencing and resequencing, which resulted in the publication of chromosomal sequences of some major vegetable crops. The order is determined by the specific locus of the corresponding gene to a marker. Based on genotyping techniques, these linked markers can be used to perform molecular marker-assisted breeding and identify genetic relationships between different traits of vegetable crops. Various genome sequencing methods also contribute to the development of new molecular markers (Saha et al. 2022). Resequencing techniques rely heavily on the reference genome and bring researchers together to analyse sequence diversity at the genomic level. The primary approach, known as bulked segregant analysis (BSA), was assumed to be whole-genome resequencing employing mass separation analysis. BSA is based on the gene identification and marker development procedures, tested on a variety of vegetable crops. Creating the F_2 progeny's divergent phenotypes acquires the SNP index of the two diversified gene pools and matches them to the vegetable reference genome. Besides this, QTLseq and MutMap can also be utilised. As a result, there is a lot less doubt about other genes and phenotypes (Takagi et al. 2013). MutMap was also used to build a DNA pool from a single individual with the F_2 isolation mutant phenotype and compare it to wildtype and parental reference sequences (Abe et al. 2012). It can also be used to locate the markers inside the genome. Large-scale resequencing has evolved into a more generic strategy based on improved approaches for finding markers linked with vegetable crop attributes.

Transcriptome and metabolic analyses help the researchers to domesticate genes and comprehend molecular regulatory networks at the genomic and transcriptional levels by altering gene expression patterns and analysing metabolic pathways. Existing molecular markers and reference genomes for vegetable crops can be employed to alter the vegetable genomes. CRISPR/Cas9 is a standard genome editing technique used to improve a variety of vegetable crops' undesirable traits (Khan et al. 2019; Satish Chhapekar et al. 2022). Compared to other breeding methods, this form of targeted breeding is more efficient and time-saving (Chen et al. 2019; Zahid et al. 2022). This chapter summarises the progress of research on molecular methods used to create vegetable crops resistant to abiotic stress, including molecular breeding and genome editing approaches.

13.2 Signal Transduction Mechanism Against Abiotic Stresses in Vegetable Crops

Plants respond to stress in various ways, including altered gene expression, cellular metabolism, growth rates, and vegetable crops yields. A sudden change in environmental conditions typically causes plant stress. Abiotic stress imposed on plants by environmental factors can be physical or chemical. Drought, flood, extreme temperatures, salt and mineral toxicity, are the abiotic stresses impacting vegetable crops yields and seed production. The roots are the plant‘s first line of defence against abiotic stress. The disruption of the Na + / K + ratio in the cytoplasm (Sahoo and Mohapatra 2020) of plant cells is one of the major responses to abiotic stress, including excess salt. Signalling is divided into three stages. First, according to the information received, the cell recognises extracellular signalling molecules. When a signalling molecule binds to a receptor, the signalling mechanism modifies the receptor protein and the response when the signal elicits a specific cellular response. Sensors' perception of the signal is the first step in the signalling pathway, and the generation of secondary signalling molecules follows it. It is usually a non-protein molecule such as Ca^{2+}, IP (Inositol phosphate), or ROS (reactive oxygen species). Each secondary signalling molecule can initiate a protein phosphorylation cascade that regulates the activity of specific transcription factors. Given the abundance of stress at the cellular level and its individual effects, cells develop a sensor that can detect stress (cold, drought, salt) and selectively facilitate the transmission of specific stress signals to cellular targets. A typical two-component system includes HIK (Histidine kinase), which is located on the membrane and senses the input signal, and R_{reg} (response regulator), which mediates the output signal (Sahoo and Mohapatra 2020).

13.2.1 ROS and Calcium

ROS are formed as a by-product of respiration and photosynthesis, and they are required for average plant growth. Single-electron transfer converts the O_2 molecule to superoxide anions, then reduced to hydroxyl radicals by H_2O_2. These three molecules are reactive oxygen species (ROS), which cause oxidative damage to proteins, DNA, and lipids. Drought, low and high temperatures, and other stressors activate ROS, leading to oxidative stress (Sahoo and Mohapatra 2020). Ca^{2+} is another non-protein molecule that influences how vegetable crops respond to abiotic stress. The interaction of inflow and outflow produces and maintains Ca^{2+} spikes in the cytosol. Plants become hypersensitive to ionic and cold stress when Ca^{2+} homeostasis is disrupted due to overexpression of the Ca^{2+}/H^+ antiporter calcium exchanger 1 (CAX1), which loads Ca^{2+} into the vacuole. ABA and mechanical stress signals mobilise Ca^{2+} from intracellular storage, and extracellular Ca^{2+} influx is crucial in cold stress signal transmission (Sahoo and Mohapatra 2020).

13.2.2 Phospholipids, CDPKs and MAPKs

These are critical components of the plasma membrane that can generate signalling molecules. Phosphorylated phosphatidylinositol (PI) is a significant and complex class of signalling precursors. PIP (Phosphatidylinositol phosphate) and PIP2 (Phosphatidylinositol bisphosphate) plant PI isomers complicate signal transduction. PLC (Phospholipase C) catalyses phospholipid degradation, resulting in IP_3 (Inositol-1, 4, 5-triphosphate) and DAG (Diacyl glycerol). Individually, these serve as second messengers. IP_3 levels in the cell have a direct impact on ABA-induced gene expression (Sahoo and Mohapatra 2020). Plants that overexpress the enzyme involved in IP_3 catabolism delay ABA induction of KIN1, RD29A, and RD22. Calcium-dependent protein kinases (CDPKs) are among the most numerous plant protein kinase subfamilies. It has a Ca^{2+} sensor kinase hybrid structure, a calmodulin-like domain, and a ser / thr protein kinase domain at the N-terminus (Sahoo and Mohapatra 2020). It is crucial in the signalling of abiotic stress. MAP kinase is a key player in signalling pathways initiated by various surface receptors. The MAPK target can be found in a variety of intracellular compartments. MAPK acts as a physical link between the cytoplasmic and nuclear signalling pathways (Sahoo and Mohapatra 2020).

13.3 Salinity Tolerance in Vegetable Crops

Excessive salt in agricultural land has been a problem since agriculture's inception. Irrigation has enabled agriculture to be expanded to semi-arid and arid lands and has contributed to a significant increase in food production over the last 40 years, resulting in the accumulation of large amounts of water and high salt. Soil degradation due to increased salinity now affects about 20% of the world's irrigated areas, instead of arid areas and deserts, which currently occupy 1/4th of the planet's total land area (Yeo et al. 1999). SOS3, SOS2, and SOS1 were identified as three significant additives that maintain ion homeostasis across salinity stress by molecular and biochemical mechanisms (Yamaguchi and Blumwald 2005; Flowers 2004). The membrane-bound Ca^{2+} sensor SOS3, which recruits the ser/thr protein kinase SOS2 to the moving membrane, detects Ca^{2+} signalling induced by the salt stress. SOS3 and SOS2 activate the plasma membrane Na^+/H^+ antiporter SOS1 and restores mobile ion balance via Na^+ ion outflow (Sahoo and Mohapatra 2020). The SOS3/SOS2 complex regulates the Na^+ region of the cytosol further by activating and dispersing these ions *via* the vacuolar transporter NHX1. Access to Na^{2+} ions is further complicated by the recreational inhibition of the plasma membrane transporter HKT1. SOS2 also regulates the Ca^{2+} ion domain in the cytosol by controlling the vacuolar Ca^{2+} channel, CAX1. The entire mechanism results in vegetable crops salt tolerance.

13.4 Cold Tolerance in Vegetable Crops

Cold stress, is the most significant biological stress, reducing vegetable crops productivity by affecting plant quality and postharvest lifespan. Plants adapt to such lethal cold stresses by acquiring cold and frost resistance through a process known as acclimation. This cold stress is transmitted via multiple signalling pathways, including ROS, protein kinases, protein phosphatases, ABA, and Ca^{2+}. Moreover, ABA has proven to be the best (Sahoo and Mohapatra 2020). Plants have a cold acclimation mechanism that helps them survive below-freezing temperatures, and this mechanism is induced by the COR (Cold response) gene. COR78 (cold induction) or RD29A (dehydration reaction) are the critical COR gene for studying gene regulation in cold and osmotic stress. The RD29A promoter region contains a 9-base pair sequence known as the dehydration response element (DRE), which response to cold stress. The CBF gene is activated by ICE1 (Inducer of CBF expression). ICE1 is a constitutive transcription factor that binds to the CBF3 promoter and induces its expression when activated by cold stress. CBF binds to the CRT / DRE cis-element of the COR gene and induces gene expression to provide freeze resistance.

13.5 Drought Tolerance in Vegetable Crops

The global climate is changing due to rising temperatures and CO_2 levels in the atmosphere. Because of the severe drought, the soil moisture available to the plant is constantly increasing, causing the plants to die prematurely. Stunted growth is a plant‘s first reaction after a drought has been imposed on the crop. ABA is an important plant hormone that aids in responding to various stress signals during drought stress. The use of ABA on plants mimics the effects of stressful conditions. In vegetable crops, ABA-mediated gene expression can be explained by two types of signalling pathways, *i.e.,* ABA-dependent and independent signalling pathways. AREB / ABF and MYC / MYB are the ABA-dependent regulons (Sahoo and Mohapatra 2020). CBF / DREB and NAC / ZFHD are ABA-independent regulons.

13.6 Genomics of Major Vegetable Crops and Identification of Genes for Abiotic Stresses

Plant genomic information research has bolstered the field of life sciences. Whole-genome sequencing can be used to investigate a species' entire genome and determine gene function. It is a valuable tool for figuring out how plants grow, develop, and differentiate at the molecular level. The advancement of high-throughput sequencing and the reduction of sequencing costs have made genome sequencing projects on various plant species more feasible. Due to their critical economic relevance and high nutrient content, vegetable crops have become an attractive subject for genetic research. Genome studies of numerous vegetable crops have been performed, including wild relatives and current cultivars. These sequenced vegetable crops can be grouped principally into Solanaceae, Cucurbitaceae, Brassicaceae, and other families (Dias and Ortiz 2021). Many major vegetable species in the Solanaceae family, including tomato, pepper, potato, and eggplant, have their genomic sequences published (Fig. 13.1).

On the other hand, wild tomatoes have a higher stress tolerance than farmed tomatoes. This discovery suggests that some critical wild tomato genes can be adapted to survive in abiotic stress (Hao et al. 2020; Pradhan et al. 2021). The following are the primary genome-based methodologies for finding genes relevant to vegetable crops. BSAseq is a popular method for resequencing the whole genome. This entails generating a new batch of descendants and comparing the resequence results to the compiled reference genome. This technique relies mainly on the reference genome to swiftly identify potential regions. Multiple candidate genes for significant features, such as in tomato for internode length (Schrager-Lavelle et al. 2019), Grey press (Chen et al. 2017a, b) and Carcass count (Gao et al. 2016a, b; Yu et al. 2021) in cucumber and, fruit shape in watermelon (Dou et al. 2018b) etc., by using this method. Some other genes are also identified by using this method in vegetables which can be useful during the phenotypic selection of genotypes in abiotic stresses (Table 13.1).

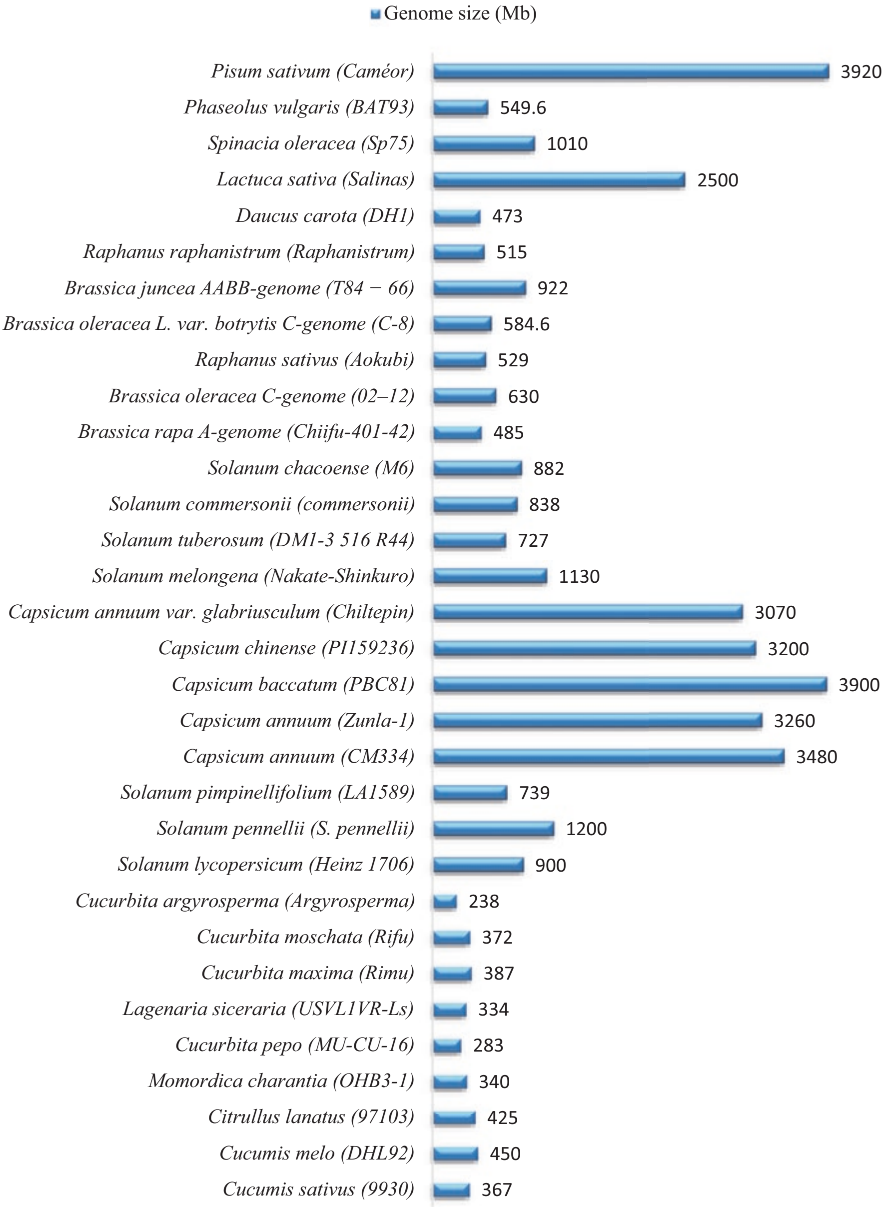

Fig. 13.1 List of reference genome information in vegetable crops. (Adapted from Hao et al. 2020); Left side: Crop name with sequence accession; Right side: Genome size in Mega Base pair (Mb)

Table 13.1 Gene discovery by genome-based approaches in major vegetable crops for changing climate

Crop species	Morphological target trait related to abiotic stresses for gene and marker discovery	Genome-based approaches	Reference
Tomato	Early flowering	QTL-seq	Ruangrak et al. (2018)
	Internode length	BSA-seq	Schrager-Lavelle et al. (2019)
	Yellow-coloured fruit	MutMap	Garcia et al. (2016)
	Fruit weight	QTL-seq	Illa-Berenguer et al. (2015)
	Leaf mold	QTL-seq	Liu et al. (2019a, b)
Cucumber	Early flowering	QTL-seq	Lu et al. (2014)
	Carpel number	BSA-seq	Li et al. (2016)
	Golden leaf	BSA-seq	Gao et al. (2016a, b)
	Tendril-less	BSA-seq	Chen et al. (2017a, b)
	Fruit length	BSA-seq	Xin et al. (2019)
	Subgynoecy	QTL-seq	Win et al. (2019)
	Yellow-green fruit peel	MutMap	Hao et al. (2018)
	Leaf variegation	MutMap	Cao et al. (2018)
	Light green coloration	MutMap	Lun et al. (2015)
	Light green peel	MutMap	Zhou et al. (2015)
	Curly leaf	MutMap	Rong et al. (2019)
	Organ size	BSR-seq	Yang et al. (2018)
	Fruit thickness	SLAF-seq	Xu et al. (2015a, b)
	Waterlogging	SLAF-seq	Liang et al. (2016)
Melon	Striped rind	BSA-seq	Liu et al. (2019a, b)
	Flavor-related	SLAF-seq	Zhang et al. (2016)
Watermelon	Fruit shape	BSA-seq	Dou et al. (2018b)
	Fruit skin color	BSA-seq	Dou et al. (2018a)
	Seed coat color	QTL-seq	Paudel et al. (2019)

(continued)

Table 13.1 (continued)

Crop species	Morphological target trait related to abiotic stresses for gene and marker discovery	Genome-based approaches	Reference
Pepper	Male sterile	BSA-seq	Cheng et al. (2018)
	Fruit colour	BSA-seq	Borovsky et al. (2019)
Ornamental kale	Lobed leaf	QTL-seq	Ren et al. (2019)
Chinese cabbage	Golden leaf	MutMap	Fu et al. (2019)
Cabbage	Purple colour trait	BSR-seq	Yan et al. (2019)
Radish	Restorer-of-fertility	BSR-seq	Lee et al. (2014)
Broccoli & cabbage	Early flowering	QTL-seq	Shu et al. (2018)

QTL Quantitative trait locus, *BSA* Bulked segregant analysis, *BSR* Bulked segregant RNA, *SLAF* Specific-locus amplified fragment, *seq* Sequencing

Other BSAseq-derived approaches, such as the QTLseq quantitative trait and the ethyl methane sulfonate (EMS) mutant MutMap, have been used to develop abiotic stress tolerance vegetable crops. QTLseq has been frequently utilised to find genes that control the quantitative features of vegetable crops since publishing reference genomes for numerous vegetable crops. This method has successfully identified quantitative features that suggest continuous phenotypic changes in different offspring of vegetable crops. It was also used to find the linkage marker Ef2.1 (Shu et al. 2018) linked to broccoli and cabbage blooms for tolerance to abiotic stress.

Significant QTL linked to cucumber early flowering during the abiotic stresses, particularly drought, has also been identified (Lu et al. 2014). This makes it easier to choose early-blooming cucumber types and shortens the cucumber growing cycle. Fruit weight and quantity of tomato loci (Illa-Berenguer et al. 2015), as well as several genes for other qualities such as ornamental cabbage locus leaves (Illa-Berenguer et al. 2015), has also been identified. In addition, QTLseq identified watermelon seed coat colour, cucumber sub-gynecology, and cucumber sub-gynecology (Win et al. 2019). The relevance of the reference genome for rapid molecular breeding is further demonstrated by the identification of candidate genes from carcinogenic EMS vegetable variations. Several pooled sequencing approaches have also been established (Abe et al. 2012), and MutMap has been proposed as a standard gene identification approach based on NGS technology. Individuals with mutant traits in the isolated F_2 group can pool their DNA. Two light green shell genes (Lun et al. 2015; Zhou et al. 2015) are found in cucumber by using MutMap technique (Hao et al. 2018), and leaf-altered genes that control cucumber fruit or leaf colour (Cao et al. 2018) has also been identified. MutMap is also used to find genes for Chinese cabbage fruits, golden leaves, and yellow tomato fruits (Fu et al. 2019). MutMap also successfully identifies random genes for plant height and leaf morphological variants.

To construct a high-density linkage map and uncover candidate genes for the Rfd1 gene, researchers used the BSRseq approach. BSAseq and BSRseq were also employed on Bell peppers at the same time to develop chloroplast and immature Bell pepper colours (Garcia et al. 2016). SLAFseq is another method for simplifying the genome and performing whole-genome resequencing. For SLAFseq applications to succeed, it is also necessary to have a known reference genome and bioinformatics foundation. SLAFseq may analyse a species' genetic diversity by simplifying its genome, and bioinformatics opens up new paths for investigating genomic alterations in evolutionary species (Xu et al. 2014). Cucumbers, peppers, and watermelons can all benefit from SLAFseq to help them figure out their complex features against abiotic stresses. For example, genes associated with cucumber fruit thickness, aphid resistance, and flooding were discovered using SLAFseq (Liang et al. 2016; Xu et al. 2015a, b; Zhu et al. 2016). It was also utilised to create a high-density map with 2634 watermelon SNPs and significantly lower distances between linked markers (Shang et al. 2016). Furthermore, SLAFseq, in conjunction with other genome-based sequencing technologies, can produce accurate and modest linkage mapping. SLAFseq and BSAseq, for example, have been used to define genes linked to pepper's first floral segment (Xu et al. 2016) and the melon flavour gene (Zhang et al. 2016; Abe et al. 2012). These finding suggests that, a combination of BSAseq and RNAseq is required, including a reference genome to identify candidate genes for abiotic stress tolerance in vegetable crops (Table 13.1).

13.7 Genome-Wide Association Analysis in Major Vegetable Crops for Abiotic Stresses

Genome-wide association analysis (GWAS) is an effective method based on genotype-phenotype correlation in a group of individuals, which looks upon genetic variation of complex traits in vegetable crops in the reference genome sequence (Saidou et al. 2014). This can be done by collecting a variety of cultural accessions, crossing lines, sequencing, and comparing genetic diversity between them, especially for traits influenced by various factors. For example, bitterness in cucumbers is an undesirable feature, hence cultivars that are not bitter after long periods of domestication were chosen. Critical GWAS studies on cucumbers have also aided in understanding the genetic mechanism of bittern production using 115 cucumber varieties and the rapid and precise detection of bitterness using linked molecular markers (Shang et al. 2014), particularly during the employment of abiotic stress.

GWAS can also be used to uncover links between fructose and volatile organic acids, which are prevalent in tomato fruit flavours during drought and salinity stress (Zhang et al. 2015; Zhao et al. 2019). Capsaicinoid content is a crucial component of pepper flavour, and GWAS has been used in several studies to explore capsaicinoids. Many transport factors and ankyrin-like proteins may be involved in capsaicinoid synthesis, and the *C. annum* accession has been used to find markers connected to capsaicin and dihydrocapsaicin levels (Nimmakayala et al. 2016). Another GWAS sample, including the *C. annuum* accession, discovered candidate genes or QTLs that modulate capsaicinoid concentration. High-density SNP mapping identified 69 QTL regions and 5 candidate genes (Han et al. 2018) during abiotic stresses. GWAS, on the other hand, has several drawbacks. Some GWAS markers produce false-positive results, and others are not repeatable among cultivars. As a result, GWAS-identified molecular markers in vegetable crops will need to be confirmed through genotyping or polymorphism amplification while studying them in the abiotic stress environment.

13.8 Genome Based Molecular Marker Discovery in Vegetable Breeding

Marker-assisted selection (MAS) has become a popular genotype-based breeding approach for increasing vegetable crops breeding performance. MAS can preemptively eliminate undesirable genetic backgrounds or nudge alleles back to the intended genetic region (Fig. 13.2). A sufficient number of molecular markers linked with the trait and their polymorphisms are also essential considerations. Molecular markers integrating RLFPs or SSRs were previously advanced without

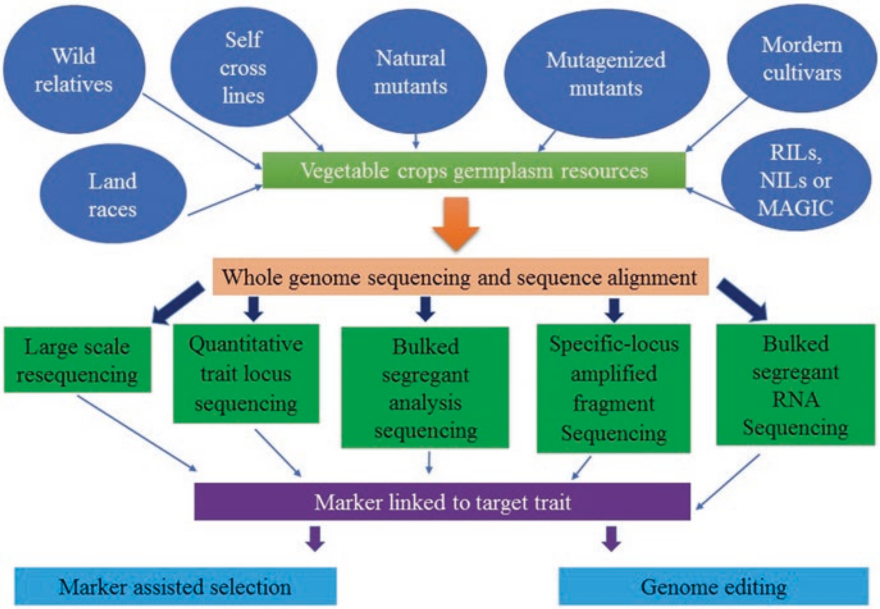

Fig. 13.2 Flowchart depicting the molecular breeding process in vegetable crops using genome-based approaches

genomic information. On the other hand, those molecular markers are far less polymorphic and have a narrow range of expression.

With the introduction of the reference genome for maximal vegetable vegetation and the advancement of the NGS era for genome sequencing and resequencing, the number of SSR markers has increased dramatically. For the black spikes of ripe cucumber fruit and the uniform colour of orange and immature fruit, near-range SSR markers were mapped (Li et al. 2013; Yang et al. 2014). In addition, in *Brassica rapa* L. var. purpurea, a high-density map using SSR markers was employed to identify the markers linked to traits related to abiotic stresses (Wang et al. 2017). In tomatoes, OVATE has been discovered to be a good indicator for fruit shape, as well as CYC B, SlMYB12, and SlMYB75 for fruit colour (Rodríguez et al. 2013; Ballester et al. 2010; Fernandez-Moreno et al. 2016; Hwang et al. 2016; Jian et al. 2019). For cucumbers, a novel targeted SSRseq approach has been devised (Jian et al. 2019). It also has higher coverage in high-throughput sequences and is less expensive than previously advanced SSR markers, allowing genotyping of many SSR markers across different accessions. This procedure can also broaden markers so that distinct cucumber ecotypes can be distinguished. SNPs, and SSR markers are important markers for vegetable plants because of the vast range and frequency of genomic modifications (Hwang et al. 2016).

As a result, SNP markers can be used to accurately genotype vegetables and plants and create accurate genetic maps for abiotic stresses (Nimmakayala et al. 2014).The molecular linkage map of tomato was also constructed in the presence of an excessive density map with more than one molecular marker (SSR, and SNP) from the preliminary 2 cM distance among the markers (Tanksley et al. 1992). As a result of the disclosure of the complete genome collection of several pepper cultivars, the genetic map has advanced dramatically (Zhang et al. 2019b). There are now 5569 SNPs in those saturation maps (Zhang et al. 2019b) available for different abiotic stresses. The essential qualities of Chinese cabbage are also linked to some molecular indications. For example, in Brassica plant breeding, flower colour is a flag function that boosts production by attracting pollinating insects. Zhang et al. (2019a) discovered markers in Chinese cabbage orange flowers and followed them through marker assisted breeding to discern different flower colour styles. These comprehensive genetic maps gave markers for inclinations in vegetable crops and increased MAS breeding for abiotic stresses. Table 13.2 summarises the genes or QTLs associated with abiotic stress tolerance in major vegetable crops.

13.9 Application of Transgenic and Gene-Editing Technology in Vegetable Breeding

Physical mutagenesis, EMS mutagenesis, and TDNA insertion can all produce a large number of mutagens, but the mechanisms behind them are yet understood (Chaudhary et al. 2019). Finding the correct strain takes a long time and many

Table 13.2 Genes identified for abiotic stress tolerance in major vegetable crops

Crop species	Name of the genes or TF or QTLs	Trait	Reference
Broccoli	BoiCesA (RNAi)	SST	Li et al. 2017
Broccoli	BoC3H	SST	Jiang et al. 2020
Broccoli	BoC3H4	SST	Jiang et al. 2019
Broccoli	BoERF1	SST	Jiang et al. 2020
Tomato	AREB cupidadehydrine	TDS	Hsieh et al. 2010
Tomato	14–3-3 genes	TDS	Xu et al. 2018
Chilli	Dreb 1A TF	TDS	Maligeppagol et al. (2016)
Tomato	bspA gene	TDS	Roy et al. (2006)
Chilli	Osmotin gene	SST	Subramanyam et al. (2011)
Tomato	HsfA1a	TDS	Wang et al. (2015)
Tomato	microRNA169	TDS	Zhang et al. (2011)
Tomato	Transcription factor SlNAC4	SST, TDS	Zhu et al. (2014)
Potato	28 drought-specific QTLs	TDS	Anithakumari et al. (2012)
Tomato	SlGATA17	TDS	Zhao et al. (2021)
Tomato	CBF/NHX1/DREB1 genes	TDS	Solankey et al. (2015)

SST Salinity stress tolerance, *TDS* Tolerance to drought stress

individuals. A genome-based gene editing approach for vegetable crops is currently being used to knock off-target genes in vegetable crops. Because of their stable gene transfer method and rich genomic information, tomatoes are an appealing food crop for proving the efficacy of gene editing. Tomato CRISPR has knocked out many genes, including regulation of the drought-tolerant gene SlMAPK3 (Wang et al. 2017). PROCERA is a gene that responds to gibberellin (Tomlinson et al. 2019) in significant vegetable crops during abiotic stresses (Soyk et al. 2017). Future studies on the domestication of wild tomatoes will also employ genome editing techniques. Wildtype tomatoes with good resistance properties can be genetically modified (Li et al. 2018; Zsögön et al. 2018). The cucumber is a model plant for squash, and its solitary nature makes reproduction difficult. As a result, selecting a female cucumber variety as a breeding target can increase cucumber yields while saving time and money. According to Hu (2017), all-female cucumber materials are conserved by boosting the cucumber genetic transformation mechanism and knocking down CsWIP, which regulates the whole female phenotype during multiple stresses. This method was also used to knock out the cucumber-specific short fruit genes sf1 and sf2 and provide the framework for molecular fruit development regulation (Xin et al. 2019; Zhang et al. 2019a). The CRISPR technique can benefit other Cucurbitaceae vegetable crops (Tian et al. 2018). For example, changing the watermelon genome revealed ClWIP1's genetic role, and female plants were kept to promote hybrid plant purity (Zhang et al. 2019a). CRISPR technology has also helped salt-tolerant squash varieties (Huang et al. 2019).

13.10 Conclusion

With the completion of the genetic sequencing of major vegetable crops, genomic information has significantly accelerated molecular breeding. By utilizing genetic data, genomic sequencing, and genotyping, several new identification approaches have been developed and applied to the majority of vegetable crops in order to identify major genes tolerance to abiotic stresses. For marker assisted breeding, several molecular markers that are directly related to essential properties of vegetable crops and linked to abiotic stress tolerance genes have also been established for major vegetable crops. Advances in gene-editing technology have also paved the way for developing new vegetables varieties with improved characters. However, in the case of vegetable farming, the breeding strategy must be improved.

Even though the genetic sequences of the majority of vegetable crops have been identified, many approaches, such as MutMap Plus and MutMap Gap, have yet to be successfully applied to vegetables for identifying genes associated with abiotic stress tolerance in order to combat climate change. These methodologies, which are reliable in other model cultures, should be used to discover target genes and related molecular markers in vegetable crops. Researchers and breeders can improve communication and information exchange by using connected data. Molecular identifiers can thus be effectively transformed into widely used markers in this manner. Superior traits in vegetable crops and cultivar genotypes can also been studied to better understand the molecular process of superior trait development and to provide a theoretical foundation for molecular breeding.

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