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Full Length Research Paper

Molecular Breeding for Biotic and Abiotic Stress Resistance in Vegetable Crops

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Abstract

Molecular breeding, utilizing molecular markers, holds immense promise in revolutionizing plant breeding programs, particularly in the context of vegetable crops. This approach necessitates appropriate marker systems, mapping populations, and software for genotypic data analysis. DNA markers, offering insights into genetic variations unaffected by environmental factors, are pivotal in crop improvement efforts. Vegetable crops, heralded as protective foods due to their richness in essential vitamins and minerals, play a crucial role in addressing malnutrition, especially among children in India. Despite India's status as the second-largest producer of vegetable crops globally, productivity remains constrained, with per capita availability significantly lower than in developed nations. Biotic and abiotic stresses contribute substantially to yield reduction, with losses attributed to insects, weeds, diseases, and pathogens.

Traditionally, classical breeding methods have been employed to develop resistance in vegetable crops against biotic stresses. However, these approaches suffer from limitations such as slow progress, high costs, and issues of linkage drag. In response, molecular genetics techniques have been embraced, offering faster and more precise methods for developing resistance traits. DNA markers, in particular, facilitate marker-assisted selection (MAS), enhancing breeding efficiency by streamlining screening procedures. Moreover, abiotic stresses like drought, salinity and temperature extremes pose significant challenges to vegetable crop productivity. Many plant species have evolved resistance mechanisms against these stresses, and molecular tools provide avenues for deciphering these mechanisms and transferring resistance traits to cultivated varieties.

Keywords: Molecular Breeding; DNA Markers; Biotic; Stress; Abiotic

Introduction

Molecular breeding refers to the use of molecular markers in the plant breeding program. An appropriate marker system, mapping populations and suitable software for analysis of genotypic data are the major requirements in the molecular breeding. Molecular (DNA) markers reveal the site of variation in the DNA and are practically unlimited in number, not influenced by the environmental factors make there usage effectively in crop improvement program.

Vegetable crops are considered as a protective food since they are rich in in vitamins and minerals as a result they are considered as major weapon to eliminate the problem of malnutrition which is alarming particularly amongst the children in India (UNICEF, 2019). Though India is the second largest producer of vegetable crops next to China, with the production of 193.61 million tons in an area of 10.7 million hectare (Ministry of Agriculture, first advanced estimates, 2020-21) but the average productivity and per capita availability of vegetables in India is comparatively lower than the developed economies and is about half of the productivity of USA (31.4 tons) (MOSPI). The biotic and abiotic factors contribute more to the reduced productivity of vegetables in India. The losses caused by biotic factors is nearly about 40%, in that 15% attributable to insects, 10% to weeds, 15% to other diseases and pathogens. Biotic stress factors include diseases caused by fungi, bacteria, viruses, weed plants, parasites, nematodes and insect pests. Different symptoms of biotic stress factors are, fungi- mildews, blisters, rusts, and wilts while leaf spots, fruit spots, cankers, crown galls are symptoms of bacterial infection. Virus infects the plants in the form of necrosis, chlorosis, leaf abnormalities, flower deformation, plant stunting. Insects and pests cause direct damages by eating and chewing of foliage, tender shoots, roots, and fruits and indirect cause by transmitting the viral diseases into plants. Weed plants compete with crop plants for nutrition, water, and sunlight there by decreasing the yield. Nematodes cause galls, knots, and swellings in roots so upper part of plants got affected. Vegetable plants generally experience various quality deterioration due to Stress. If the temperature of fruits exceeds 30^0C, the lycopene content decreases significantly in Tomato [1]. Exposure to stress decrease shoot length root length, number of roots, fresh weight of seedling number of leaves, chlorophyll content in chilli genotypes. In cauliflower and broccoli, warmer conditions delay the initiation of the curd and head as well as affected the quality of edible parts.

Drastic decrease was seen in fresh and dry matter contents in okra because of heat stress. The origin of new pathogens and insect races due to climatic and genetic factors is a major challenge for plant breeders in breeding biotic stress resistant vegetable crops. In the past, classical breeding approaches were utilized for this purpose. Continuous use of traditional breeding methods can narrow the gene pool, making crops more vulnerable to stress and limiting future progress. Traditional breeding takes decade to breed one variety. Seeds bred from classical breeding from F_1 hybrids can be more expensive. Therefore, molecular genetics approaches were adapted by breeders to develop effective resistance in vegetable crops within a shorter time, novel technologies such as DNA markers serve as a major tool to detect the presence of allelic variation in the genes underlying the resistance traits, markers have enormous potential to improve the efficiency and precision of conventional plant breeding via marker-assisted selection (MAS) by reducing the reliance on laborious screening and scoring procedures. Similarly, the quality and yield of vegetable crops are also affected by many abiotic stresses, like drought, salinity, low and high temperatures etc, many higher plants developed resistance mechanism against the abiotic stresses and molecular tools will helps in better understanding of these resistance mechanisms and to transfer the resistance traits to cultivated varieties of vegetable crops.

Molecular screening of germplasm for biotic stress resistance Marker assisted selection v/s phenotypic selection in biotic stress breeding

Resistance cultivar development for multiple pathogen resistance in vegetable crops is a desirable goal, the process is often challenging due to the need for large-scale population inoculation and screening and lack of available resistance genes in a cultivated genetic background. It is often further complicated by linkage drag of unacceptable characteristics tightly linked with resistance genes, emergence of new disease pathogens or new races of existing pathogens, and the necessity of selecting for resistance to multiple pathogens [2]. MAS offer an opportunity to overcome the problems associated with phenotypic selection and helps in combining multiple resistance genes.

Marker assisted selection in stress breeding

It can be defined as the use of DNA markers that are tightly- linked to target loci as a substitute for or to assist phenotypic screening. MAS will probably never replace phenotypic selection (PS) entirely. Especially for disease resistance a final testing of

breeding lines is always required, regardless how tight a marker is linked to a gene or QTL [3]. MAS can be used in early segregating populations and at early stages so it prohibits screening of the large number of populations in later stages of breeding program. Marker assisted selection allow to access, transfer and combine the resis- tance genes at faster rate. No need of performing time consuming and labor-intensive artificial inoculation tests to assess the resis- tant phenotype. No maintenance of the pathogens or the pests on the host (or alternate hosts) in marker assisted selection. Thereby it provides new solutions for selecting and maintaining desirable genotype for biotic stress. The essential requirements for develop- ing MAS system are,

- Availability of germplasm with substantially contrasting phe- notypes for the traits of interest,
- Highly accurate and precise screening techniques for pheno- typing mapping population for the trait of interest,
- Identification of flanking markers closely associated with the loci of interest and the flanking region on either side and
- Simple robust DNA marker technology to facilitate rapid and cost-effective screening of large population.

The MAS, which has greater advantages in biotic stress breed- ing, as it helps in selecting resistant traits with low heritabil- ity, substitute for laborious phenotypic screening, facilitates easy

identification and transfer of recessive genes, reduce the reduces the problem of linkage drag, pyramiding of multiple disease resis- tance genes, rapid recovery of the recurrent parent genome in the backcross breeding and identification of resistant lines at seedling stage.

It is well known that MAS helps breeders to increase selection efficiency, precision and selection intensity and selection of resis- tance gene against prevalent pest and diseases in early generation, resulting in increased genetic gain and save the cost and time.

Different MAS schemes in resistance breeding Early generation marker assisted selection

Generally, it is performed at F_2 or F_3 generations; it has great advantages to eliminate undesirable gene recombination, lacking resistance genes. Marker assisted-based early generation selection not only helps to select suitable gene combinations but also ensure a high probability of retaining superior breeding lines.

Markers assisted pyramiding

Pyramiding allows stacking multiple genes leading to the si- multaneous expression of more than one gene in a variety to develop durable resistance. Outcome of a gene pyramiding is a genotype with all of the target genes. But it is difficult to transfer all the resistant genes conventionally, hence DNA markers can be used in gene pyramiding program as it will increase the durabil- ity of disease resistance and also enhances trait performance by combining two or more resistance genes in single cultivar leading to the development of genetic stocks with precise broad spectrum resistance capabilities.

Marker assisted back cross breeding

MAB is the process of using the results of DNA tests to assist in the selection of the individuals to become the parents in the next generation of the genotyping improvement program. When all the positive alleles come from distant and un-adapted line, the marker assisted backcross (MABC) of QTLs into an elite line performed [4]. Marker assisted background selection helpful to reduce the genet- ic background of wild species in introgression. It reduces number of backcrosses required to eliminate undesirable alleles, thereby saving time and expense [5].

Marker assisted recurrent selection

In the phenotypic recurrent selection, reselection generation after generation followed with inter mating among selected plant to create the population for the next cycle of selection. Therefore, it is considered as more effective strategy for the improvement of polygenic traits by increasing the frequency of the favorable genes for various polygenic traits, however selection efficiency is not sat- isfactory as the selection is influenced by the environmental conditions and takes longer time (at least 2-3 seasons for one cycle of selection). With the use of markers, recurrent selection for com- plex traits can be accelerated considerably and several selection cycles are possible within a year by accumulating the QTL alleles in the population and here the selection is also independent of the environment. It is possible today to define an ideal genotype as a pattern of QTLs, all QTLs carrying favorable alleles from various

parents. If individuals are crossed based on their molecular marker genotypes, it might be possible to get close to the ideal genotype after several successive generations of crossings.

Combined marker assisted selection

The strategic combination of MAS with phenotypic screening is known as 'combined MAS'. It may have advantages over phenotypic screening or MAS alone in order to maximize genetic gain plant selection using such markers is useful for breeders in order to select a subset of plants using the markers to reduce the number of plants that need to be phenotypically evaluated. It is called as tandem selection. This approach could be adopted when additional QTLs controlling a trait remain unidentified or when a large number of QTLS need to be manipulated. Combined marker assisted selection saves cost and time as compared to phenotypic screening alone.

Genome selection

Genomic selection (GS) or genome-wide selection (GWS) is an upgrade form of MAS that uses marker-based selection approach that considers available markers covering the whole genome for concurrently selecting genes that are associated with at least few markers [6]. This method is rapidly gaining popularity among the breeders particularly for the traits which are difficult to measure. In GS approach, QTLs and gene identified are in linkage disequilibrium with at least one marker and help to reduce the chance of missing small-effect QTLs [7]. It facilitates refining the genetic basis of polygenic resistance to crop diseases [8]. GS is considered as the most powerful approach than MARS and may become the potential tool in the future resistant breeding programs [9].

The applications of molecular based resistant breeding programs in different vegetable crops

Tomato

Tomato is one of the major vegetable crops of Solanaceous family, cultivated throughout the world for its fruits. It is susceptible to several diseases caused by fungi, bacteria, viruses or nematodes which significantly reduce fruit yield and quality. The diseases and pests cause up to 40% and 34.4% of tomato yield loss respectively [10]. Though they can be controlled conventionally by the use of chemicals, but the indiscriminate use of hazardous chemical causes, environment pollution, health hazards (nearly one-third of total pesticide poisoning cases in the world occurred in India, emergence of new races/biotypes and economically unviable in long term. Hence molecular based resistant breeding approaches overcome all these complications and accelerate resistant varieties development compared to conventional breeding approach, till now resistance has identified and well characterized for more than 30 diseases [11,12]. Majority of fungal resistances are due to single dominant genes [13], these resistance genes or QTLs are mapped in tomato using different mapping populations as discussed below.

Early Blight caused by *Alternaria solani,* characterized by target board shaped black or brown concentric rings surrounded by yellow halo observed both on fruit and leaves, the QTLs associated with early blight resistance in wild tomato species *L. hirsutum* Humb. and *Bonpl* have been identified in backcross population by analysis with RFLP markers [14]. The resistance to soil borne diseases viz., Fusarium wilt found to be controlled by genes *I*, *I-2* mapped on chromosome 11 [15], while *Got-2* and *I – 1* mapped on chromosome 3 [16,17]. Among these *I* and *I-2* were most commonly used in the breeding program [13]. For, late blight resistance till now four genes viz., *ph-1, ph-2, ph-3* and *ph-4* have been mapped on chromosomes 7, 10, 9, and 2 respectively [18]. *Ph-3* confers high level of resistance which is widely used in resistance breeding program as *ph-1* and *ph-2* genes introgression results in

breakdown of resistance. Furthermore, three QTLs *lb4, lb5b* and *lb11b* from *L. hirsutum* accession also show quantitative resistance to *Phytophthora infestans* and were mapped on chromosomes 4, 5 and 11 respectively using NILs and Sub-NILs [19]. The powdery mildew incidence commonly observed in green house cultivated tomato caused by *Leveillula taurica and Oidium neolycopersici.* A dominant resistance gene *Lv*, was mapped on chromosome 12 us- ing RFLP markers in *S. chilense* confers resistant to *L. Taurica* [20]. The incomplete-dominant genes *Ol-1* and *Ol-3* located on chro- mosome 6 near *Mi* gene were found resistant to *oidium* species mapped from *S. habrochaites* accession using SCAR markers [21]. Further three more QTLs, *Ol-qtl1* located on chromosome 6 near *Ol-1* locus, *Ol-qtl2* and *Ol-qtl3* are mapped on chromosome 12 in the vicinity of *Lv* locus also confers resistance to powdery mildew pathogens [22]. Bacterial wilt, a major bacterial disease (*Ralstonia pseudosolanacearum*) that limits tomato production in coastal re- gions is observed to be controlled by two major QTLs located on chromosome 6 (*Bwr-6*) and 12 (*Bwr-12*), subsequently SNP-based CAPS/dCAPS markers near *Bwr-6* were developed and validated to well establish marker-assisted breeding for resistance to bacterial wilt [23]. Similarly, six resistance loci, *Ty-1, Ty-2, Ty-3, Ty-4, Ty-5* and *Ty-6* have been identified for the devastating viral disease TY-LCV (Tomato yellow leaf curl virus). Of them, *Ty-1, Ty-3* and *Ty-4* derived from *S. chilense* were mapped on short arm of chromosome 6, long arm of chromosome 6 and chromosome 3 respectively [24,25], *Ty-2* from *S. habrochaites* mapped to chromosome 11 [26], *Ty-5* reported from *Solanum peruvianum* mapped onto chromo- some 4 ([27]. Additionally, many QTLs carried resistance to TYLCV have also been detected. Likewise, many molecular markers linked to various resistant genes listed in table 1 and 2.

Disease	Gene	Marker	Marker type	Marker ID	Enzyme	Forward	Reverse	References
Alternaria stem canker	*Asc*	RFLP	Co-dominant	TG134	-	NA	NA	[29]
	Asc	RFLP	Co-dominant	TG442	-	NA	NA	[29]
Corky root rot	*py-1*	CAPS	Co-dominant	TG40	*DraI*	CGTTTAGGCAATT	AACAACAACTGTACCT	[30]
					HindIII	CACATCTAG	CAGTCC	
	py-1	CAPS	Co-dominant	TG324	*DraI*	CTTCTAGTAGTCCAAC	CACTTGGTTGATGG	[30]
						AGCAACTG	ATAGTG	
	py-1	CAPS	Co-dominant	TG479	-	GGTGATTATGGGTGA	CCAAGTGAGTACCAAC	[30]
						TCCTATG	AGTTCC	
	py-1	RAPD	Dominant	OPW-04	-	CAGAAGCGGA		[30]
	py-1	RAPD	Dominant	OPC-02	-	GTGAGGCGTC		[30]
	py-1	RAPD	Dominant	OPG-19	-	GTCAGGGCAA		[30]
Fusarium crown and root rot	*Frl*	RAPD	Co-dominant	UBC 655	-	GCA TTT CCC G		[31]
	Frl	RAPD	Dominant	UBC 116	-	TAC GAT GAC G		[31]
	Frl	RAPD	Dominant	UBC 194	-	AGG ACG TGC C		[31]
Fusarium wilt	*I*	SCAR	Dominant	At2	-	CGAATCTGTATATT	GGTGAATACCGATCA	[32]
						ACATCCGTCGT	TAGTCGAG	
	I-2	SCAR	Dominant	Z1063	-	ATTTGAAAGCGTGGTA	CTTAAACTCACCATT	[32]
						TTGC	AAATC	
	I-2	InDel	Dominant	TFus	-	CTG AAACTC TCC GTA	CGA AGA GTG ATTGGA	[33]
						TTT C	GAT	
	I-2	InDel	Dominant	Tfus	-	CTG AAACTC TCC GTA	CCT GGATGA ACA GCT	[33]
						TTT C	GAG	
	I-3	CAPS	Co-dominant	P7–43B	*NsiI*	CAGTCATTATTAACA	TCTGAGCAATAC- GTCT	[15]
						AATTTCAGGATCG	AGCAGC	
	I-3	CAPS	Co-dominant	PTG-190	*AluI*	GCAGTACACTTCTCC	AGTTTCAGTAGTTGT	[15]
						TTATCATGTG	TCCAAATTCC	

Table 1: Molecular markers associated with resistance to major diseases in tomato.

Disease	Gene	Marker	Marker type	Marker ID	Enzyme	Forward	Reverse	References
	I-3	CAPS	Co-dominant	CT226	*MaeIII*	GTGAAGGAGTGTCA	GGAATGAACAATTT	[15]
						AAGGCAAC	ATATGCAGCAG	
	I-3	SCAR	Co-dominant	P7–43DF1/R1	_	GGTAAAGAGATGCGA	GTCTTTACCACAGGA	[15]
						ATAAGCATGT	CTTTATCACC	
Late blight	*Ph-3*	CAPS	Co-dominant	TG328	*BstN1*	GGTGATCTGCTTAT	AAGGTCTAAAGAAG	[34]
						AGACTTGGG	GCTGGTGC	
	Ph-3	CAPS	Co-dominant	TG591	*AclI*	AAGGCAAAGGAAGTT	AGAGGTTGCAACTCG	[34]
						GGAGGTCA	TGGATTGAG	
Leaf mould	*Cf-6*	SCAR	Co-dominant	S374	–	CCCGCTAC ACCTTA	GCTTGGGAGATTGT	[35]
						AACTT	GTGTAGC	
	Cf-6	SSR	Co-dominant	T10	–	CTGTTTACTTCAAG	ACTTTAACTTTATTA	[35]
						AAGGCTG	TTGCGACG	
	Cf-6	SSR	Co-dominant	T12	–	GAGCGAGCAGAAA	GAGCCTGAAAAC	[35]
						GGTGAAT	ATAGAAGT	
	Cf-	CAPS	Co-dominant	CT2	*MspI*,	AAGCCTCTAATCA	TTCAGTGCAATAATA	[36]
	multiple				*HpaII*	AGAAAATGG	ATGAGGG	
	Cf-	CAPS	Co-dominant	ET32	–	AGAAGGATAAAGCTCA	AAGGAACATCTGT	[36]
	multiple					ACATCGG	GGTTCGC	
Powdery Mildew	*Ol-1*	SCAR	Dominant	SCAE16	–	TCCGTGCTGAATGAA	TCCGTGCTGATAAAA	[21]
						GATTCAAAC	CTGTTAGAC	[21]
	Ol-1	SCAR	Dominant	SCAF10	–	GGTTGGAGACGAA	GGTTGGAGACAATAGA	[21]
						TGGAAAGATGC	CTCGAGAT	[21]
	Ol-1	SCAR	Dominant	SCAB01	–	GCTTCTAGATGCAGA	CGCCCATTCCCGCA	[37]
						AAGTTGGCG	TATACAG	
	Ol-1	SCAR	Dominant	SCAG11	–	TGGGATCACAGATT	ATGTGTGCGATGAGAA	
						AACAAATGCG	ACGTGG	
	Ol-1	SCAR	Dominant	SCAK16		CAAACAAAGCAGTGG	TAAAAGCCTTAGTGG	
						ATTTTTTTCG	GACAGGGC	
Verticillium wilt	*Ve-1*	SCAR	Co-dominant	V1LeO1new	–	TACGGAGTTATTCGCT	AGAGATCAAGAGTAA	
						AAAGC	CTAGCC	

Table 2: Molecular markers associated with resistance to major diseases in tomato.

Brinjal

Brinjal is one of the highest pesticide consuming crops mainly applied to control fruit and shoot borer infestation, the develop- ment of *Bt*-transgenics will lower the shoot and fruit borer damage and ultimately the pesticide uses in brinjal. Diseases like damp- ing off, phomopsis blight, verticillium wilt, fusarium wilt, bacterial wilt, leaf spot, collar rot and little leaf cause heavy losses [38]. Com- pared to other Solanaceae vegetables, knowledge on the genetic control of many stress tolerances as well as morphological traits in eggplant is relatively poor. The genetic mapping in eggplant has only commenced in the 1990s, first molecular map of brinjal was published in 1998 by Nunome and colleagues using RAPD mark- ers, subsequently AFLP, RFLP and microsatellite (SSR) markers have also been mapped in eggplant populations [39,40] by using both intra-and interspecific populations. Tamura., *et al.* [41] used RAPD and RFLP markers to confirm the hybridity of a bacterial wilt resistant protoplast fusion product of *S. integrifolium-S. violaceum*. In the same timeframe, Inter Simple Sequence Repeat (ISSR) mark- ers were employed in conjunction with isozymes and RAPDs to ascertain the dihaploids resulting from somatic hybrids between *S. melongena* and *S. aethiopicum*, bearing fusarium wilt resistance [42]. Two QTLs responsible for verticillium wilt resistance using RAPD-AFLP map [37]. Comparative transcriptome analysis of egg- plant (*Solanum melongena* L.) and turkey berry (*Solanum torvum*) was performed to compare disease resistance genes found in egg- plant with that of turkey berry [36].

Chilli and Pepper

Both chillies and sweet peppers belongs to the same species *Capsicum annuum* L., and family solanaceae while chilli botanically known as *Capsicum annuum* L. var *longum* and sweet pepper bo- tanically called *Capsicum annuum* L. var *grossum*. Both the crops are infected by many pests like gram pod borer, tobacco caterpil- lar, spider mites, root-knot nematodes, thrips, spider mites/yellow mites,

aphids and diseases viz., damping off, die-back and anthrac- nose (fruit rot), choanephora blight/wet rot, mosaic complex, pow- dery mildew, cercospora leaf spot, bacterial leaf spot, alternaria leaf spot fusarium wilt.

Linkage was observed between partial resistance to CMV and susceptibility to TMV; however, genetic distance between them was not known. Resistance to bacterial leaf spot controlled by single dominant gene (*Bs2*) in *C. chacoense* [44] and subsequently this gene incorporated to commercial varieties. Subsequently it was reported that at least four independent dominant genes, *Bs1, Bs2, Bs3* and *Bs4* known to control hypersensitive resistance to Bacte- rial leaf spot. Furthermore, several QTLs resistance to diseases and pests has been detected in *Capsicum* sp. through the use of different molecular markers (Table 3).

Sl No	Resistant Trait	QTL	LG	Mapping populations	References
1	Cucumber mosaic virus (CMV)	Two QTLs	6 and 12 respectively	DH population from Perennial and Yolo Wonder cross.	[45]
		cmv5.1, Cmv11.1, cmv11.2, and cmv12.1	LG5, 11 and 12 respectively.	double haploid progenies from the cross of Vania (*C. baccatum*) and H3	[46]
2	Powdery mildew	Lt_5.1, Lt_6.1 Lt_9.1 Lt_10.1 and Lt_12.1	P5, P6, P9, P10 and P12 chromosomes respectively.	Double haploid progenies from the cross of H3 and Vania	[47]
3	Anthracnose	One major QTL, and three minor QTLs	-	F_2 population derived from an interspe- cific cross of *C. annuum* and *C. chinense*	[48]
4	*Phytophthora capsici*	Phyto.4.1, Phyto.5.1, Phyto.5.2, Phyto.6.1, Phyto.11.1, Phyto.12.1	Chromosome P4, two QTLs on P5, single QTL each on P6, P11 and P12 respectively.	BC population between Yolo Wonder and CM334.	[49]

Table 3: QTLs associated with resistance to different diseases of *Capsicum sp*.

Cole crops

Cole crops botanically belong to the species Brassica oleracea and family Brassicaceae, among cole crops, Cabbage (*B oleracea* L. var. *capitata*), cauliflower (*B. oleracea* L. var *botrytis*), broccoli (*B. oleracea* L. var *italica*), brussel sprouts (*B. oleracea* L. var. *gem- mifera*), knol khol (*B. oleracea* L. var *gongyloids*) and kale (*B. olera- cea* L. var. *acephala*) are the economically important and cultivated commonly throughout the world. In India, cabbage and cauliflower are the largely cultivated Cole crops with more area and produc- tion than other cole crops. One of the major causes of poor yield and quality of Brassica vegetables are diseases and pests. The crops are infected by fungal diseases like damping off/wirestem, (a com- plex disease caused by *Pythium* sp, *Phytophthera* sp, *Fusarium* sp, *Rhizoctonia* sp), black leg (*Phoma lingum*), black spot (*Alternaria brassicae*), cabbage yellow (*Fusaium oxysporim* f sp. *conglutinens*), downy mildew (*Perenospora brassicola*), clubroot (*Plasmodiophora brassicae*), stalk rot (*Sclerotinia sclerotiorum*), bacterial diseases viz., black rot (*Xanthomonas compestris pv compestris*), bacterial soft rot (*Erwinia carotova* pv *carotova*), viral diseases are cauli- flower mosaic virus transmitted by aphid and various nematode species i.e., root knot nematode, stunt nematode, insect pests that infect the crops are diamond back moth (*Plutella xylostella*), stem borer (*Hellula undalis*), cabbage caterpillar (*pieris brassicae*), cab- bage semi-looper (*Plusia orichalcea*), painted bug (*Bagranda cru- ciferarum*), aphids, cabbage fly (*Delia brassicae*).

The black rot resistance has been studied extensively and there were reports of incomplete resistance in some genotypes. They have been used in breeding program to improve resistance in cul- tivars but there is no report of complete resistance to the disease and the quantitative genetic control further complicates its use in producing resistance varieties [50].

The wild Brassica relatives (for example *B. fruticulosa*) are ma- jor sources of resistance to a number of biotic and abiotic stresses and hence they can be used as important genetic resources for the Brassica crops improvement. Backcrossing of wild relatives with elite susceptible cultivars was followed to develop commercial cul- tivars resistant to various biotic and abiotic stresses and it can be aided by molecular markers linked to the resistant genes and the process of selection of desired resistant morphotypes can be ad- vanced (Table 4). Crossing of *cry1Ac* and *cry1C*-transgenic plants, two *Bt* genes were introduced into broccoli to resist diamond black moths. Molecular analysis confirmed the expression of both genes in all progeny, offering a new avenue for DBM resistance.

Sl No	Resistant Trait	QTLs	LG	Mapping populations	References
1	Downy mildew	At the cotyledon stage, four or three dominant genes depend on source, at the 4-5 leaf stage, single dominant gene (in PI231210), two (in PI246077), or three additive dominant genes (in the broccoli-cauliflower line).		A Polish-selected broccoli-cauliflower line, susceptible cauliflower line, and their F_1 and F_2 offspring.	[51]

2	Club root				
		Three QTLs		F_2 population from cross between broccoli and cauliflower	[52]
3		pb-3 and pb-4	LG3 and 1 respectively	DH population from cross between cabbage and broccoli.	[53]
4		18 QTLs identified for 5 different isolates of *Plasmodiophora brassica*		F_1 and $F_{2/3}$ progenies of the cross C10 (resistant kale) × HDEM (susceptible broccoli)	[54]

Table 4: QTLs/genes associated with resistance to different diseases of brassica vegetables.

The transcriptome profile of Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) grown under drought conditions was analyzed the resulted in the report of several transcription factor genes for drought stress, includes *bHLHs, AP2/ERFs, NACs* and *bZIPs*, com- parative expression analysis of selected *BrbZIPs* under different stress conditions suggested that drought-induced *BrbZIPs* are im- portant for improving drought tolerance [55]. The *IQD* (*IQ67*-do- main) family shows a major role in several abiotic stress responses in plant species, 35 *IQD* genes, from *BrIQD1* to *BrIQD35*, were iden- tified in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) and were unevenly distributed on 9 of the 10 chromosomes and transgenic studies showed that plants with *BrIQD5* genes showed more tol- erance to drought stress. Similarly, Park., *et al.* [56] observed the role of *BrDSR28* gene in drought tolerance in *Brassica rapa* through microarray analysis. Salinity tolerance is a complex trait governed by multiple genes, making it quantitative in nature [57]. *Brassica* species are generally classified as moderately salt tolerant, with amphidiploid species exhibiting greater tolerance compared to diploids. The development of salt-tolerant Brassica involves sev- eral strategies: (i) screening existing tolerant genotypes, (ii) con- ventional breeding methods, and (iii) generating transgenic plants to introduce novel genes. Marker-assisted selection offers non-destructive advantages over conventional approaches by providing genotype information without subjecting plants to stress, and it can handle large sample sizes. DNA markers flanking target genes expedite breeding programs aimed at enhancing stress tolerance. Efforts to develop transgenic Brassica with increased salinity tol- erance focus on candidate genes involved in ion homeostasis and osmolyte accumulation. For instance, transforming cabbage (*Bras- sica oleracea* var. *capitata*) cultivar 'Golden Acre' with the bacte- rial *betA* gene enhances tolerance to NaCl stress [58]. Similarly, overexpression of a *B. napus* Group 3 *LEA* gene in Chinese cabbage (*Brassica campestris* ssp. *pekinensis*) improves tolerance to salinity and drought [59]. These transgenic plants exhibit delayed onset of salt stress symptoms and enhanced recovery upon stress removal. With numerous transgenic *Brassica* plants expressing salinity-re- lated genes.

Cucurbits

Cucurbits are one of the major vegetable crops belongs to cu- curbitaceae family, distributed mainly in tropical and subtropical regions of the world. They are known to be infected by downy mildew (*Pseudoperenospora cubensis*), powdery mildew (*Erysiphe cichoracearum* and *Sporothica fuliginea*), anthracnose (*Collectotri- chum lagenarianum*), fusarium wilt (*Fusarium oxysporum*), root rot (*Rhizactonia solani*), Collar rot (*Rhizactonia bataticola*), fruit rot (*Pythium* sp), alternaria blight (*Alternaria cucumerina*) caused by fungal pathogens, while bacterial diseases affect the crop are an- gular leaf spot (*Pseudomonas syringae pv lachrymans*), bacterial leaf spot (*Xanthomonas compestris* pv *cucurbitae*), viral diseases in- cludes mosaic virus, cucumber yellow vein virus, cucumber green mottle mosaic virus, watermelon bud necrosis, pumpkin yellow mosaic virus, phytoplasma diseases like witche's broom, phyllody and root knot nematodes. Among cucurbits, disease resistance genes have been intensively mapped in cucumber and melon (Ta- ble 5). The identified and validated genes/QTLs can be effectively utilized to develop resistant cultivars in a short period of time by developing molecular markers linked to them.

Sl No	Resistant Trait	Gene/QTL	LG	Mapping population/line	References
1	Fusarium wilt	*Fom-2*	LG9	MR-1 line of muskmelon	[60,61]
		Fom-1	LG9	Watermelon	[62]
2	Melon necrotic spot virus	*nsv*	LG11	F_2 population derived from cross PI161375 and Piel de Sapo	[62].
3	zucchini yellow mosaic virus (ZYMV)	*Zym-1*	LG5	Muskmelon and cucumber	[63]

4	Cucumber mosaic virus (CMV)	Seven QTLs		RIL population obtained by crossing a Charentais-type, Vedrantais and the resistant Korean line PI 161375.	[64]
5	*Fusarium oxysporum* f. sp. *melonis*	Nine QTLs	five linkage groups	recombinant inbred line population developed with Isabelle (resistant) and Vedrantais (susceptible)	[31]
6	Powdery mildew	four QTLs	Two QTLs on LG2 and single QTL each on LG3 and 4.	RIL population derived from a cross between Santou (susceptible) and PI197088-1 (resistant) lines	[65]
7	Cucumber mosaic virus	*cmv6.1*	LG6	RIL population generated from a cross between '65G' and '02245'	[66]
8	Powdery mildew	Six QTLs		$F_{2:3}$ population of two cucumber inbreeds	[67]
		4 QTLs *pm1.1*, *pm2.1, pm5.1 and pm6.1*	LG1, 2, 5 and 6 respectively.	RIL population from cross between PI 197088 and 'Coolgreen'.	[47]
9	Downy mildew	four QTLs viz., *dm2.1, dm4.1, dm5.1,* and *dm6.1*	LG2, 4, 5 and 6 respectively	F_2 population from cross between 2 inbred lines TH118FLM and WMEJ	[68]
		11 QTLs	-	RIL population from cross between PI 197088 and 'Coolgreen'.	[47]
10	Gummy stem blight	five QTLs namely *gsb-s1.1, gsb-s2.1, gsb-s6.1, gsb-s6.2,* and *gsb-s6.3*	*gsb-s1.1* and *gsbs2.1* mapped onto LG1 and 2, respectively, while remaining three mapped to LG6,	RIL population derived from the cross of wild cucumber resistant accession (PI 183967) and susceptible accession (931	[69]
11	Six QTLs *gsb3.1, gsb3.2, gsb3.3, gsb4.1, gsb5.1,* and *gsb6.1*	Three QTLs on LG3, remaining on LG4, 5 and 6 respectively.	RIL population from cross between PI 183967 (*C. sativus var. hard- wickii*) and 931 (*C. sativus*).	[70]	
12	Three QTLs *ClGSB3.1, ClGSB5.1 and ClGSB7.1*	LG3, 5 and 7 respectively	$F_{2:3}$ mapping population derived from a cross between Crimson Sweet (*C. lanatus*) and resistant PI 482276 (*C. amarus*)	[71]	
13	Melon-cotton aphid	Four additive and two pairs of epistatic QTLs.	-	[72]	

Table 5: QTLs/genes associated with resistance to different pests and diseases of Cucurbits.

Further, Cucurbits are also highly sensitive to environmen- tal constraints and immediate abiotic stresses viz., drought, high salinity, low or chilling temperature, high temperature which se- riously limit the quality as well as quantity of the cucurbits par- ticularly cucumber yield, temperature and drought affects the sex expression in plant thereby reduces the fruit yield. Thus, increased tolerance of cucurbits to the abiotic stresses will considerably im- prove their production. The plant utilizes three types of drought response mechanisms such as drought escape, drought avoidance and drought tolerance. The plants tolerate drought by way of re- ducing water loss and osmotic adjustment maintenance and it is a complex trait controlled by many genes. Several species/ geno- types of cucurbits act as sources of drought tolerance. The genetic diversity found in cucurbits serves as primary source for screen- ing against the drought tolerance; traditionally it is carried out based on phenotype and through biochemical analysis; however, they were affected by environmental factors hence development of molecular markers linked with the genetic regions controlling drought tolerance considered as an effective approach for screen- ing and molecular breeding approaches also to develop drought tolerant varieties.

The NAC (standing for no apical meristem [NAM], Arabidopsis transcription activation factor [ATAF] and cup-shaped cotyledon [CUC]) proteins are the plant-specific transcription factor families which are needed mainly for the development of plant and abiotic stress resistance. Zhang., *et al.* [69] observed the tissue specific ex- pression of *CsNAC* genes in response to multiple abiotic stresses in cucumber using in silico tools, and qPCR method. Three to five De- hydrin (DHN) genes that belongs to late embryogenesis abundant (LEA) protein family identified in cucurbits through genome-wide searches and are valuable to understand different abiotic stress re- sponse mechanisms in cucurbits [73].

Root crops

The root crops are rich source of dietary nutrients in the form of plant pigments like carotenoids, anthocyanins, and other fla- vonoids. The major impeding factors in their cultivation are pest and diseases. The carrot is found to be infected by many pests such as carrot fly (*Psila rosae*), leaf hopper (*Empoasca punjabenensis*), aphids (*Aphis gossypi*), cut worm (*Agrotis ipsilion*) and diseases comprising of powdery mildew (*Erysiphe heraclei*), cercospora leaf blight (*C. carotae*), alternaria leaf blight (*A. dauci*), cavity spot (*Pythium sulcatum*) bacterial leaf spot (*Xanthomonas campestris* pv. *carotae*), aster yellows (amycoplasma) and nematodes, mainly the root-knot nematode (*Meloidogyne incognita, M. javanica* and *M. hapla*) infects the crop. Another root crop radish is also dam- aged by various pests and diseases. The major pests od radish are mustard sawfly (*Athalia lugens proxima)*, flea-beetles (*Monolepta signata; Phyllotreta chotanica*), aphids (*Brevicoryne brassicae, My- zus persicae, Lipaphis erysimi,* and *Toxoptera aurantia*). Apart from these, diamond back moth (*Plutella xylostella*), painted bug (*Bagrada cruciferarum*), leaf webber (*Crocidolomia binotalis)* infes- tation also noticed. The most common fungal diseases infect radish includes white rust (*Albugo candida*), *alternaria* blight (*Alternaria alternata; Alternaria brassicae*), sclerotinia rot (*Sclerotinia scleroti- orum*), Yellows disease (*Fusarium oxysporum* f. sp*. raphani*), rhizoc- tonia rot *(Rhizoctonia solani)* and nematodes particularly root knot nematode (*Meladogyne incognata*) infestation is reported. Beetroot (*Beta vulgaris* L*. subsp. vulgaris*) is also one of the major root crops of European countries, cultivated in northern and southern parts of India during winter season the roots are used as cooked vegetable, fresh salad and for pickles making. The crop is affected by fungal diseases cercospora leaf spot (*Cercospora beticola*), downy mildew (*Perenospora sachatii*), seedling rot (*Pythium* sp*., Sclerotium rolfsii, Rhizactonia solani*), bacterial blight (*Pseudomonas syringe* pv *ap- tata*), viral diseases such as beet mosaic, curly top virus and beet yellow and insect pests includes leaf miner (*Pegoniyia hyocyami*), aphid (*Aphis* sp), semi looper (*Plusia nigrisigna*) and web worms (*Hymenia fascialis*) and cyst nematodes (*Heterodera schachtii*) are reported to cause the damage to crop.

Several previous studies have identified genes/QTLs involved in governing various biotic stresses along with molecular markers linked to them in root crops (Table 6). Introgression of these genes by means of different molecular breeding strategies can be effec- tively used to develop the resistant cultivars.

Sl No	Resistant Trait	Gene/QTL	LG	Mapping population/line	References
Carrot					
1	Root knot nematode (*Meloidogyne javanica*)	*Mj-1*	LG8	Brazilian cv "Brasilia"	[74]

2		*Mj-2*	LG8	Carrot accession PI652188	[75]
3	Powdery mildew	*Eh*			[76]
Radish					
4	Yellows disease caused by *Fusarium oxysporum f. sp. raphani*				
		Single QTL	LG1		[77]
		Eight QTL*s*			[78]
Beetroot					
5	Cyst nematode	*Hs1, Hs2* and *Hs3*	LG1 of three species in the section Patellares, LG7 of and LG8 of *B. webbiana* respectively		[79]
6	Cercospora leaf spot				
		Seven QTL*s*.			[80]
		Four QTL*s*	LG3, 4, 7 and 9.		[81]
7	Beet necrotic yellow vein virus	*Rz1*		Rizor hybrid	[82]
		Rz2		Sea beet (*Beta vulgaris ssp. maritima*) germplasm 'WB42'	[82]
8	Powdery mildew	Monogenic		Beet root	[83]

Table 6: QTL*s*/genes associated with resistance to different pests and diseases of root crops.

Root crops are also affected by several abiotic stresses like heat, cold, drought, salinity, heavy metal toxicity and anoxia. Hence it is necessary to increase its adaptation to various abiotic stresses. The response mechanism of plants to abiotic stresses commences with the perception of stress and subsequent signal transduction, influ- encing the activity of transcription factors. This, in turn, modulates the expression levels of genes involved in physiological responses. Additionally, abiotic stresses can be regulated via epigenetic mechanisms [84]. Accumulation of heavy metals causes phytotoxicity and also reduced the nutrients accumulation in root crops, it was noticed that heat shock proteins also involved in protection against heavy metal stress, particularly against lead and arsenic [85]. Hypoxia the condition where the oxygen is deficient in the root zone affects plant growth in turn root quality and yield. Que., *et al.* [86] reported three genes encoding alcohol dehydrogenases (*ADH1–3*) were up-regulated in roots affected from hypoxia.

Bulb crops

All the bulb crops are monocotyledonous vegetables, belongs to the family Alliaceae and the genus *Allium*. Onion and garlic are the major bulbous vegetables cultivated from ancient times and are cultivated mostly in rabi season in plains and March to July in hills of India [87]. The major insect pests of these crops are thrips (*Thrips tabaci*), cut worm (*Agrotis ipsilion*), maggots (*Delinia an- tiqua*), head borer (*Heliothis armigera*), fungal disease that affect crops are downy mildew (*Perenospora destructor*), purple blotch (*Alternaria porri*), *Stemphylium* blight (*Stemphylium vesicarium),* smut (*Urocystis cepulae*), smudge (*Collectotrichum ciricinans*), black mould (*Aspergillus niger*), white rot (*Sclerotium cepivorum*), basal rot (*Fusarium oxysporum* f. sp*. cepae*), bacterial diseases in- cludes stalk rot (*Pseudomonas gladioli* pv *alliicala*) and soft rot (*Erwinia carotovara* pv *carotovara*) and yellow dwarf is the viral disease infect both at bulb and seed crop. The pests and disease af- fect the, quality, yield as well as storage life of bulbs, and also seed yield and quality.

Resistance or tolerance source for many pests and diseases are poorly characterized in cultivated *Allium* germplasm with some exceptions [88]. Some of molecular characterization studies results in the dissection of genetic architecture of *Allium* sp. in response to various biotic stresses (Table 7). The relation is observed between bulb pigmentation and smudge resistance, in which the colored bulbs (yellow and red varieties) were resistant to smudge, while it is common in white bulbed varieties. The linkage was reported between thrips resistance loci and glossy foliage, conditioned by a recessive gene (*gy*) was observed but the glossiness was also as- sociated with undesirable allele, *y1* governs for yellow lethal [89]. Apart from this, two separate was reported loci for scape glossi- ness and glossiness was defined by recessive alleles at the loci, *gls1* and *gls2* where *gls1* was found epistatic to *gls2*. It was observed that two loci located on chromosome 2 and 5 control the waxiness through acyl reduction and decarbonylation pathways, respective- ly and the

regions were flanked by SNP markers which facilitate the marker-assisted breeding to develop thrips resistant cultivars without the problem of linkage drag [90]. Anjomshoaa., *et al.* [91] carried out study on genetic diversity analysis for rust resistance in the 16 Iranian garlic clones (*Allium sativum* L.) using 12 primers (NBS-LRR) reported the substantial diversity in the homologues of resistance genes in the Iranian garlic clones.

Resistant Trait	Gene/QTL	LG	Mapping population/line	References
Downy mildew	Two recessive loci *s1* and *s2*		Calred	[92]
Pink root	A single recessive locus *pr1*			[93]
Purple blotch	*ApR1*		Arka kalyan	[94]

Table 7: QTLs/genes associated with resistance to different pests and diseases of bulb crops.

Pertaining to abiotic stresses, several onion inbreds were high- ly resistant to ozone damage and speculated that it was controlled by dominant loci which prevent the damage by closing of stomata, subsequently the dominant gene was labeled as *Oz*.

Leafy and salad vegetable crops

Leafy and salad vegetables group are the richest source of nu- trition to humans as they are rich in vitamins such as vitamin A (beta carotene), B1 (riboflavin), B9 (folic acid), C (ascorbic acid and minerals like calcium, potassium, magnesium, iron and others, they are very essential for the pregnant women and children and helps to cure the problem of night blindness.

Downy mildew is one of the serious diseases of spinach that significantly reduces the yield if uncontrolled, till now 17 races of this pathogen has been reported 17 [95]. Systematic research on identification of downy mildew inheritance in spinach was initi- ated by Smith and coworkers in 1950s with years of their effort, resulted in the identification of single dominant gene to control the resistant to race 1 and 2, subsequently two tightly linked dominant genes has been reported to control resistance to race 1 [96]. The resistance of a dominant gene *Pfs-1,* was characterized and noti- fied to control the resistance to race 6 of the pathogens by using NIL population, bulk segregant analysis revealed a SCAR marker, named *Dm-1*, was closely associated with the *Pfs-1* locus (approxi- mately 1.7 cM) and can differentiate the resistant and susceptible genotypes. Over a period of time different research groups, identi- fied multiple resistant loci i.e. from *RPF2* to *RPF10*, found to con- fer resistance against the most races of downy mildew fungi [97]. Feng., *et al*. [95] developed molecular markers linked with three downy mildew resistance genes (*RPF1, RPF2* and *RPF3*). Molecu- lar breeding approaches such as marker assisted selection, marker assisted backcrossing and marker assisted pyramiding techniques can be effectively used to develop DM resistant spinach cultivars. Similarly in lettuce downy mildew resistance governed by qualita- tive (single dominant genes, *Dm* or the resistance factors, *R*) and quantitative (governed by multiple genes). Many race-specific re- sistant genes exist, with most mapped *Dm* genes clustered at link- age groups 1, 2, and 4, except for *Dm13* which is located at *LG3*. Mo- lecular markers tightly linked with *Dm* genes have been identified and converted into SCAR markers to aid marker-assisted selection. Lettuce Big-vein is a viral disease transmitted by the soil-borne fungus *Olpidium brassicae* reported to be controlled by three QTLs, of them one QTL was located on chromosome 3 and two on chro- mosome 4. Additionally, two more QTLs were located on chromo- some 5 and 6 in a population derived from resistant Thompson and susceptible cv. Cisco.

The powdery mildew resistance in pea was reported to be con- trolled by two single recessive genes (*er1* and *er2*) and one domi- nant gene (*Er3*). Most of the PM resistance breeding programs uses *er1* gene, because *er-2* is temperature sensitive and the locus *er1* has been mapped onto linkage group VI of Pea. Powdery mildew- resistant pea stocks were developed by incorporating the resis- tant genes *er1* and *er2* into the Pb89 and Bonneville backgrounds through marker-assisted selection. These stocks serve as valuable pre- breeding material for creating resistant cultivars and can be further utilized for pyramiding *er1* and *er2* genes for long-lasting resistance through intercrossing. Bruchid is the major storage pest of cowpea causing considerable loss in yield as well as affect the germination of cowpea seeds. The resistance to bruchid in cow- pea is observed to be controlled by two pairs of recessive genes. Similarly pod borer (*Maruca vitrata*) resistance was observed in some of *Vigna vexillata* accessions but it is not readily crossable with cultivated species make it difficult to develop resistance in cultivated varieties. However, agrobacterium mediated transfer of crystal proteins (*Cry*) and vegetative insecticidal proteins (*Vips*) from *Bacillus thuringiensis (Bt)* helps to develop pod borer resis- tance transgenic varieties. For introgression of these complex trait marker assisted recurrent selection and pyramiding multiple QTLs found beneficial as both takes comparatively less period of time [98].

Potato

Potato (*Solanum tuberosum* L.) is herbaceous annual tuber crop belongs to the family solanaceae. The major insect pests causing damage to crop directly by sucking, chewing of plant parts or indi- rectly through transmitting viruses are aphids (*Aphis gossypii* and *Myzus persicae*), jassids (*Empoasca fabae*, Seriana equate), cut- worm (*Agrotis ipsilion*), leaf eating caterpillar (*Spilosoma oblique*), epilancha beetle (*Henocepilancha vigintioctopunctata*) and potato tuber moth (*Phthorimia opercullela*), root knot nematode (*Meliodogyne incognata, M javanica, M hapla*), cyst nematode (*Glo- bodera rostochinensis*), the crop is infected with many pathogens, economically important ones are early blight (*Alternaria solani*), late blight (*Phytophthora infestans*), charcoal rot (*Macrophomina phaseoli*), black scurf (*Rhizactonia solani*), powdery scab (*Spon- gospora subterannea*), wart (*Synchytium endobioticum),* bacterial diseases such as bacterial wilt *(Pseudomonas solanacearum*), common scab (*Streptomyces scabies*), viral diseases includes po- tato virus-X, Y, S, A, potato leaf roll virus and mycoplasma diseases such as phyllody, purple top roll, marginal flavescence. The prog- ress in molecular biology over the years helps in providing bet- ter knowledge on genomic regions accompanying with resistance and susceptibility to pests and diseases. Different wild species act as source for late blight resistance *Solanum chacoense, Solanum acaule, Solanum berthaultii, Solanum brevidens, Solanum demissum, Solanum bulbocastanum, Solanum sparsipilum, Solanum microdon- tum, Solanum spegazzinii, Solanum sucrense, Solanum vernei, So- lanum, stoloniferum, Solanum toralapanum, Solanum verrucosum*. The resistance among them controlled monogenically (*R* genes) as well as polygenically (QTL's) (Table 8). But rapid break down of resistance was observed in the plants introgressed with *R* genes, sub- sequently the study shifted to *Rpi* genes (resistance to *P. infestans*) from other wild species used to develop resistance. The present studies on late blight resistance mainly concerned with pyramid- ing of multiple *R* genes in one cultivar which might increase both durability of resistance and delay the onset of symptoms. At CPRI, Shimla molecular markers tightly linked to *R1, R2* and *R3* were used for pyramiding these genes in single potato variety background for improved late blight resistance. Similarly, four genes conferring ex- treme resistance (ER) to PVY, namely *Rychc*, *Ryadg*, *Rysto*, and *Ry- hou*, have been identified. Additionally, four N genes, *Nychc*, *Nctbr*, *Nydms*, and *Nyadg*, have been reported to exhibit high resistance to PVY. Notably, the Nyadg gene is epistatic to *Ryadg*, resulting in genotypes carrying both *Ryadg* and *Nyadg* displaying extreme re- sistance to PVY. In India, a marker-assisted breeding program was used to develop a triplex (YYYy) potato parental line containing the *Ryadg* gene, known for its extreme resistance to PVY.

Mechanism of stress tolerance in vegetable crops

Plants have evolved various mechanisms for thriving under stress conditions. Plants sense the stress through the direct and indirect effects of stress on sensor molecules positioned in differ- ent cellular components. In response to stress, plants have evolved different avoidance and tolerance-based mechanisms. In order to survive under stressful conditions plants have evolved multiple of intrinsic tolerance mechanisms to adapt to the high temperature stress. The understanding of various physiological, molecular and biochemical pathways can facilitate the development of superior tolerant varieties to stress conditions. Producing an economically significant yield under heat stress conditions depends on several plant physiological parameters and mechanisms that contribute to heat tolerance in the field, such as amendments to essential processes such as photosynthesis, and concomitant increases of transcripts coding for proteins involved in protection. In many cases, a tolerant variety is characterized by higher photosynthetic rates, improved membrane thermostability, the ability to sustain leaf gas exchange.

Severe Stress conditions generate ROS, such as hydrogen per- oxide and superoxide radicals. as byproducts of the aerobic metabolism, which adversely affect cellular metabolism, such as lipid membrane peroxidation, and damage nucleic acids and proteins [99]. Plants respond to ROS production by activating enzymatic and non-enzymatic ROS scavenging systems. The main ROS scavenging enzymes are superoxide dismutase (SOD), catalase (CAT), peroxidase (POX), ascorbate peroxidase (APX) glutathione reductase (GR), whereas non-enzymatic chemical are ascorbic acid (ASC) and glutathione (GSH). In response to HS, plants synthesize molecular chaperones including HSPs that recognize hydrophobic amino acid residues of non-native proteins and promote folding and refolding of denatured proteins. They are also responsible for assembling of multi-protein complexes, transporting, and sorting of proteins into correct compartments, controlling cell cycle and signal-transduction under various stress conditions. The different classes of HSPs play complementary and sometimes overlapping roles in protein stabilization under stress.

Conclusion

molecular breeding presents a promising avenue for enhancing vegetable crop productivity, addressing malnutrition challenges, and mitigating the impact of biotic and abiotic stresses. By leverag- ing the power of molecular markers and genetic insights, breeders can

expedite the development of resilient and high-yielding vege- table varieties, thereby contributing to food security and nutrition improvement efforts in India.

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