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Genes, *QTLs* and linked molecular markers conferring the resistance for various biotic stresses in tomato cultivar

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Abstract
Tomato (*Solanum lycopersicum* L.) is one of the important consumable vegetable after potato. Tomato is frequently grown across the world for fresh vegetable and industrial processing. Tomato is the richest source of vitamins (vitamin A and C) and other nutritive minerals. Cultivated tomato is highly susceptible to several biotic stresses like insects, fungi, bacteria, viruses and nematodes. Development of biotic stress resistance cultivar of tomato is one of the challenging efforts. In this context, traditional breeding is not successful tools for development of multiple disease resistant tomato cultivars. Molecular markers based breeding for the incorporation of desirable traits conferring the resistance for biotic threats is one of the powerful tools in tomato breeding programmes. Wild relatives of tomato having many resistance genes and QTLs which conferring the resistance against pathogens and the diseases. However, utilization of linked molecular markers associated to resistance traits is one of the wonderful strategies for pyramiding of genes for multiple biotic stresses as well as future breeding programmes.

Keywords: Tomato, resistance genes, QTLs, biotic stresses, desirable traits, molecular markers

Introduction
Tomato (*Solanum lycopersicum* L.) is widely grown for vegetable purposes across the tropical and sub-tropical region of the world. The commercial farming of tomato is one of the strategic opportunities to increase the income of growers, (Fan *et al*., 2013) [10]. There are more than 7500 tomato cultivars are available for cultivation but most of them are susceptible to bacterial, fungal, and viral pathogens that reduces yields, fruit quality, shelf-life, and nutritional content. The major diseases of tomato are *Tomato mosaicvirus* (ToMV), *Tomato yellow leaf curl virus* (TYLCV), *Tomato spotted wilt virus* (TSWV), *Tomato chlorotic spotvirus* (TCSV) and *Groundnut ring spot virus* (GRSV), *Cucumber mosaic virus* (CMV), *Tobacco etch virus* (TEV), *Potato virus Y* (PVY), *Fusarium wilt* (FW), *Verticillium wilt* (VW), *late blight* (LB), *Bacterial wilt* (*Rs*), *Bacterialspot* (Xcv), *leaf mold* (Ff), *Root-knot* (*Mi*) and bacterial speck. Development of multiple disease resistance cultivar of tomato is one of the challenging issues. The genomic study for the identification of desirable resistance genes and loci for various diseases and pathogens and incorporation of these resistance sources in the cultivated varieties can change the scenario of tomato production.

In the series of genomic study, it has been characterized that tomato having the genome of approximately 950 Mb (Olmstead R.G, *et al*., 2008) [28]. DNA markers have wide range of plant species including tomato. Use of molecular markers in the construction of high-density linkage maps are a useful tools for association analysis, QTL analysis and marker assisted backcross breeding. However, the development of large number of molecular markers for saturation of the linkage map with respect to particular traits and use in the identification of candidate resistance genes may determine the future breeding strategy for development of disease resistant tomato cultivars. Validation of molecular markers across the tomato genomes for trait of interest and identification of linked markers which segregate with particular trait should be helpful in the development of disease resistant tomato cultivars. Using the powerful tools of molecular markers it has been clarified that the some wild species of the tomato like *Solanumperuvianum, Solanum chilence, Solanum pimpinellifolium, Solanum pennellii* and *Solanum habrochaites* conferring the resistance for more than twenty five diseases of the tomato caused by viruses, fungus, bacteria's, insects and nematodes (Gururani M.A *et al*., 2012) [14].

However, the molecular markers linked to the particular genes and whose inheritance has also been detected for various oligogenic traits in the wild sources. The molecular markers study employs across the all tomato chromosomes has been successfully done for the identification of the resistant candidate gene by the workers (Tanksley S.D, *et al*. 1995) [39]. Several molecular markers like RAPD, SSR, ISSR, SNPs, SCARS, InDel, dCAPS etc. have been frequently used for the screening of the disease resistance loci on the various chromosomal position of the chromosome of the wild tomato species. Utilization of the these molecular markers associated with resistance gene and their incorporation through marker assisted backcross breeding may recover the yield loss of tomato cultivars caused due to different diseases (Arens P *et al*., 2010) [3]. The proper application of marker assisted breeding steps like fore ground selection, background selection; parental polymorphism survey and recurrent parent genome recovery during the gene pyramiding using the particular donor source may definitely confer the resistance.

In this article, we have discussed about the candidate resistance genes(S), linked QTLs and associated molecular markers linked to the particular genes for resistance against bacteria, fungi, nematodes and viruses in tomato cultivars. This article will be useful to the tomato breeders for development of multiple disease resistance cultivars of the tomato employing marker assisted breeding for gene pyramiding and also in the development of breeding lines like RILs, NILs and segregation analysis in future breeding programmes.

Molecular marker system for biotic stress resistance breeding

Molecular markers are DNA segments linked with the particular genes and whose inheritance would be detected. Most of the molecular markers are used for the characterization of germplasm for various oligogenic and polygenic traits. Some of molecular markers linked to particular genes, which conferring the resistance for pathogens and diseases are frequently used in the marker assisted backcross breeding for incorporation and validation. Ideal molecular markers are frequently distributed throughout the genome, co-dominant in nature as well as easy, fast and cheap to detect. In the developmental series of molecular markers associated to the tomato genomes have been identified and conferring the presence of resistance genes in the particular location on chromosome. These markers include the varieties like restriction fragment length polymorphisms (RFLPs), randomly amplified polymorphic DNAs (RADPs), microsatellites like simple sequence repeats (SSRs) and other moderns like SCARs, STS, InDel, dCAPS etc. (Andersen, 2013) [2], Lateef, 2015) [23].

In the tomato breeding programme for development of disease resistant tomato cultivars, wild tomato species are the wide source of resistance gene. A huge collection of tomato wild species and their relatives, number of candidate genes have been identified and validated using gene linked and gene based molecular markers again disease resistance. However, some dominant markers like STS, RAPD and AFLP having the limitation due to narrow genetic base in the progenies used in the breeding programs for parental polymorphism survey (Jehan T, *et al*., 2016) [19]. Some QTL linked molecular markers are highly useful for marker assisted selection for the incorporation of resistant genes in the useful cultivars from wild source (Li T.H, *et al*., 2008) [25]. The gene based marker system and their particular association with the single nucleotide polymorphism is one of the robust ways to provide accurate information and future breeding program for marker assisted incorporation of disease resistance genes in the popular cultivars (Hamilton *et al*., 2012) [15] and (Shirasawa *et al*., 2010b) [36]. The next generation markers and SNPs are recently identified with respect to genetic variations at nucleotide sequence level (Kumar J, *et al*., 2011) [22].

The first genetic linkage map in tomato was first constructed by Bernatzky and Tanksley in (1986) [7] using RFLP marker in the mapping population derived from the crosses of *S. lycopersicum* and *S. pennellii*. Several other genetic maps have been developed in tomato using RFPLs, CAPs, SSRs, SNPs markers for localization of resistance genes in the wild relatives of tomato species for future breeding programmes (Gonzalo and van der Knaap, 2008, Shirasawa *et al*. 2010a, and Sim *et al*., 2012) [13, 35, 37].

The resistance genes for various mapping population derived lines may confer the form various mapping populations. Some of the identified candidate genes have been validated using DNA markers could be useful for marker assisted breeding. Several functional markers have been found across the 12 chromosome of the tomato genome conferring the availability of resistance genes for various biotic threads (Rodríguez *et al*., 2011) [31]. One of the important loci commonly known as resistance gene analogs (RGA) have been mapped on the chromosome 9 to 12 chromosome of the tomato genome (Foolad M *et al*., 2002) [11]. These loci are found as group of 29 RGAs showing the numerous resistance genes and several quantitative trait loci in the tomato genome across the different location in the chromosome (Zhang L.P. *et al*., 2002) [45].

However, development of new elite breeding lines and varieties of the tomato for multiple biotic stress resistance, used of molecular markers is one of the powerful tools to achieve durable resistance by pyramiding several major and minor genes into cultivars. These markers are also useful in easy selection of donor source and screening of tomato cultivars for numerous diseases and pathogens. Recurrent parent genome recovery with targeted trait of interest using backcross breeding can also be done for recovery of most of genomic proportion of the recurrent parents. The future strategy for introgression of useful traits can also be achieved by the tomato breeders to develop disease resistant tomato cultivars.

Genes, QTLS and Molecular marker associated with resistance to fungal diseases

Cultivated tomato is severely influenced by several fungal diseases like *Verticillium wilt*, *Fusarium wilt*, *Late blight*, *Early blight*, *Leaf mold*, *Powdery mildew*, *Gray leaf spot*, *Fusarium crown* and *Root rot*, and *Corky root rot*. These devastating diseases reduce the satisfactory and economic yield of the cultivated tomato cultivars. Many resistance genes have been indentified form the wild source of tomato for these fungal diseases. The identified wild resistance source, resistance genes, chromosomal location of the resistance genes and linked molecular markers are given in the table 1.

Verticillium wilt is one of the severe fungal diseases of the tomato, there are two candidate genes namely *Ve1* and *Ve2* conferring the resistance for *Verticillium Wilt* from *S. lycopersicum*. These genes are linked with cleaved amplified polymorphism (CAPS) markers. The genome wide surgery

for *Verticillium wilt* using CAPS marker conferring the visibility of *Ve1* and *Ve2 I* genes on the chromosome 9 of the tomato genome (Uribe P, *et al*., 2014) [20].*Fusarium wilt* is another devastating fungal disease of tomato spread around the world. *Fusarium wilt* is soil born disease caused by fungus *Fusarium oxysporum* f. Four resistance genes namely *I-1, I-2, I-3* and *I-7* have been identified against *Fusarium wilt* from different wild species of tomatoes. The resistance gene *I-1* and *I-2* have been identified on chromosome 11 of *S. pennellii* using SCAR marker. Another resistance gene for *Fusarium wilt I-3* is located on chromosome 7 of *S. pennellii* has been validated using SCAR marker (Arens P, *et al*., 2010) [3], the *I-7* is also conferring the resistance against *Fusarium wilt* located on the chromosome 8 of the tomato genome (Barillas A.C. *et al*., 2008) [5].

Early and late blight of tomato is dangerous disease damage the leaf of tomato plants and later affects the fruits. The early blight of tomato is caused by *Alternaria solani.* Resistance against have also been recognized in the wild species of tomato. Two candidate genes *Ph2* and *Ph3* have been identified for the wild source *Solanum pimpinellifolium.* These genes are confirmed and validated using CAPS markers. *Ph2* is located on the chromosome 9 of the *Solanum pimpinellifolium* while*Ph3* on chrmomosome 10 (Gonzalez-Cendales Y *et al*., 2016) [12].

Leaf mold is other fungal disease of the tomato affects tomato leaves by molding them. Many resistance genes for these severe pathogens have been identified form the wild tomato species and some are indentified from the cultivated tomato verities. The genes available in the resistance source can easily be used for the introgression in the susceptible verities to achieve durable resistance. The major genes *cf1, cf2, cf4, cf5, cf9, cf19, Hcr-9-4E* have been identified from different tomato species. Expect for *cf2, cf5, cf9* and *cf9*, no other tightly linked markers has been identified for their accurate validation. The resistant gene *cf1* is found on the chromosome 1 of the *S. lycopersicum var. cerasiforme, cf2* on chromosome 6 of *S. pimpinellifolium* and SSR marker system has been developed for the validation of *cf2* on the chromosome 6. The gene *cf4* and *cf9* conferring the resistance against lead mold have been validated on chromosome 1 of the *S. pimpinellifolium* but no any tightly linked markers has been identified for *cf4* gene. Whenever, *cf9* is tightly linked with SCAR markers. Another important resistance gene cf9 found on the chromosome 2 of the *S. lycopersicum* has been validated and closely linked with SCAR marker (Gonzalez-Cendales Y *et al*., 2016) [12].

The genes for *Powdery mildew* resistance in tomato have been identified from wild species *S. habrochaites, S. chilense, S. peruvianum* and some genes from *S. lycopersicum*. Most of the genes conferring the resistance against powdery mildew have been found on the chromosome 6 and 12. The resistance gene *lv* is found on the chromosome 12 of *S. chilense, Ol-3* and *Ol-4* on chromosome 12, *Ol-1* on chromosome 6 of *S. habrochaites* but no any tightly linked markers has been identified for these genes (Gonzalez-Cendales Y *et al*., 2016) [12]. Only *Ol-2*, found on the chromosome 6 of *S. lycopersicum* has been identified as ideal genes for *powdery mildew* resistance because of the closely association with highly resolution melt molecular marks dCAPS (Barone A *et al*., 2007) [6].

Molecular marker system have been also developed for other fungi born diseases of tomato viz. *Gray leaf spot, Fusarium crown* and *Root rot*, and *Corky root rot.* The soil born disease like *Corky root rot* is a soil borne disease caused by *Pyrenochaeta lycopersici.* This disease influence the tomato crop when temperature below to normal. The exact resistance sources of this fungal pathogen are not exactly known but *S. lycopersicum* having the resistance gene Py-1 for this disease. Due to lack of closely linked markers this is not yet to be totally resistance (Gonzalez-Cendales Y *et al*., 2016) [12]. Root rot and Fusarium crown are also soil borne diseases caused by *Fusarium oxysporum* spreading around the world. Only a single candidate gene *Frl* has been identified from *S. lycopersicum* on chromosome 9 which sowing the resistance for this particular fungal pathogen. Closely linked CAPS and SCAR marker system are also available for this gene (Mutlu N, *et al*., 2015 and Devran Z, *et al.* 2018) [24, 26]. Another fungal disease of tomato is Gray leaf spot having less infection as comparsion to other fungal pathogens. This gene was mapped on chromosome 11of *S. lycopersicum* using InDel markers. The InDel marker is closely linked to these particular genes but no any evidence are available for the marker in the marker assisted breeding (Su X, *et al*., 2018) [38].

Table 1: Fungal diseases, resistance genes and associated molecular markers in tomato (Source: Su X, *et al*., 2018) [38]

Disease	Resistance gene	Linked markers	Chromosomal location of genes	Resistant source
Verticilliumwilt	*Ve1*	CAPS	9	*S. lycopersicum*
	Ve2	CAPS	9	*S. lycopersicum*
Fusarium wilt	*I-1, I-2*	SCAR, ---	11	*S. pennellii*, ----
	I-3	SCAR	7	*S. pennellii*
	I-7	CAPS	8	---
Late blight	*Ph2, Ph3*	CAPS	10, 9	*S. pimpinellifolium*
Leaf mold	*Cf4, cf9*	---, SCAR	1	*S. pimpinellifolium*
	Cf1, Hcr9-4E	---,---	1	*S. lycopersicum*
	Cf2	SSR	6	*S. pimpinellifolium*
	Cf5	SSR	6	*S. habrochaites*
	Cf19	SCAR	2	*S. lycopersicum*
Powdery mildew	*Ol-3, Ol-4, Ol-5*	---	12	*S. habrochaites*
	Ol-1	---	6	*S. habrochaites*
	Ol-2	dCAPS	6	*S. lycopersicum*
	Lv	---	12	*S. chilense*
Gray leaf spot	*Sm*	InDel	11	*S. lycopersicum*
Fusarium crown and root rot	*Frl*	CAPS, SCAR	9	*S. lycopersicum*
Corky root rot	*Py-1*	-	3	*S. lycopersicum*

Genes, QTLS and Molecular marker associated with bacterial disease resistance

Tomato plant is infected by numerous bacterial diseases and decreases in yield have been recorded by several bacterial diseases. Both gram-positive and gram-negative bacteria are proven as devastating source of bacterial pathogen to the tomato cultivars in the nature. Bacterial wilt, bacterial spot, bacterial speck and bacterial cancer are the major diseases of tomato. Number of molecular markers associated to these bacterial diseases have been reported from tomato genome on the different chromosomal locations and some of the markers are closely linked to the particular genes which conferring the resistance. However, breeders are used molecular markers in the breeding purpose for introgression of several major and minor genes from wild species to cultivated species to achieve durable resistance for the diseases caused by bacterial pathogen (Yang W, *et al*., 2007) [44]. The use of molecular markers tightly linked to the bacterial diseases of tomato will be also useful in the development of mapping population and in marker assisted backcross breeding. The identified wild resistance source, resistance genes, chromosomal location of the resistance genes and linked molecular markers are given in the table 2.

Bacterial wilt is the well known disease of tomato observed in the many temperate zone of the world. Bacterial wilt is soil borne disease of cultivated tomato crop caused by *Ralstonia solanacearum.* Number of resistance source of bacterial wilt has been reported and the genes showing resistance for bacterial wilt is polygenic in nature has also been reported. The genes conferring the resistance for bacterial wilt are earlier reported in the some tomato cultivars of Hawaii in the back of more than two decayed. Mainly two genes *Bwr-6* and *Bwr-12* have been have been reported from *S. lycopersicum* on the chromosome 6 and 12 respectively. These resistant genes are linked with several SCAR markers and some SNPs are also reported for these genes (Kim B, *et al*., 2018) [21]. These reported genes will be helpful for future breeding programmes in the development of wilt resistant cultivar of tomato.

Bacterial cancer is important disease of the tomato caused by bacterium *Clavibacter michiganensis* sub-sp. *Clavibacter michiganensis* is a gram-positive bacterium and no any extensive studies have been carried out for the proper development of the bacterial cancer disease resistant cultivars. Bacterial cancer severely infects the plant during cold season due to very low temperature. These are several QTLs have been reported from the chromosome 1, 6, 7, and 8 of the *Solanum peruvianum* and *S. lycopersicum*. Cmm1.1- Cmm 0.1 is the major gene/QTLs have been validated and reported by RFLP marker system. However, Cmm is the gene based marker system having the information of resistance for bacterial cancer pathogens (Balaji V, *et al*., 2008) [4].

Bacterial speck is other bacterium derived disease of the controlled and uncontrolled environment of the cultivated tomato genotypes. The causal organism of bacterial speck is *Pseudomonas syringae (Pst)*. Several genes have been reported and extensively used for the marker assisted selection studies for introgression of genes in to the cultivated varieties of the tomatoes from the wild sources. The resistance gene includes the *Pto*, *Prf*, *Fen* and *Pti1* from wild sources. The wild source of *Pto*, *Prf* and *Fen* is S. *pimpinellifolium*, *Prf and Fen* are located on the chromosome 5 of *S. pimpinellifolium* while *Pto* on the chromosome 6. Another important gene for the bacterial speck resistance is *Pti1*, located on the chromosome 12 of the *S. lycopersicum* and linked with marker Oth-R (reported like protein) (Balaji V *et al*., 2008) [29]. The gene *Pto* is closely linked with CAPS marker system (Yang W *et al*., 2005) [43] while, *Prf* and *Fen* genes are validated and associated with Oth-R (reported like protein) marker system (Lee J.M. *et al*., 2015) [24].

Bacterial spot is the well known disease of the tomato because of the loss in yield across the world. Bacterial spot is caused by bacterium *Xanthomonas campestris* pv. *Vesicatoria* (*Xcv). Xanthomonas campestris* is the gram-negative bacteria, difficult to control due to the complex genetic background. However, several genes (*Rx-1, Rx-3, Rx-4, Rx-4, Xv-3, Bs-4, Xv-4*) have been reported. The QTLs (*Bac-spo-QTL*) has also been reported from *S. lycopersicum* var. *cerasiformae* on chromosome 11 with the help of tightly linked SSR marker system (Hutton S.F *et al*., 2010) [18].The resistant gene *Rx-1* and *Rx-2* have been reported in *S. lycopersicum* on chromosome 1, 2 respectively (Barone A *et al*., 2007) [6], *Rx-4* and *Xv-3* on chromosome 11 (Wang H *et al*., 2011) [40] and *Rx-3*&*Bs-5* on chromosome 5 of *S. lycopersicum* (Schornack S, *et al*., 2004) [32]. These resistant genes are linked with the series of molecular markers like CAPS, InDel (Pei C, *et al*., 2012) [29].

Table 2: Bacterial diseases, resistance genes and associated molecular markers in tomato (Source: Wang H *et al*., 2011) [40]

Disease	Resistance gene	Linked markers	Chromosomal location of genes	Resistant source
Bacterial wilt	*Bwr-6*	---	6	*S. lycopersicum*
	Bwr-12	SNP, SCAR	12	*S. lycopersicum*
Bacterial speck	*Prf, Fen*	RLP RES	5	*S. pimpinellifolium*
	Pto	CAPS	6	*S. pimpinellifolium*
	Pti1	Other RES	12	*S. lycopersicum*
Bacterial canker	*Cmm 0.1 to 1.1*	RFLP	1,6,7,8	*S. lycopersicum*
Bacterial spot	*Rx-1. Rx-2*	---	1,2	*S. lycopersicum*
	Rx-3, Bs-4	CAPS	5	*S. lycopersicum*
	Rx-4, Xv-3	InDel, CAPS	11	*S. lycopersicum*
	Xv-4	CAPS	3	*S. lycopersicum*
	Bac-sp-QTL	SSR	11	*S. lycopersicum* var. *cerasiformae*

Genes, QTLs and Molecular marker involved invirus resistance

Among all the pathogens, viral pathogens are involved in the severe loss of tomato yield. A group of viral diseases that can be transmitted from various sources causing harmful effect on the tomato cultivars throughout the worlds. Some of the important viral diseases of tomato are TYLCV, TSWV, ToMV, CMV, TCMV and some poty viruses. The indentified wild resistance source, resistance genes, chromosomal location of the resistance genes and linked molecular markers

are given in the table 3.

Tomato yellow leaf curl virus is one of the devastating diseases of tomato transmitted by *Bemisia tabaci.* This virus belongs to geminivirus, having bipartite genome. Geminivirus also causes papaya leaf curl disease and other leaf curl diseases have been reported in the some solanaceae plants. The resistant sources of TYLCV have been reported from the wild species of tomato. Several genes (*Ty1, Ty2, Ty3, Ty4, Ty5, Ty6*) have been reported from wild species of tomatoes *viz.S. chilense*, *S. habrochaites*, *S. peruvianum* and *S. lycopersicum* on the different chromosomal location of the tomato genomes (Prasanna H.C. *et al*., 2015) [30]. Large numbers of CAPS, SCAR, AYC, InDel and SNPs have been identified to numerous resistant genes. The resistant gene Ty1 and Ty3 are located on the chromosome 6 of *S. chilense* and closely linked with CAPS and ACY molecular marker system (Jung J, *et al*., 2015 and Nevame A.Y.M. et at., 2018) [20, 27]. Other TYLC genes *Ty5*, showing the resistance against pathogen has been observed on chromosome 4 of *S. peruvianum* and linked with several types of molecular markers InDel, CAPs and SNPs (Wang Y, *et al*., 2018) [41].

However, some special genes *Ty6* which conferring the resistance against TYLCV located on chromosome 10 of the *S. lycopersicum* and linked with SNP marker are one of the robust gene for future breeding programs in the marker assisted backcross breeding (Hutton S.F. *et al*., 2015) [17].

Some viral diseases of the tomato like TCSV, PVY, AMV and ToMV have been recorded as severe disease. The resistant source of the ToMV has been identified from the wild species *S. habrochaites*. The *S. habrochaites* has resistance genes Tm-1 against ToMV are located on the chromosome 2 and closely linked with the SCAR marker (Arens P, *et al*., 2010) [3]. Other ToMV resistance gene Tm-2 and Tm2a have been reported on chromosome 2 of *S. peruvianum* and are closely linked with the CAPS marker (Shi A, *et al*., 2011)[34].

Some other viral diseases of tomato caused like CMV and AMV have limited information due to unavailability of accurate resistance source germplasm. Moreover, *Cmr* genes located on the chromosome 12 of the *S. chilense* linked with RFLP molecular marker system has been reported as resistance gene for CMV. The resistance gene (*Am*) has been reported on the chromosome 6 of *S. habrochaites* but no any robust markers linked to these are reported. The resistance gene (*Pot-1*) for poty virus resistance is reported on the chromosome 3 of *S. habrochaites* but lack of any associated and linked markers to this resistance gene may not be easy to further use in the marker assisted breeding programmes (Shi A, *et al*., 2011) [34].

Table 3: Viral diseases, resistance genes and associated molecular markers in tomato (Source: Shi A, *et al*., 2011) [34]

Disease	Resistance gene	Linked markers	Chromosomal location of genes	Resistant source
TPY	*Pot-1*	---	3	*S. habrochaites*
AMV	*Am*	---	6	*S. habrochaites*
CMV	*Cmr*	RFLP	12	*S. chilense*
ToMV	*Tm-1*	SCAR	2	*S. habrochaites*
	Tm-2, Tm2a	CAPS	9	*S. peruvianum*
TSW	*Sw-5*	SCAR	9	*S. peruvianum*
TYLCV	*Ty-1, Ty-3*	CAPS, ACY	6	*S. chilense*
	Ty-2	SCAR	11	*S. habrochaites*
	Ty-4	CAPS	3	*S. chilense*
	Ty-5	CAPS, InDel, SNP	4	*S. peruvianum*
	Ty-6	SNP	10	*S. lycopersicum*
	Ty-1/3	CAPS	6	*S. lycopersicum*

Genes, QTLs and Molecular marker associated with nematode and insect resistance

A wide range of insects and nematodes are involved in the damage of cultivated tomato crops around the world. The major nematodes and insects affecting tomato crops are *Meloidogyne spp., Macrosiphum euphorbiae, Bemisia tabaci, Bactericerca cockerelli, Root-knot* nematodes, Potato cyst etc. Loss in yield and quality of tomato fruits have been observed by these nematodes and insects. The limited numbers of resistance sources are available for these biotic threads in the nature. Only few resistant genes (*Mi* and *Hero*) have been identified from the wild sources and associated markers linked to these genes have also designed for the detection and validation (Seah S, *et al*., 2007) [33]. The indentified wild resistance source, resistance genes, chromosomal location of the resistance genes and linked molecular markers are given in the table 4.

The *Mi* gene has different relatives having the resistance for *Meloidogyne spp., Macrosiphum euphorbiae, Bemisia tabaci, Bactericerca cockerelli,* Root-knot nematodes, and potato cyst. The *Mi* genes are designated on the basis of resistance to different nematodes and viruses viz. *Mi-1* for *Meloidogyne spp., Macrosiphum euphorbiae, Bemisia tabaci, Bactericerca Cockerelli, Mi-j and Mi-1.2 for Bemisia tabaci, Bactericerca Cockerelli, Mi-3, Mi-9 and Mi for Root-knot* nematodes (Ammiraju J, *et al*., 2003) [1]. The resistance gene *Mi-1* and *Mi* are located on the chromosome 6 of *S. peruvianum* and linked with CASR and CAPS marker (Seah S, *et al*., 2007) [33]. The resistant gene *Mi-3* has been observed on chromosome of *S. peruvianum* using SCAR marker (Yaghoobi J, *et al*., 2005) [42]. The resistant genes *Mi-j, Mi-1.2* and *Mi-9* linkedwith SCAR and CAPS marker system have been identified on the chromosome 12 of *S. peruvianum* (Hoogstraten J.G.J., *et al*., 2005) [16].One other gene (*hero*) showed the resistant for tomato cyst caused by Globodera rostochiensis identified from the wild tomato species S. pimpinellifolium (Ernst K, *et al*., 2002) [9].

Table 4: Insects and nematodes, resistance genes and associated molecular markers in tomato (Source: Ammiraju J, *et al*., 2003) [1]

Disease	Resistance gene	Linked markers	Chromosomal location of genes	Resistant source
Bemisia tabaci, Bactericerca Cockerelli, Meloidogyne spp.	*Mi-1*	SCAR	6	*S. peruvianum*
Root-knot nematodes	*Mi-3*	SCAR	3	*S. peruvianum*
	Mi	CAPS	6	*S. peruvianum*
	Mi-9	---	12	*S. peruvianum*
Bemisia tabaci, Bactericerca, Cockerelli	*Mi-j, Mi-1.2*	CAPS, SCAR	12	*S. peruvianum*
Potato cyst	*Hero*	---	---	*S. pimpinellifolium*

Conclusion and future perspectives

The use and proper utilization of the molecular markers in tomato breeding for various biotic stresses would be proven as marvelous gift. It is concluded that from this literature, the wild species of tomatoes have number of resistance genes and genes conferring the resistance for several biotic stresses. However, the molecular markers are frequently available for the various gene governing the resistance for diseases caused by fungi, bacteria, viruses insects and nematodes should must be helpful in marker assisted breeding and gene pyramiding of several major and minor genes to achieve durable resistance in the future breeding programmes.

References

1. Ammiraju J, Veremis J, Huang X, Roberts P, Kaloshian I. The heat-stable root-knot nematode resistance gene Mi-9 from Lycopersicon peruvianum is localized on the short arm of chromosome 6, Theoretical and Applied Genetics. 2003; 106(3):478-484.
2. Andersen SB. Plant breeding from laboratories to fields. International Conference on Innovative technologies California, 2013, 47-48.
3. Arens P, Mansilla C, Deinum D, Cavellini L, Moretti A, Rolland S *et al*. Development and evaluation of robust molecular markers linked to disease resistance in tomato for distinctness, uniformity and stability testing, Theoretical and Applied Genetics. 2010; 120(3):655-664.
4. Balaji V, Mayrose M, Sherf O, Jacob-Hirsch J, Eichenlaub R, Iraki N *et al*. Tomato transcriptional changes in response to Clavibactermichiganensis subsp. michiganensis reveal a role for ethylene in disease development. Plant Physiology. 2008; 146(4):1797-1809.
5. Barillas AC, Mejia L, Sanchez Perez A, Maxwell DP. CAPS and SCAR markers for detection of I-3 gene introgression for resistance to *Fusarium oxysporum* f. sp. *lycopersici* race 3. Tomato Genetics Cooperative Report. 2008; 58(2):11-17.
6. Barone A. and Frusciante L., Marker-assisted Selection: Current Status and Future Perspectives in Crops Livestock. Forestry and Fish, FAO, Italy, 2007, 153-164.
7. Bernatzky R, Tanksley SD. Toward a saturated linkage map in tomato based on isozymes and random cDNA sequences. Genetics. 1986; 112:887-898.
8. Devran Z, Kahveci E, Hong Y, Studholme DJ, Tor M. Identifying molecular markers suitable for Frl selection in tomato breeding. Theoretical and Applied Genetics. 2018; 131(10):2099-2105.
9. Ernst K, Kumar A, Kriseleit D, Kloos DU, Phillips MS, Ganal MW. The broad-spectrum potato cyst nematode resistance gene (Hero) from tomato is the only member of a large gene family of NBS-LRR genes with an unusual amino acid repeat in the LRR region. Plant Journal. 2002; 31:127-136.
10. Fan S, Brzeska J, Keyzer M, Halsema A. From Subsistence to Profit: Transforming Smallholder Farms. Food Policy Report. International Food Policy Research Institute, Washington DC, 2013.
11. Foolad M, Zhang L, Khan AA, Nino-Liu D, Lin G. Identification of QTLs for early blight (Alternaria solani) resistance in tomato using backcross populations of a *Lycopersicon esculentum L.* hirsutum cross. Theoretical and Applied Genetics. 2002; 104(6):945-958.
12. Gonzalez-Cendales Y, Catanzariti AM, Baker B, Mcgrath DJ, Jones DA, Identification of I-7 expands the repertoire of genes for resistance to F usarium wilt in tomato to three resistance gene classes. Molecular Plant Pathology. 2016; 17(3):448-463.
13. Gonzalo MJ, van der Knaap E. A comparative analysis into the genetic bases of morphology in tomato varieties exhibiting elongated fruit shape. Theoretical and Applied Genetics. 2008; 116:647-656.
14. Gururani MA, Venkatesh J, Upadhyaya CP, Nookaraju A, Pandey SK, Park SW. Plant disease resistance genes: current status and future directions, Physiology and Molecular Plant Pathology. 2012; 78:51-65.
15. Hamilton JP, Sim SC, Stoffel K, Van Deynze A, Buell CR, Francis DM. Single nucleotide polymorphism discovery in cultivated tomato via sequencing by synthesis. Plant Genome Journal. 2012; 5:17-29.
16. Hoogstraten JGJ, Braun C, McDonough H. Methods for coupling resistance alleles in tomato. US Pat Journal. 2005, 15.
17. Hutton SF, Ji Y, Scott JW. A tomato breeding line with begomo virus resistance gene Ty-3 in a 70-kb Solanum chilense introgression. Horticultural Science. 2015; 50(8):1257-1259.
18. Hutton SF, Scott JW, Yang W, Sim SC, Francis DM, Jones JB. Identification of QTL associated with resistance to bacterial spot race T4 in tomato. Theoretical and Applied Genetics. 2010; 121(7):1275-1287.
19. Jehan T, Lakhanpaul S. Single nucleotide polymorphism (SNP)–methods and applications in plant genetics: a review, 2006.
20. Jung J, Kim HJ, Lee JM, Oh CS, Lee HJ, Yeam I. Gene-based molecular marker system for multiple disease resistances in tomato against Tomato yellow leaf curl virus, late blight and verticillium wilt. Euphytica. 2015; 205(2):599-613.
21. Kim B, Hwang IS, Lee HJ. Lee JM, Seo E, Choi D *et al*. Identification of a molecular marker tightly linked to bacterial wilt resistance in tomato by genome-wide SNP analysis. Theoretical and Applied Genetics. 2018; 131(5):1-14.
22. Kumar J, Chaudhary AK, Solanki RK, Pratap A. Towards marker-assisted selection in pulses: A review, Plant Breeding. 2011; 130(3):297-313.
23. Lateef D. DNA marker technologies in plants and applications for crop improvements. Journal of Biological

sciences Medicine. 2015; 3:7-18.
24. Lee JM, Oh CS, Yeam I. Molecular markers for selecting diverse disease resistances in tomato breeding programs. Plant Breeding & Biotechnology. 2015; 3(4):308-322.
25. Li TH, Li YX, Li ZC, Zhang HL, Qi YW, Wang T. Simple sequence repeat analysis of genetic diversity in primary core collection of peach (*Prunus persica*). Journal of Integrative Plant Biology. 2008; 50(1):102-110.
26. Mutlu N, Demirelli A, Ilbi H, Ikten C. Development of co-dominant SCAR markers linked to resistant gene against the Fusarium oxysporum f. sp. radicis-lycopersici. Theoretical and Applied Genetics. 2015; 128(2):1791-798.
27. Nevame AYM, Xia L, Nchongboh CG, Hasan MM, Alam M, Yongbo L *et al*. Development of a New Molecular Marker for the Resistance to Tomato Yellow Leaf Curl Virus. Bio Med Research International, 2018. doi: 10.1155/2018/8120281.
28. Olmstead RG, Bohs L, Migid HA, Santiago-Valentin E, Garcia VF, Collier SM. A molecular phylogeny of the Solanaceae. Taxon. 2008; 57(1):1159-1181.
29. Pei C, Wang H, Zhang J, Wang Y, Francis DM, Yang W. Fine mapping and analysis of a candidate gene in tomato accession PI128216 conferring hypersensitive resistance to bacterial spot race T3. Theoretical and Applied Genetics. 2012; 124(3):533-542.
30. Prasanna HC, Sinha DP, Rai GK, Krishna R, Kashyap S, P, Singh NK *et al*. Pyramiding T y-2 and T y-3 genes for resistance to monopartite and bipartite tomato leaf curl viruses of India. Plant Pathology Journal. 2015; 64(2):256-264.
31. Rodríguez GR, Muños S, Anderson C, Sim SC, Michel A, Causse M *et al*. Distribution of SUN, OVATE, LC, and FAS in the tomato germplasm and the relationship to fruit shape diversity. Plant Physiology. 2011; 156:275-285.
32. Schornack S, Ballvora A, Gürlebeck D, Peart J, Ganal M, Baker B *et al*. The tomato resistance protein Bs4 is a predicted non-nuclear TIR-NB-LRR protein that mediates defense responses to severely truncated derivatives of AvrBs4 and over expressed AvrBs3. Plant Journal. 2004; 37(1):46-60.
33. Seah S, Williamson VM, Garcia BE, Mejía L, Salus MS, Martin CT *et al*. Evaluation of a co-dominant SCAR marker for detection of the Mi-1 locus for resistance to root-knot nematode in tomato germplasm. Tomato Genetics Coop Rep journal. 2007; 57:37-40.
34. Shi A, Vierling R, Grazzini R, Chen P, Caton H, Panthee D. Identification of molecular markers for Sw-5 gene of tomato spotted wilt virus resistance, American Journal of Biotechnology Molecular Sciences. 2011; 1(1):8-16.
35. Shirasawa K, Asamizu E, Fukuoka H, Ohyama A, Sato S, Nakamura Y*et al*. An interspecific linkage map of SSR and intronic polymorphism markers in tomato. Theoretical and Applied Genetics. 2010a; 121:731-739.
36. Shirasawa K, Isobe S, Hirakawa H, Asamizu E, Fukuoka H, Just D *et al*. SNP discovery and linkage map construction in cultivated tomato. DNA Research. 2010b; 17:381-391.
37. Sim SC, Durstewitz G, Pliesle J, Wieseke R, Ganal MW, Van Deynze A *et al*. Development of a large SNP genotyping array and generation of high-density genetic maps in tomato. PLoS One. 2012; 7:e40563.
38. Su X, Zhu G, Huang Z, Wang X, Guo Y, Li B *et al*. Fine mapping and molecular marker development of the Sm gene conferring resistance to gray leaf spot (*Stemphylium* spp.) in tomato. Theoretical and Applied Genetics. 2018; 132(4):871-882.
39. Tanksley SD, Ganal MW, Martin GB. Chromosome landing: A paradigm for map-based gene cloning in plants with large genomes, Trends in Genetics. 1995; 11(2):63-68.
40. Wang H, Hutton SF, Robbins MD, Sim SC, Scott JW, Yang W. Molecular mapping of hypersensitive resistance from tomato 'Hawaii 7981'to Xanthomonas per forans race T3. Physiopathology. 2011; 101(10):1217-1223.
41. Wang Y, Jiang J, Zhao L, Zhou R, Yu W, Zhao T. Application of Whole Genome Resequencing in Mapping of a Tomato Yellow Leaf Curl Virus Resistance Gene. Scientific Report. 2018; 8(1):9592.
42. Yaghoobi J, Yates JL, Williamson VM. Fine mapping of the nematode resistance gene Mi-3 in Solanum peruvianum and construction of a S. lycopersicum DNA counting spanning the locus. Molecular Genetics & Genomics. 2005; 274(1):60-69.
43. Yang W, Francis DM. Marker-assisted selection for combining resistance to bacterial spot and bacterial speck in tomato, J Am. Soc. Hortic. Sci. 2005; 130(5):716-721.
44. Yang W, Francis DM. Genetics and breeding for resistance to bacterial diseases in tomato: prospects for marker assisted selection, Genetic Improvement. 2007; 2:153-164.
45. Zhang LP, Khan A, Nino-Liu D, Foolad MR. A molecular linkage map of tomato displaying chromosomal locations of resistance gene analogs based on a Lycopersicon esculentum Lycopersicon hirsutum cross. Genome. 2002; 45(1):133-146.