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The Leaf Curling in *Capsicum* Species : A Review

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Abstract

Among the commercial crops grown in India, chilli is widely used in cooking, seasoning, pharma and cosmetic industries. Among the pests that invade chilli cultivation, chilli leaf curl virus (ChLCV) is a major impediment in realizing economic returns. Infection of virus vectored by whiteflies, cause curling of interveinal regions distorting the phyto-morphology under severe cases. The virus potentially manifests cent percent yield loss either alone or coupled with thrips and mites, called as leaf curl syndrome. Attempts to manage vectors and in turn the virus have been spurious due to their quick ability to develop resistance. This necessitates the use of genetic resources that can tolerate or resist the virus. There are several reports on availability of varieties and germplasm collections rendering resistance. Based on the genetic background, resistance to ChLCV has been reported as mongenic dominant, monogenic recessive and two recessive loci interacting in duplicate dominance epistatic fashion. Although genetic determinants controlling ChLCV resistance is of high relevance, there have been limited attempts to map genomic regions controlling resistance. Two linked markers are now available in public domain, which can surrogate phenotypic selections to near precision. In the present review, an attempt is made to dissect ChLCVD in resistance breeding facets.

Keywords: Capsicum, Chilli leaf curl virus, Genetics

Chilli, *Capsicum annuum*, has been an indispensable ingredient in Indian cuisines and preparations. It is widely found garnished on dishes. The word *Capsicum* is derived from Greek, meaning 'to bite' (Nigam *et al*., 2015). Chilli fruits are used both unripe and ripe dried. Red chilli is used as spice for seasoning and as ingredients in curries. While, green chilli is used in curries, chutneys and often in seasoning. Paprika, Byadagi chilli, Warangal chapatta and similar high colour, less pungent varieties are extensively used for colour extraction, which is used extensively in bakery and beverages. Enzymes isolated from chilli fruits are used to treat certain types of cancer (Spice Board, 2019).

This species stands out from other members of family solanaceae in production of vanilloid compound capsaicin, which binds specifically to mammalian transient receptor potential vanilloid 1 (TRPV1). This ability of capsaicin has been tapped for its potential use in pharmaceuticals as a painkiller (Borbiro *et al*., 2015). In addition, capsaicin when treated to skin, results in vasodilation increasing blood flow to skin (Roberts *et al*., 1992). In cosmetic industry, extracts from fruits have been used in lipsticks, postulating the irritating effect to cause inflammation resulting in plumpy appearance of lips (The cosmetic chemist, 2016). Apart from its pharmaceutical and industrial usages, consumption of green chilli provide plethora of health benefits. Dietary inclusion of green chilli aids in weight loss, controlling blood sugar level, supports healthy heart and aids in digestion (NDTV Food, 2020). Some varieties of green chilli are sources of vitamin C, B_6 and K to considerable extent along with minerals like copper and manganese. A serving of pepper (45 g) gives 18 kcal of energy (Herbazest, 2019). Similarly, red chilli is known to maintain blood pressure and burn fat.

Chilli originated in South America and Portuguese introduced to India through Brazil at the end of fifteenth century. India is considered as secondary center of diversity especially for the extensively cultivated species, *C. annuum* (Dhaliwal *et al*., 2014). Farm grown peppers can be grouped into two, based on pungency. The species *C. annuum* is known to bear

pungent (hot pepper) and non-pungent (sweet pepper) fruits. India is the largest producer, consumer and exporter of dry chilli in the world (Linkedin, 2017). Present scenario of chilli production in India is lead by Andhra Pradesh followed by Karnataka. In 2018-19, the country was estimated to witness 3.66 lakh ha of green and 7.39 lakh ha of red chilli cultivation, yielding 37.37 lakh MT and 21.72 lakh MT of green and red chillies, respectively (NHB, 2018-19). In Karnataka, Belgaum and Haveri are the leading districts in area and production of the crop (Anonymous, 2018).

Pests and pathogens including plethora of viruses infect chilli. The genus Begomovirus under family Geminiviridae is one among the 65 viruses reported to infect chilli plants. This virus induces cupping and curling of leaves viewed as chilli leaf curl virus disease (ChLCV) and is reported throughout the world (Nigam *et al*., 2015). It is the most devastating virus in terms of incidence and loss caused. Potentially, it could cause 100 per cent yield losses (Greenleaf, 1986; Senanayake *et al*., 2013; Kumar *et al*., 2015). The virus is obligate on whiteflies for transmission. The vector allows rapid and efficient transmission of virus due to its indiscriminant feeding. The vector population thrives and multiplies best in natural conditions of 25-35 ^{0}C. Hence, ChLCV is mostly severe to summer crop. However, other season cultivations are infected sufficiently to cause economic losses (Nigam *et al*., 2015) demanding scientific attentions and interventions. In this review, Chilli leaf curl virus (ChLCV) is explained in view of symptoms, management, resistance and breeding strategies.

Symptoms

Pepper plants when harbor ChLCV display symptoms subject to the genetic resistance it carries. Based on the kind of alleles they carry, plants show immune (no symptoms) to severe morphological distortions resulting in total yield loss. Typically, presence of the virus can be manifested by leaf curling, rolling and puckering (Fig. 1). Blistering of the interveinal areas is mostly apparent along with thickening and swelling of veins along with leaf distortion. Young plants infected by ChLCV show elongated basal leaves followed by shortened internodes and petioles resulting

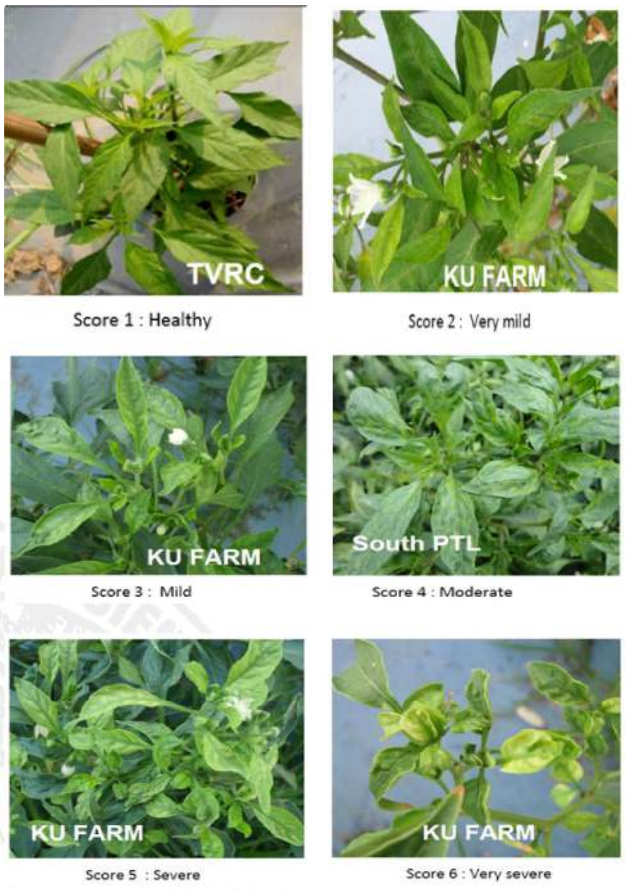

Fig. 1 Symptoms of ChLCV along with scale

in crowded leaves and stunted growth (Thakur *et al*., 2018). Vein clearing symptoms are also being reported, these samples were observed with typical geminate particles (Senanayake *et al*., 2007). In severe cases, the infected plants remain stunted and fail to flower and fruit (Kumar *et al*., 2015) resulting in cent percent losses. Older leaves in plants become leathery and brittle (Sinha *et al*., 2011). The virus depends on white flies (*Bemisia tabaci*) for its transmission.

Incidence of ChLCV along with non-insect pests forms a complex syndrome called murda complex. The tarsonemid mite (*Polyphagotarsonemus latus* Banks) and yellow thrips, (*Scirtothrips dorsdalis* Hood) are most destructive and are considered major pests (Berke and Sheih, 2000). Thrips and mites, respectively cause upward (Fig. 2) and downward (Fig 2B) curling of leaf margins, resulting in leaf curl syndrome along with ChLCV (Sarkar *et al.,* 2008). Thrips and mites in pepper severely distorts plant

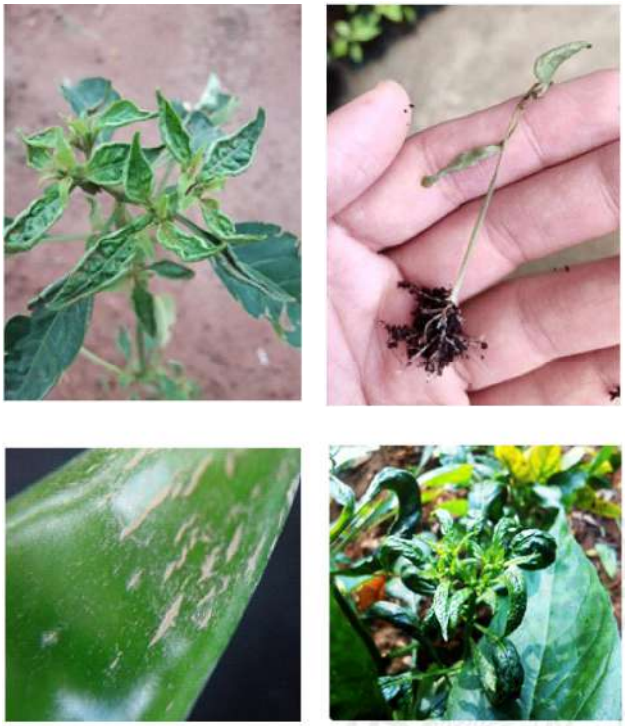

Fig. 2. Symptoms of leaf curl syndrome caused by thrips and mite infestation in pepper. Manifestation of feeding of A. thrips on leaves; B. thrips on young seedlings resulting in silvering C. thrips causing bronzing in fruits D. mite in festation on pepper

geometry. Thrips nibble the lower surface of leaves to cause cup shaped leaves, curling upwards at the margins. Also, rasping of thrips causes silvering of leaf and bronzing of fruit surface (Fig. 2). Flowers of pepper are also known to be infected by thrips. Mites, on the other hand, are habituate and multiply on lower leaf surface to cause curling of leaf margins downwards. Mites prefer pubescence of the leaves and stem while pubescence deters thrips. The economic losses caused are quantitatively 11-75 percent and 60-80 per cent qualitatively (Ghosh *et al*., 2009).

Distribution of Virus and Vector

The virus, being continuously devastating in chilli crop, has evolved into numerous strains. Though apparently it manifests leaf curling, genome level modifications render them their severity. The mutated forms across the world are given names based on their region of first report. Initially, Vasudeva (1954) reported ChLCV in India. For long, there were reports on four ChLCV strains infecting pepper. Tomato leaf curl New Delhi virus (ToLCNDV), Chilli leaf curl virus (ChiLCV), Cotton leaf curl Multan virus (CLCuMV) and Tomato leaf curl Joydebpur virus (ToLCJoV) from Pakistan (Khan *et al*., 2006; Senanayake *et al*., 2007; Hussain *et al*., 2004). Further, upon sequence comparison among the viral strains prevailing in Mirzaapur, Gorakhpur, Varanasi and Maharanjganj, Rai *et al*. (2010) reported ChLCV Varanasi as a different strain. Apart from these, ChLCV Guntur strain, ChLCV Bengaluru strain and ChLCV Madhya Pradesh strains are of economic relevance. Other strains prevailing across the world are pepper yellow leaf curl Indonesia virus from Indonesia and Cabbage leaf curl virus from Cuba (Zubiaur *et al*., 2006). Strains reported in Sri Lanka by Senanayake *et al*. (2007) are named as Chilli leaf curl Sri Lanka virus.

Apart from causing feeding damage to pepper, whiteflies (*Bemisia tabaci* (Gennadius)) transmit the viral particles. This complex cryptic species are vector to 111 Begomoviruses (Tiwari *et al*., 2013). In India, 9 out of 31 indistinguishable species are reported, which can be distinguished based on genetic makeup, mating behaviour and range of infecting host plants (Ellango *et al*., 2015). They have been identified based on ribosomal internally transcribed spacer 1 sequence, well known as ITS-1 (Li *et al*., 2005) and mtCO1 (Jun *et al*., 2012). Initial occurrence of whiteflies in India was reported from Kolar region of Karnataka causing epidemics by spreading tomato leaf curl virus (Banks *et al*., 2001). The distribution pattern of white fly genetic groups are most diverse in southern and eastern India which harbour most of the pepper growing regions. The genetic groups and their distributions in major parts of India are mentioned in Table 1 (Ellango *et al.,* 2015).

Though the flies are less mobile, cryptic species have migrated across the globe due to anthropogenic carriers. Different genetic groups are known to co-exist even in the same field. Thus, Table 1, indicates prevalence of several cryptic species in the same region.

TABLE 1
Distribution of genetic groups of *Bemicia tabaci* in India

Genetic groups of whiteflies	Location
Asia I	Ludhiana, Indore, Havery, Kolar, Bengaluru, Bagalkot, Guntur
Asia I-India	Coimbtore
Asia II 1	Ludhiana, Varanasi, Lucknow, Prakasham, Kottayam
Asia II 5	Coimbatore, Kottayam, Thiruvananthapuram
Asia II 7	Delhi, Bengaluru, Ahmadabad, Ranibennur
Asia II 8	Dharwad, Ranibennur, Erode, Chikkaballapura
Asia II 11	Dharwad, Gadag
China 3	Birbhum
MEAM1	Bengaluru, Kolar

Management of ChLCVD

In order to put a break for the virus from infecting, the vector (whitefly) that transmits the virus has to be controlled first. Several management practices have emerged to control the vector such as use of systemic insecticides, physical barriers, use of yellow sticky traps, biological control, and certain agronomic practices. However, the pest being polyphagous, alternate hosts like weeds and other crops act as major sources of inoculum to pepper. Several reports on the management of chilli leaf curl viral disease (ChLCVD) focusing majorly on virus control have been made available by researchers. The benefits of applying several synthetic and natural insecticides to control whitefly were found rewarding in the past. Improvement in growth and yield performance of treated plants was noticed as compared to the non-treated plants. Regular spraying of insecticide, malathion at every 21 days interval was found to be effective for management of the disease (Khan *et al*., 2006). However, a continuous spray of insecticides may result in residue accumulation in fruits and soil leading to tainted environment. Frequent sprays indeed adds further to the cost of pepper cultivation. In recent past, the vector has been found to rapidly head towards insecticide resistance. Thus, several insect growth regulators and new pyrethroid insecticides have appeared promising to manage this pest. However, due to rapid means of developing resistance by the pest, efficiency of newer insecticides remains for limited duration (Thakur *et al*., 2018). Accordingly, chemical control measures have remained partially effective in managing whiteflies durably. As a result, integrated pest management strategy has to be developed to check the pest most effectively.

For controlling virus diseases, as many preventive measures as possible should be taken as they are economically justified, since a single method of control is not likely to keep crops entirely free from virus infection (Heathcote, 1973). Integrated pest management strategy to control chilli leaf curl virus disease is presented in Table 2 (Thakur *et al*., 2018).

Screening Methodology

Phenotyping germplasm for responses to the trait under selection is of utmost importance in resourcing the genes. Accurate phenotyping can aid in precise selection and can further assist in mapping. Since ChLCV is often associated with complex curling syndrome, it is of paramount importance to design strategies in screening plants for response to viral inoculation. Vector population increases and reaches highest peak in *summer* during fruiting stages while in *kharif*, the vector density is high during vegetative and fruiting stages (Srivastava *et al*., 2017). High temperature coupled with humidity results in cresting of whitefly population (Srinivasan, 2009). Hence, it is appropriate to screen genetic resources at peak vector density to identify resistance sources.

For effective phenotyping in identifying resistance genotypes, two approaches are used. First, transplanting 30 days old seedlings to be screened in hot spots during summer. Followed by infection through whiteflies, naturally. Observations are recorded after 30, 60 and 120 days for either incidence (Kumar *et al*., 2011) or severity (Adluri *et al.*, 2017) based on the objectives. Incidence recorded are converted into coefficient of incidences and interpreted. While,

TABLE 2

Integrated pest management strategies to control chilli leaf curl virus disease

Method	Treatment/Practice	Reference
Cultural control	• Use of healthy seeds • Growing nursery in protected structures/ nets • Removal of infected seedlings and weed hosts from nursery • Treatment of seedlings with proper systemic insecticides to control vector • Use of yellow sticky traps just above the nursery to control insect vectors • Destroying previous year susceptible crops, particularly Solanaceous weeds and volunteer plants • Good weed control in the crop to ensure non availability of alternative host to virus and vectors • Transplanting dates should be adjusted to avoid peak season of the vector population • Use of reflective (silver colour) plastic mulch • Use of live mulches, border crops or hedges which are more attractive to the vectors than pepper crop	Reviewed by Kenyon *et al*. 2014
Biological control of vector	• Predators: *Coccinella septempunctata*, *Clitostethus arcuatus*, *Orius* spp*, Chrysoperla carnea*, *Chrysopa* spp., *Sinea confusa*	Reviewed by Gerling *et al*. 2001
	• Parasitoids: *Eretmocerus emiratus*, *Eretmocerus eremicus*, *Encarsia accenta*, *Encarsia adusta* etc. • Pathogens (Fungi): *Verticillium lecanii* and *Paecilomyces fumosoroseus*, *Paecilomyces farinosus* • Mycoinsecticides: BotaniGard, Bea-Sin, Boveril PM, Mycotal, Ago Biocontrol Verticillium, Pae-Sin	Reviewed by Faria and Wraight 2001
Chemical control of vector (Synthetic)	• Difenthiuron 50 WP @ 0.75 g per litre	Heathcote (1973)
	• Spraying diazinon, malathion, metasystox at 10 days interval	Devi and Reddy (1995)
	• 0.07% monocrotophos with 0.25% wettable sulphur	Bhattiprolu and Rahman (2006)
	• Diafenthiuron @ 200 ml/litre	Hussain *et al*. (2017)
	• Imidacloprid 17.8 SL (0.003%)	Pandey *et al*. (2010)
	• Imidacloprid (0.05%), acephate (0.1%) and malathion (0.05%)	Ahmed and Ram (2016)
Natural extracts	• Neem oil, neem guard, repellin and biosol	Chakraborti (2000)
	• Raw cow milk and Trichoderma	Kumar (2006)
	• Neem seed kernel extract (5%)	Pandey et al. (2010)
	• Seed extract of *Sapindus trifoliatus* and *Solanum trilobatum*	Ahmed and Ram (2016)
	• Clerodendrum aculeatum (leaf extract), Terminalia arjuna (bark extract)	Chaubey et al. (2017)

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severity scored are converted into percent disease index (PDI). Alternatively, seedlings can be challenge inoculated with viruliferous whiteflies either by single or by mass inoculation. Non-viruliferous whitefly culture are maintained on healthy cotton plants (*Gossypium hirsutum* L.) in insect proof glass house. The inoculation of ChLCV is maintained in a separate insect proof cage on susceptible plants. Simultaneously, the seedlings to be screened are sown in pro trays with coco pit (Sharma *et al*., 2018). The seedlings at 2-3 leaf stage (approximately 20 days after emergence) are used for inoculation. Non-viruliferous white flies are collected from cotton plants and released in the cage with susceptible plant for virus acquisition for 24 hours. Further, they are released in a closed structure containing seedlings to be screened, healthy cotton plant and a susceptible infected plant. This procedure is repeated 2-3 times to avoid escape of inoculum. At 4-6 leaf stage (approximately 45 days old seedlings), data are recorded on severity using prescribed scale. Among the two methods, challenge inoculation is more reliable as it overcomes false positive phenotyping of resistance due to escape.

Challenged seedlings, in either field or artificial conditions, are sorted as susceptible or resistant based on the Horsfall-Barratt (HB) scale like any other disease. Researchers have used this ordinal scale with five (1-5; 0-4) and six (0-5; 0-9) distinct classes. However, all types of scoring methods arrive at common value of weighted averages, called disease severity index (DSI) or per cent disease index (PDI) expressed in percentage. Use of HB scale for capturing disease severity ought to be subjective depending on symptoms and variability, in scoring the response to ChLCV infection. Most researchers have modified the 0-5 scale given by Banerjee and Kalloo (1987) for tomato leaf curl virus. However, Chaubey and Mishra (2017) have used 0-9 scale. Recently, Thakur *et al*. (2020) have used 1-5 scale for evaluating the segregating populations for response to the disease. In our studies, we use 6 point scale (1-6) scale, (1- immune to 6- highly susceptible) provided by AVRDC (Fig. 1). Ordinal classification of chilli plants based on Banerjee and Kalloo (1987) is given in Table 3.

TABLE 3

Classification of responses of chilli accessions to ChLCV infection given by Banerjee and Kalloo, 1987 and modified by Kumar *et al.* 2006

Class	Grade	Description of symptoms
Immune	0	Immune
Highly resistant	1	0 to 5% curling and clearing of upper leaves
Resistant	2	6 to 25 curling, clearing of leaves and swelling of veins
Moderately susceptible	3	26 to 50% curling, puckering and yellowing of leaves and swelling of veins
Susceptible	4	51 to 75% leaf curling and stunted plant growth and blistering of internodes
Highly susceptible	5	More than 75% curling and deformed small leaves, stunted plant growth

Sources of Resistance to ChLCV

Pre requisite for an effective breeding program aimed at developing disease resistance is a dependable source of resistance. This can be obtained from wild relatives, germplasm and often from farmer's varieties. Among the cultivated species, *C. frutescens* (Anandhi and Khader, 2011) and *C. chinense* (Adluri *et al*., 2017) harbour resistance against ChLCV. However, *C. annuum* varieties Punjab Lal and CV2 are also being found symptom less (Kumar *et al*., 2009). A list of resistance sources reported by various studies is given in Table 4 (Thakur *et al.,* 2018).

Genetics of ChLCV Resistance

Knowledge of inheritance (monogenic, oligogenic, polygenic) and mode of gene action is key to choose a breeding method in ameliorating traits. The basic step in identifying a putative resistant source involves

TABLE 4

Chilli germplasm accessions and breeding lines exhibiting resistance/tolerance to leaf curl viruses in India

Sources of resistance	References
Puri Red, Puri Orange	Mishra *et al*. (1963), Chattopadhyay *et al*. (2008)
Jwala	Tewari and Ramanujam (1974)
Surjamani, Perennial, S 118, S 114 (derived from Perennial 9 Long red)	Sooch *et al*. (1976)
Perennial, S 5-4, S 20-1, S 41-1, S 118-2-also resistant to Tobacco mosaic virus (TMV) and Cucumber mosaic virus (CMV)	Singh and Thakur (1977)
Pant C-1, Pant C-2-tolerant to leaf curl virus	Mathai *et al*. (1977)
Delhi Local-tolerant to leaf curl virus-also tolerant to TMV-immune to CMV and PVX	Konai and Nariani (1980), Tewari and Viswanath (1986)
Cross 218, EC 121490, IC 18253, IC 18885, JCA 196, Karanja, Pant C-I-less than 30% leaf curl incidence in the field	Bhalla *et al*. (1983)
CA-960, G-4, Jwala	Dhanju (1983)
Lorai, Longi, Pant C-I, Perennial, S 118-2-resistant/tolerant to leaf curl virus-also resistant/tolerant to CMV and TMV	Sharma and Singh (1985)
JCA 196, JCA 218, JCA 248, NP-46-A, Pant C-I, Pusa Jwala	Sangar *et al*. (1988), Brar *et al.* (1989)
Bangla Green (BG-1), CH-1, Indonesian Selection, Laichi-1, Laichi-2, Lorai, LS-l, MF41-1, MS13, Pant C-I, Perennial, Punjab Lal, S 20-1, Surjamani-field resistant to leaf curl virus-also field resistant to CMV	Singh and Kaur (1990)
Surajmukhi, Japani Loungi, Pant Chilli-1, Pusa Jwala and PBC-473	Awasthi and Kumar (2008)
Punjab Sindhuri and Punjab Tej-moderate resistant to leaf curl virus	Dhaliwal *et al*. (2013)
CH-27-F1 hybrid highly resistant to leaf curl virus	Dhaliwal *et al*. (2015)
Saurian 2010, Perennial and Japani Loungi	Ahmad *et al*. (2016)
DLS-Sel-10, WBC-Sel-5 and PBC-142	Srivastava *et al*. (2017)

extensive evaluation of germplasm under natural conditions with adequate quantity of vector population and virus inoculum. Once identified, resistance can be further confirmed by artificial inoculation. Subsequently, those lines with a certain level of resistance can be used in chilli breeding programmes for transferring the resistance employing mass selection, pedigree method, single-seed descent, backcross method, recurrent selection, and hybridization. From the above-mentioned methods, the backcross method has proven to be very promising and effective for incorporating disease-resistant gene (s) to elite genetic background.

Understanding the genetic basis of resistance to ChLCV is prerequisite for rational utilization of naturally occurring disease resistance. Disease resistance mechanisms can be of monogenic (qualitative) or polygenic (quantitative). The former is based on single gene, whereas later, depends on two or more genes (Keller *et al*., 2000). Monogenic resistance offers race specific and complete resistance. In other words, genes are not operative against all the races of the pathogen and follow gene for gene hypothesis (interact with *avr* gene from pathogen). This kind of resistance eases working out genetics. However, monogenic resistance is not

durable. It is quite contrasting with polygenic inheritance which offers relatively durable resistance as it delays the disease development by increasing latency and other parameters related to the epidemic along with expressing no obvious molecular interaction with the pathogen. Therefore, quantitative inheritance is more favourable than monogenic inheritance.

Several studies have been conducted to unravel the genetics of ChLCV. Genetic analysis of virus resistance against chilli mosaic and leaf curl viruses in Punjab during 1989-90 indicated that resistance was controlled by monogenic recessive genes (Bal *et al*., 1995; Kumar *et al*., 2009; Rai *et al*., 2010). The inheritance study of resistance to PepLCV in a partially compatible inter-specific cross (PBC-535 × Bhut Jolokia) also revealed monogenic recessive nature against pepper leaf curl virus (Rai *et al.,* 2014). Governance of resistance was also reported to be monogenic recessive in cross DLS Sel. 10 × Phule Mukta. Further, it was confirmed in backcrosses of the same cross (Maurya *et al*., 2019).

Extensive screening of breeding lines by Jindal *et al.* (2018) under natural conditions against ChLCV resulted in the identification of FL-201 and S-343 as highly susceptible and highly resistant, respectively. Genotype FL-201 was crossed with S-343, the resulting F_1 hybrid was found to be resistant even after 30-40 days of inoculation suggesting disease resistance under dominant gene control. Further screening of F_2 population of 200 plants under artificial conditions, resulted in resistant and susceptible plants segregating as 139 resistant (HR, R, MR) and 61 susceptible (HS, S, MS) plants. Further, these ratios were found to be in accordance with null hypothesis of chi-square test for a 3:1 hypothesised segregation ratio. This suggests that the resistance carried by S-343 is controlled by a single dominant gene (Jindal *et al*., 2018). Hence, S-343 is reported to serve as potential resistant donor in breeding programmes for developing resistant/tolerant varieties for ChLCVD. Resistance in S-343 was also reported as dominant in another investigation by Hament *et al*. (2019).

In the study conducted by the Department of Genetics and Plant Breeding, College of Agriculture, GKVK, an interspecific cross between Byadgi kaddi (a local collection from Karnataka) and Bhuth jolokia (collection from north east India) was affected to study the genetics. The inheritance of resistance to ChLCV is found to be due to interaction between two genes in duplicate dominant epistasis. This was evident from obtaining 15:1 F_2 ratio segregating for and susceptibility and resistance, respectively. Further F_3 progenies were screened for confirmation and these plants exhibited segregation for susceptibility and resistance in the expected 15:1 ratio (Ravikiran, 2019). The disagreement of these results with previous reports could be accountable to the genetic background and allele present in the donor against the viral strain used in the study of genetics of resistance to ChLCV.

Deducing genetics of resistance can also be attempted from generation mean analysis. In six generations derived from MS-341 (susceptible) and S-343 (resistant), additive × additive (i), additive × dominance (j) and dominance × dominance (l) interaction were present. In the best fit model of joint scaling test, both the additive (d) and dominance (h) gene effects were significant. Moreover, the magnitude of [h] component was higher than the [d] component suggesting the presence of dominance and additive effects in the inheritance of resistance to ChLCV. The role of dominance × dominance type of interaction was predominant in the inheritance with duplicate type of epistasis. The positive sign of (l) effects indicated higher frequencies of resistance increasing alleles. Hence, it can be concluded that disease incidence is controlled by dominance, additive and epistatic effects. Hence to improve the trait, methods like recurrent selection, multiple cross or diallel selective mating system may be adopted in chilli improvement programmes.

Attempts to Map

Though ChLCV has been a serious and economical threat in pepper cultivation, less attempts are reported regarding mapping of the region governing resistance to the virus (Wang and Bosland, 2006). Considering the synteny between tomato and pepper genomes and genomic regions governing resistance to Tomato leaf curl virus mapped (Ty genes), Mangal *et al*. (2017)

shortlisted 86 markers linked to Ty genes in Tomato. These markers were used in F_2 population derived from crosses of PM × DLS-Sel-10 as well as Anugraha × WBC-Sel 5 for analysis of marker trait association using BSA. None of the markers could differentiate the bulks indicating absence of association. These results are likely due to the influence of genome rearrangements in shuffling the micro collinearity among members of same family. Recently, Thakur *et al*. (2020) have reported two SSR markers CA 516044 and PAU-LC-343-1, situated 15.7 cM apart harbouring the gene for resistance to ChLCV. In the process, $F_{2:3}$ was used as mapping population derived from susceptible MS-341 and resistant S-343. Initially, 685 SSR markers were used for screening the resistant and susceptible bulks. The linked markers were further used for linkage analysis. Further, the markers were validated through NCBI BLAST. The reported markers are linked, with considerable probabilities of false positive selections due to distant location. However, these are the only reported markers available in the public domain, which can surrogate the genic markers until others are available.

Pepper, being a commercial crop, is valued for both green and dry chillies. Among the biotic stresses that plant ails, ChLCV causes severe distortion of plant morphology and cent per cent loss of marketable fruits. The virus has evolved into several stains to cause the disease across the world. Although several strategies have been devised against the virus, none of them could impart complete control. Moreover, chemical means of control degrades the environments and pouches residues in the produces. Genetic resistance is the remedy for such difficult-to-manage viral diseases. Genes governing resistance are reported to be mono and oligo genic with dominance and recessiveness. DNA markers linked to dominant gene are now available, which can potentially bypass the phenotyping process. Though it is a menace since years resistance breeding for ChLCV is still at infancy, opening up a large scope for studies in this arena.

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