Screeningofchilligenotypesforresistancetoleafcurlviru

s

Abstract

Leaf curl virus disease is a most destructive threat to chilli production. In the presentinvestigation 54 chilli genotypes were screened for leaf curl virus resistance in the naturalepiphytoticfieldconditionsandartificialinoculationusingviruliferouswhitefliesatHorticulture Research and Extension Centre (University of horticulture science, Bagalkot)during 2020-2023. The genotypes DCA-262, Khandhari and Bhoot Jolokia were found to beimmune and genotypes EC 391087 (9%), IC 342426 (5%), Punjab Lal (7%), Punjab Surkh(9%) were found to be highly resistant to leaf curl virus under natural conditions. Screeningwith artificial inoculation confirmed that the genotypes Khandhari and Bhoot Jolokia werefoundtobeimmuneandgenotypesEC391087(11%),PunjabLal(10%),PunjabSurkh(10%)were highly resistant to leaf curl virus. The checks Byadgi Dabbi (100%) and ByadgiKaddi(98%)were foundto be highly susceptible in bothnatural and artificial conditions.

Keywords: Chillileafcurlvirus,resistance,screening,genotypes,whitefly,hostplantresistance

Introduction

Thechillicropyieldisadverselyaffectedduetoleafcurldisease,causedbyChillileafcurlvirus (Kumar*etal.*,2015)belongingtogenusBegomovirusandfamilyGeminiviridae(Raj*et al.,* 2005). It causes the greatest damage regarding disease incidence and yield loss. Therehavebeenreportsof100%lossesofmarketablefruitinextremecircumstances(Senanayake*etal.*,2007,Zehra*etal.*,2017).Whitefly(*Bemisiatabaci*)actsasavectorforthetransmission

of virus into the host plant. Common symptoms include leaf puckering, curling, and rolling;blisteringoftheveinousregions;veinthickeningandswelling;internodeandpetioleshortening;leafcrowding;andoverallplantstunting(Peiris1953,JoshiandDubey1976,Sinha*et al.,* 2011, Srivastava *et al.,* 2020). Evasive techniques have been attempted with varyingdegreesofsuccess,includingagronomictreatments,sickplantremoval,andpesticideapplications to suppress vectors. Managing the disease with pesticides is great challengingbecause of recurrent development of resistance against pesticides by whitefly[22,23,24,25]. Utilizing hostplant resistance is a long-term, cost-effective, environmentally secure, and reliable method ofmanagingdiseases,particularlythosebroughtonbyviruses.Wildrelativesoraccessionsofthecultivated species are renowned for their wealth of useful genes including those of diseaseresistant(Mammadov*etal.*,2018).Therefore,thegoalofthecurrentstudywastoscreenchilligenotypes under natural epiphytotic and artificial conditions using viruliferous whiteflies toidentifythesourceofresistanceto thechilli leafcurl virus.

Materialsandmethods

Thepresentinvestigationon screeningandidentificationofchillileafcurlvirusresistant genotype in chilli was carried out at Horticulture Research and Extension Centre,(University of Horticulture Science, Bagalkot) during 2020-2023. The experimental materialconsistingof54genotypesduring2020-21.TheexperimentwaslaidoutinRandomisedBlockDesign with two replications and two checks. Seedlings of chilli genotypes were raised inprotrays and 35 days old seedlings were transplanted at a distance of 60 x 45 cm in the monthof January during the summer season. The experimental site and season were found to befavourable for white fly build up in the past years (Sirawata and Karcho 2023). Susceptiblecheckgenotypeswereplantedatevery6throwafter5rowsofchilligenotypesunderinvestigation. All the recommended cultural practices were followed. The virus scoring wascarriedoutatanexperimentalplotduringearlyandgrandgrowthstages.Forartificialscreeningundermassinoculationconditions,chilligenotypeswereraisedandchallengedbyviruliferouswhite fly population maintained on susceptible symptomatic chilli plants in the wooden cagecovered with nylon net. Adult virulent whiteflies collected from the symptomatic plants weregiven an acquisition access period (AAP) of 48 hrs on the genotypes under investigation.Seedlings were inoculated at the three-leaf stage, using 10–12 viruliferous whiteflies perseedling for an inoculation access period (IAP) of 48 hrs. Seedlings were then transplanted inanopen field condition and diseaseincidenceswerescored.

Fig1.Screeningthegenotypesunderartificialinoculationmethod

Observationrecorded

Ten plants in each genotype in each replication were randomly selected, tagged andthediseaseindexobservationswererecordedfromthetaggedplantsinbothnaturalscreeningas well as artificial screening. The leaf curl index was calculated for each chilli genotypesbased on the ratings using the scale followed by Kumar *et al.,* (2006). From the recordedobservation percent disease incidence (PDI) and disease severity were calculated. Based onthe genotype performance against leaf curl virus reaction, they were categorized into sixcategoriesbyadopting the method of Reddy*etal.*(2001).

Percentdiseaseincidence(PDI):Theincidenceofleafcurlviruswascalculatedbyusingthefollowing formuladevelopedby(Kumar*etal.,* 2006)and statisticallyanalysed.

$$\text{Percentdiseaseincidence (\%)} = \frac{\text{Numberofdiseasedplants}}{\text{Totalnumberofplantsobserved}} \times 100$$

Diseaseseverity: Theseverityofchillileafcurlviruswascalculatedbyusingthefollowingformuladev eloped by(Wheeler, 1969)andstatistically analysed.

$$\text{Diversityseverity} = \frac{\sum(\text{Diseaseclass} \times \text{No.ofplants ineachclass})}{\text{TotalNo.ofplantsselected} \times \text{Maximumdiseasegrade}} \times 100$$

Table1:Indexingofleafcurlvirusinchilli

Symptom severitygrade	Symptoms	Reaction(%)	Category
0	Nosymptom	0	Immune
1	0-5%Curlingandclearingofupper leaves	1 – 10	HighlyResistant
2	6-25%Curling,clearingofleaves and swelling ofveins	11–25	Resistant
3	26-50% Curling, puckering and yellowingofleavesandswellingof veins	26 – 40	ModeratelyResistant
4	51-75% leaf curling andstunted plant growth andblisteringofinternodes	41 – 60	Susceptible
5	>75%curlinganddeformedsmallleaves,stunted plant growth withsmallflowers andnoorsmallfruit set	>60	HighlySusceptible

Resultsanddiscussion

There was high phenotypic variation for leaf curl virus disease incidence and severityamongchilligenotypesstudied.Itrangedfrom0to100percentwithintheevaluatedgenotypes. No disease incidence and severity were observed in Bhoot Jolokia (*Capsicumchinense*), Khandhari, DCA-262 (*Capsicum frutescence*). In species *Capsicum annuum* EC391087 (9%), IC 342426 (5%), Punjab Lal (7%), Punjab Surkh (9%) were found to be highlyresistanthaving leastdisease incidenceandseverity.

Under artificial screening, a significant variance was observed in the leaf curl virusincidence and severity among the genotypes investigated. The disease severity ranged from 0to 100 per cent, lowest was observed in Khandhari (*Capsicum frutescence*) and Bhoot Jolokia(*Capsicumchinense*)with0percentdiseaseincidenceshowingimmunitytovirus.Genotypes DCA-262 (6%), Punjab Lal (10%) and Punjab Surkh (10%) were found to be highly resistantto leaf curl virus. The highest per cent of disease incidence was observed in ByadgiKaddi,Byadgi Dabbi and followed by Shankershwar with disease severity of 100%, 98% and 97%respectivelyand werefound to be highlysusceptible.

Based on the observed data and calculated disease incidence and severity it wasobtained that Bhoot Jolokia, Khandhari and DCA-262 were immune to leaf curl virus disease.Similarresultswereobservedby(Rai*etal*.,2014;Thakur*etal*.,2019).GenotypesEC391087, IC 342426, Punjab Lal and Punjab Surkh were found highly resistant to virus. Similar resultswere observed by several workers (Singh and Kaur, 1990; Hundal *et al.*, 1995; Kumar *et al.*,2006; Thakur *et al*., 2019). The native resistance of these genotypes to the virus was furtherconfirmedwiththeartificialinoculationinthepresencestudies.Hence,theresistanceobserve dwas not due to any kind of escape or non-preference of whitefly during screening but due toresistance mechanism present in these genotypes that either hinder virus replication or itsmovementthroughouttheplant(Verlaan*etal*.2013).Theresistancegeneorallelethatprevailsinth esegenotypesisthemostappropriatereasonforobservedresistanceandimmunitytoleafcurl virus. Identification of new and stable chilli genotypes that are immune to leaf curl virusinfectionthroughdifferentmethodsofscreeningisquitecrucialforadoptingtheminchillicropi mprovementprogram.

Fig2.Susceptibilityofchilligenotypestochillileafcurlvirus

Fig3.Resistanceof chilligenotypestochillileafcurlvirus

Table2:Reactionofchilligenotypesscreenedagainstleafcurlvirus

Sl No	Genotypes	Naturalscreening			Artificialscreening		
		Per cent diseaseindex (%)	Diseaseseverity (%)	Disease reaction	Per centdiseasein dex (%)	Diseaseseverity (%)	Disease reaction
1	EC 378633	86.67	80	HS	91.67	83	HS
2	EC 378688	73.33	54	S	78.33	61	HS
3	EC 391082	23.33	17	R	28.33	23	R
4	EC 391083	30.00	20	R	30.00	24	R
5	EC 391087	10.00	9	HR	20.00	11	R
6	EC 596952	76.67	51	S	81.67	58	S
7	EC 599993	70.00	69	HS	75.00	74	HS
8	IC 214965	36.67	36	MR	45.00	39	MR
9	IC 214966	26.67	17	R	31.67	23	R
10	IC 284628	20.00	12	R	23.33	21	R
11	IC 342426	10.00	5	HR	18.33	14	R
12	IC 342464	23.33	12	R	33.33	19	R
13	IC 537595	76.67	54	S	86.67	64	HS
14	IC 537657	46.67	36	MR	56.67	43	S
15	IC 537658	36.67	29	MR	45.00	37	MR
16	IC 537659	43.33	32	MR	50.00	40	MR
17	IC 537661	40.00	36	MR	48.33	45	S

18	IC 570388	60.00	45	S	66.67	60	S
19	IC 572454	66.67	52	S	78.33	65	HS
20	IC 572465	63.33	50	S	73.33	58	S
21	IC 572466	56.67	39	MR	65.00	50	S
22	IC 572475	90.00	80	HS	95.00	88	HS
23	IC 572477	93.33	84	HS	96.67	90	HS
24	Nic23897	83.33	73	HS	91.67	77	HS
25	Nic23906	90.00	80	HS	93.33	83	HS
26	DCA-111	33.33	26	MR	38.33	34	MR
27	DCA-245	90.00	80	HS	93.33	87	HS
28	DCA-299	80.00	57	S	88.33	65	HS
29	DCA-226	36.67	21	MR	45.00	31	MR
30	DCA-255	43.33	25	R	53.33	33	MR
31	DCA-92	83.33	59	S	90.00	68	HS
32	DCA-86	86.67	82	HS	95.00	90	HS
33	DCA-195	86.67	79	HS	91.67	88	HS
34	DCA-257	76.67	58	S	85.00	70	HS
35	DCA-107	73.33	55	S	80.00	66	HS
36	DCA-131	83.33	60	S	91.67	68	HS
37	LCA305	30.00	20	R	43.33	28	MR
38	LCA324	36.67	27	MR	46.67	32	MR
39	KDSC210-10	46.67	31	MR	53.33	34	MR

40	HissarVijay	30.00	21	MR	35.00	25	R
41	PantC1	26.67	19	R	35.00	25	R
42	PusaJwala	33.33	17	R	35.00	23	R
43	G-4	93.33	87	HS	96.67	90	HS
44	DCA-262 (Capsicumf rutescence)	0.00	0	I	13.33	6	HR
45	Khandhari	0.00	0	I	0.00	0	I
46	Bhoot Jolokia	0.00	0	I	0.00	0	I
47	PunjabLal	6.67	7	HR	13.33	10	HR
48	PunjabTej	23.33	13	R	28.33	20	R
49	PunjabSindhuri	20.00	12	R	25.00	19	R
50	PunjabSurkh	16.67	9	HR	20.00	10	HR
51	SurajMukhi	36.67	23	R	46.67	30	MR
52	ByadgiKaddi	100.00	98	HS	100.00	98	HS
53	ByadgiDabbi	100.00	100	HS	98.33	100	HS
54	Shankeshwar	96.67	97	HS	93.33	95	HS
	S.Em±	1.50	1.50		3.38	3.38	
	C.D.at5%	4.24	4.24		9.58	9.58	
	C.D.at1%	5.65	5.65		12.76	12.76	

Table3:Categorizationofchilligenotypesforresistancetoleafcurlvirusbasedonvirussymptomsundernatural condition

Diseasereaction	No. ofgenotypes	Genotypes
Immune	3	DCA-262(*Capsicumfrutescence*),Khandhari,Bhoot Jolokia
Highlyresistant	4	EC391087,IC342426,PunjabLal,PunjabSurkh
Resistant	12	EC391082,EC391083,IC214966,IC284628, IC342464,LCA305,PantC1,PusaJwala,PunjabTej, PunjabSindhuri,DCA-255,SurajMukhi
Moderatelyresistant	11	IC214965,IC537657,IC537658,IC537659,IC537661,IC572466,DCA-111,DCA-226,LCA 324,KDSC210-10,HissarVijay
Susceptible	11	EC378688,EC596952,IC537595,IC570388,IC572454,IC572465,DCA-299,DCA-92,DCA-257,DCA-107, DCA-131
Highlysusceptible	13	EC378633,EC599993,IC572475,IC572477,Nic-23897, Nic-23906, DCA-245, DCA-86, DCA-195,G-4,ByadgiKaddi,ByadgiDabbi,Shankeshwar

The genotypes were categorized into 6 groups based on their reaction to leafcurl virus. From disease severity per cent, it is evident that 3 genotypes were found to beimmune to virus, 4 genotypes were highly resistant, 12 were resistant, 11 were moderatelyresistant, 11 were susceptible and 13 were found to be highly susceptible to leaf curl virusduring natural screening. In case of artificial screening by mass inoculation of virulent whiteflies, it was observed that 2 genotypes were found to be immune, 3 genotypes were highlyresistant, 12 genotypes were resistant, 10 genotypes were moderately resistant, 6 genotypesweresusceptibleand21genotypesexhibitedhighlysusceptiblereactiontoleafcurlvirus.Total18 genotypes exhibited different reaction to leaf curl virus in natural and artificial screening,thisisbecauseofforcedinoculationtovirusesintotheplantsystemthroughvectorsinartificialscreening.Incaseofnaturalscreeningtheremaybechancesofescapismofvirusinfestation

byvectors(Koeda*etal.*,2021).Totalof36chilligenotypesexhibitedsimilarreactiontovirusin both natural and artificial screening imparting the resistance is due to the genetic make upof these genotypes against virus. The standard susceptible check Byadgi Dabbi and ByadgiKaddiexhibitedcompletesusceptibilitytoleafcurlviruswhichconfirmstheeffectivescreeni ngprogram.

Table4:Categorizationofchilligenotypesforresistancetoleafcurlvirusbasedonvirussymptomsun derartificial condition

Diseasereaction	**No. ofgenotyp es**	**Genotypes**
Immune	2	Khandhari(*Capsicumfrutescence*),BhootJolokia
Highlyresistant	3	DCA-262,PunjabLal,PunjabSurkh
Resistant	12	EC 391087,IC 342426,EC 391082,EC 391083,IC214966,IC284628,IC342464,HissarVijay ,Pant C1,PusaJwala,PunjabTej,PunjabSindhuri
Moderatelyresistant	10	IC214965,IC537658,IC537659,DCA-111,DCA-226,LCA324,KDSC210-10,LCA305,DCA-255, SurajMukhi
Susceptible	6	EC596952,IC537657,IC537661,IC572466,IC 570388,IC572465,
Highlysusceptible	21	EC378688,EC378633,IC537595,EC599993,IC 572475,IC572454,IC572477,Nic-23897,Nic-23906,DCA-299,DCA-92,DCA-257,DCA-107,DCA-131,DCA-245,DCA-86,DCA-195,G-4, ByadgiKaddi,ByadgiDabbi,Shankeshwar

Conclusion

Identification of new and stable chilli genotypes that are immune to leaf curl virusinfection through different methods of screening and adopting in breeding program is crucialfor chilli crop improvement.The investigation on chilli genotypic reaction for leaf curl virusinfection,sourcesofresistance,wereconductedforeffectiveresistancebreedingprogram.The promisinggenotypesidentifiedthatareresistanttoleafcurlvirusincludeEC391087,IC-

342426, Punjab Lal, Punjab Surkh, IC-284628, IC-342464, Punjab Tej and Punjab Sindhuri.These genotypes can be further utilised for effective breeding and development of multiplediseaseresistant chilli varieties.

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