DEVELOPMENT OF CHILLI (*Capsicum annuum* L.) HYBRIDS WITH LEAF CURL VIRUS RESISTANCE, HIGH YIELD AND QUALITY

by

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(2015-22-008)

THESIS

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COLLEGE OF AGRICULTURE

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2019

DECLARATION

I, hereby declare that this thesis entitled **"DEVELOPMENT OF CHILLI (*Capsicum annuum* L.) HYBRIDS WITH LEAF CURL VIRUS RESISTANCE, HIGH YIELD AND QUALITY"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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LIST OF ABBREVIATION

&	-	and
µg	-	Microgram
ANOVA	-	Analysis of variance
AVRDC	-	Asian Vegetable research & Development Center
a.m.	-	Anti meridian
BP	-	Better parent
CD (0.05)	-	Critical difference at 5 % level
CD (0.05)	-	Critical difference at 1 % level
cm	-	Centimeter
DAT	-	Days After Transplanting
d.f	-	Degrees of freedom
et al.	-	and co-workers/co-authors
Fig	-	Figure
F_1	-	First filial generation
g	-	gram
GCA	-	General combining ability
ha	-	hectare
IIVR		Indian Institute of Vegetable Research
i.e.	-	that is
kg	-	Kilogram
KAU	-	Kerala Agricultural University
mm	-	Milli meters
MP	-	Mip parent
NBPGR	-	National Bureau of Plant Genetic Resources
SCA	-	Specific Combining ability
SE	-	Standard error
S.E.D	-	Standard error difference
S.E.M	-	Standard error mean
SH	-	Standard heterosis
sp.	-	Species
t.	-	tone
viz.,	-	namely

Introduction

1. INTRODUCTION

Chilli (*Capsicum* spp.) is a major vegetable and spice crop of family *Solanaceae*. The genus *Capsicum* comprises of at least 34 wild species (Qin *et al.*, 2014; da Costa Batista, 2016), and five species *viz.*, *Capsicum annuum* (Linnaeus), *C. frutescens* (Linnaeus), *C. chinense* (Jacquin), *C. pubescens* (Ruiz & Pavon) and *C. baccatum* (Linnaeus) have been domesticated and cultivated (Bosland, 1992; Bosland and Votavo, 2012). Most of the cultivated and wild species of *Capsicum* have chromosome number 2n=2x=24 (Pickersgill, 1997). *C. annuum* L. is the most cultivated species throughout the world (Wang and Bosland, 2006) and they are categorised as sweet pepper or bell pepper (non-pungent fruits) and hot pepper or chilli pepper (pungent fruits) (Dhaliwal and Jindal, 2014). Hot pepper is widely grown as a spice crop in tropical and temperate region, whereas sweet pepper as high-value greenhouse crop. In Kerala three species, *C. annuum* L., *C. frutescens* L. and *C. chinense* Jacq. are widely cultivated.

Chilli is native to Central and South America (Pickersgill, 1991), and major center of diversity is Mexico (Costa *et al.* 2009). India is taken into consideration to be the secondary center of diversity for *C. annuum* L. (Dhaliwal *et al.* 2014). The out-crossing in chilli ranges from 7-90 per cent under field conditions, therefore considered as facultative cross-pollinating species (Singh *et al.*, 1994; Tanksley, 1984). Portuguese traders for the first time introduced chilli to India towards the end of 15^{th} century and its cultivation became popular in 17^{th} century. Chilli is the second largest commodity after black pepper in international spice trade on economic terms. Chilli is used in lots of forms, which include fresh or cooked vegetables, spices or herbs and as numerous processed products (Hazra *et al.*, 2016). Chilli is a wealthy source of vitamins (A, C and E) and minerals (potassium, magnesium and iron). It has high nutritional and antioxidant values, so being used in medicine industry and health pharmacology (Takashi *et al.*, 2001).

India is the world's largest producer, consumer and exporter of chillies. In India, green chillies are grown in an area of 0.31 million hectares with a production of 3.76 million tonnes and dry chillies in 0.83 million hectares with a production of 1.87 million tonnes (NHB, 2017). Globally, dry chillies occupies an area of 1.68 million hectares with a production of 3.81 million tonnes whereas, green chillies are grown in an area of 1.93 million hectares with production of 32.32 million tonnes (FAO, 2015). In India, Karnataka accounts for the major share (~17.85 %) of green chilli production followed by Madhya Pradesh, Andhra Pradesh, Bihar and Maharashtra whereas for dry chilli production Andhra Pradesh (~47.16%) leading in production followed by Telangana, Madhya Pradesh, West Bengal, Karnataka (NHB, 2017). Productivity of dry chilli has expanded by 90% from 1.18 tonnes hectare^{-1} in 2000 to 2.25 tonnes hectare^{-1} in 2016 (NHB, 2017). The increase in productivity is due to cultivation of high yielding and disease resistant F_1 hybrids in place of open pollinated cultivars. Globally, fruit yield in chilli has been increased by 35-50 per cent due to heterosis breeding (Dhaliwal and Jindal, 2014).

In the latest years, chilli hybrids have become very popular with the farmers due to their superior *per se* performance. Chillies grown from hybrid seeds are uniform and high yielding (Bosland and Votava, 2012). Superior performance of hybrids is manifested because of better plant vigour, high growth and development, earliness, increased productivity and higher degrees of resistance to biotic and abiotic stresses (Yordanov 1983).

Globally, more than 35 viruses have been reported under natural conditions. (Green and Kim, 1991). Among these, the occurrence of Chilli leaf curl disease (ChiLCD) caused by white fly (*Bemisia tabaci* G.) transmitted geminivirus, namely, *Chilli leaf curl virus* (ChiLCV) is one of the serious production constraints in tropics and subtropics of the world. The disease inflicts both the quantitative and the qualitative yield losses which often reach 100 per cent (Meena *et al.*, 2006; Senanayake *et al.,* 2007). The disease appears in

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epidemic form in autumn season in North Indian plains and in summer season in South India. The characteristic symptoms of ChiLCD include upward curling, reduced size of leaves, puckering, stunted growth with no flowers and fruits in severely affected plants.

Hitherto, in India five chilli leaf curl viruses predominantly infecting chilli have been reported. These include *Chilli leaf curl virus* (ChiLCV), *Chilli leaf curl India virus* (ChiLCINV), *Chilli leaf curl Vellanad virus* (ChiLCVV), *Tomato leaf curl Joydebpur virus* and *Tomato leaf curl New Delhi virus* (ToLCNDV) (Khan *et al.*, 2006; Senanayake *et al.*, 2007; Kumar *et al.*, 2012; Shih *et al.*, 2007). A recent survey and molecular characterization of chilli infecting virus revealed that a new begomovirus species, namely, *Chilli leaf curl Vellanad virus* (ChiLCVV) is responsible for ChiLCD in Vellanad area of Kerala (Kumar *et al.*, 2012).

Diverse cultural and chemical tactics were attempted to manage the disease without plenty achievements. Managing the disease with pesticides has been a hard challenge because of recurrent development of resistance against pesticides by white fly (Horowitz *et al.,* 2005). Exploitation of host-plant resistance is safe, durable and economic feasible approach to manage the disease. Availability of resistant donor(s) is a prerequisite for any resistance breeding programme. In general, wild relatives or accessions of the cultivated species are renowned for their wealth of useful genes including those for disease resistant.

The success of disease resistance breeding solely depends on the genetic variability and the evaluation tests employed for identification of the resistant sources from the germplasm. Screening of germplasm under natural epiphytotic and glass house conditions using viruliferous whiteflies and or graft inoculation is followed to identify the source of resistance against the ChiLCV (Kumar *et al.*, 2006; Kumar *et al.*, 2009; Rai *et al.*, 2014). A clear understanding of the underlying mechanism of disease resistance and its inheritance pattern helps to

select appropriate breeding strategies for successful introgression of the resistance genes.

A wide range of variability in chilli was exhibited for various economic and quality traits encouraging the breeders to exploit the variation for genetic improvement of the crop (Borgohain *et al.*, 2005). To break productivity limitations and to develop hybrids with desirable characters, selection of the parents is one of the important and most critical responsibilities for plant breeders. The common technique for selecting the parents on the basis of mean performance does not always produce good hybrids. Therefore, parents should be selected on the basis of their combining ability potential. Moreover, knowledge of gene action helps in the selection of appropriate breeding strategy for the genetic improvement of diverse quantitative traits. In plant breeding, gene action is commonly measured in terms of components of genetic variance or combining ability effects and variances. The varieties or strains could be evaluated in several ways based on the combining ability of their parents and one of them is line × tester analysis (Kempthorne, 1957). By using this analysis promising lines could be selected from the germplasm. As compared to diallel technique, this approach could evaluate more number of breeding lines at once. This in turn suggest the breeder whether to go for F_1 hybrid development or selection in subsequent generations to realize homozygous promising lines. The information on combining ability effects (general and specific combining ability) could be helpful for interpretation of the genetic basis of promising traits.

Information on the involvement of type of epistatic genetic effects in the inheritance of yield, quality and ChiLCD resistance is crucial for adopting suitable breeding procedures to develop hybrids/varieties having resistance/tolerance to ChiLCD with high yield and quality. Line × Tester analysis fails to identify epistasis gene interactions. Generation mean analysis (Hayman, 1958) offers a complete picture of gene action governing the character.

This approach is a simple first degree statistically analyzed technique to detect the predominant gene effects that are governing a particular trait.

Keeping in view of these facts and need, the present investigation was planned with following objectives:

- To identify the sources for ChiLCV resistance in a collection of germplasm through natural and artificial screening
- Identification of potential parents for ChiLCV resistant hybrid breeding based on mean performance and general combining ability (GCA) effects.
- To identify superior performing ChiLCV resistant hybrids on the basis of expressed heterosis and specific combining ability (SCA) effects.
- To study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and for ChiLCV resistance using generation mean analysis.

Review of Literature

2. REVIEW OF LITERATURE

The literature pertinent to the present investigation entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" has been reviewed under the following heads:

2.1 VIRUSES AFFECTING CHILLI

Chilli is known to be affected by more than 35 viruses (Green and Kim, 1991). Twenty-four viruses are reported to affect chilli naturally, among them 11 have been reported from India namely *Pepper vein bending virus*, *Pepper veinal mottle virus*, *Chilli leaf curl virus* (Senanayake *et al.*, 2006), *Cucumber mosaic virus*, *Tomato leaf curl New Delhi virus*, *Tobacco leaf curl virus*, *Indian chilli mosaic virus*, *Potato virus X*, *Potato virus Y* and *Tobacco ring spot virus*. Among all these viruses, the chilli leaf curl virus (ChiLCV) is the most destructive virus in terms of disease incidence and fruit yield loss. In severe conditions, 100 percent marketable fruits loss have been reported.

2.1.1 Chilli leaf curl virus

Begomoviruses infecting a large quantity of economically essential dicot plants worldwide, including India. The genus Begomovirus belongs to the family Geminiviridae vectored by the whitefly, *Bemisia tabaci* Gennadius. The Begomovirus members characterized by twin icosahedral particles (18 × 30 nm size) and the genome consist of one or two circular, ssDNA components (2.5-3.0 kb) known as DNA A and DNA B (Hanley-Bowdoin *et al.*, 1999; Navot *et al.*, 1991; Mayo and Pringle, 1998). In bipartite begomoviruses the two components DNA A and DNA B share highly conserved common region (200 nucleotides) called iterons and non-nucleotide stem-loop (TAATATTAC) (Moffat, 1997; Fauquet *et al.*, 2003).

Betasatellites or satellite molecules (~1.4 kb) are usually associated with monopartite Begomoviruses. These betasatellite assisted by the helper virus for its encapsidation, replication and cell-to-cell movement (Mansoor *et al.*, 2003; Saunders *et al.*, 2004; Briddon and Stanley, 2006).

Chilli leaf curl disease on chilli plant has been reported from India (Dhanraj and Seth, 1968; Raj *et al.*, 2005). A strain of *Chilli leaf curl virus-Pakistan* (ChiLCV-PK) was associated with chilli leaf curl disease. The partial DNA-A sequences analysis indicated that this strain was monopartite (Khan *et al.,* 2006; Senanayake *et al.,* 2006). Later, Chattopadhyay *et al.* (2008) sequenced and cloned complete virus and they found 95% sequence identity with ChiLCV-PK (*Chilli leaf curl virus-Pakistan*). The infectivity of this virus also demonstrated in the natural host. Meanwhile, *Tomato leaf curl Joydebpur virus*, reported from tomato in Bangladesh, was also found to be associated with Chilli leaf curl disease in Punjab (Shih *et al.,* 2007). Till date genome sequence of four begomoviruses infecting chilli have been characterized from India *viz., Chilli leaf curl virus* (ChiLCV), *Tomato leaf curl New Delhi virus* (ToLCNDV), *Tomato leaf curl Joydebpur virus* (ToLCJV) and recently *Chilli leaf curl Palampur virus* (ChiLCPV) (Khan *et al.,* 2006; Senanayake *et al.,* 2007, Kumar *et al.,* 2011).

2.1.2 Variability in begomoviruses

In chilli under natural infestation conditions 34 recognized and 18 tentative species of begomoviruses have been reported. Among them, *Tomato leaf curl virus* are the highly destructive ones. Tomato leaf curl disease (ToLCD) in tomato was caused by eight different viruses. Three of these viruses, *Tomato leaf curl India virus* (ToLCIV), *Tomato leaf curl New Delhi virus* (ToLCNDV) and *Tomato leaf curl Gujarat virus* (ToLCGV) were predominant in North India while the other three, *Tomato leaf curl Karnataka virus* (ToLCKV), *Tomato leaf curl Bangalore virus* (ToLCBV), and *Tomato leaf curl Vellanad virus* (ToLCVV) occur in southern India (Srivastava *et al.,* 1995; Padidam *et al.,* 1995; Kumar *et al.,* 2012). The chilli leaf curl disease is due to complex which consists of Chilli leaf curl virus (monopartite) and a DNA-β satellite (Chattopadhyay *et al.*, 2008). Menike and De costa (2017) identified two chilli leaf curl virus isolates (CL-14 and CL-15) based on DNA homology analysis. The identified isolates were more genetically closer to *Chilli leaf curl-Bhavansagar-India and Chilli leaf curl Salem virus-India.*

2.2 SYMPTOMATOLOGY

The diseases caused by begomoviruses are easily recognized by their distinctive symptoms in infected plants. The symptoms are broadly of three types: a) leaf curling, b) vein yellowing and c) yellow mosaic. Reduction in leaf size, vein clearing and leaf margin curling was reported in India, USA and Sri Lanka (Puttarudraiah, 1959). The typical symptoms consist of leaf curling, puckering, rolling, shortening of internodes and petioles, blistering of interveinous areas, thickening and swelling of the veins, older leaves turned out to be leathery and brittle, crowding of leaves and stunting of whole plants (Sinha *et al.,* 2011). The typical leaf curl symptoms and increase in disease severity in infected plants are due to the presence of cognate betasatellites associated with the virus (Kumar *et al.*, 2011; Kumar *et al.*, 2015).

2.3 SCREENING OF GENOTYPES AGAINST ChiLCV AND RESISTANT SOURCES

The success of disease resistance breeding depends on the genetic variability and the reliable evaluation tests employed for identification of the resistant sources. It is important to employ most reliable tests of resistance when dealing with destructive diseases like ChiLCV. Various methods have been employed to screen *Capsicum* germplasm for resistance to ChiLCV *viz.*, screening under natural epiphytotic conditions and artificial inoculation (grafting inoculation and white fly mediated inoculation). Breeding for ChiLCV resistance was started in late sixties in India and natural field screening was mostly used to identify resistance sources based on disease incidence and severity.

Mishra *et al.* (1963) conducted artificial screening by using viruliferous whiteflies under greenhouse conditions. Two chilli varieties namely Puri Red and Puri Orange showed resistant reaction to Chilli leaf curl virus. The resistance of these varieties was also confirmed by graft inoculation i.e. grafting the infected scions on the test plant rootstocks (Puri Red and Puri Orange).

Tewari and Ramanujam (1974) developed a chilli variety Pusa Jwala, which was resistant to viruses, followed by two other resistant varieties Pant C 1 and Pant C 2 developed by Mathai *et al.* (1977). Tewari and Viswanath (1986) identified a selection named Jwala, which was found resistant to Chilli leaf curl disease and this selection was derived from a cross NP46 A × Puri Red. The lines from *C. annuum* L. S38.3.19, S42.2.4 were tolerant to leaf curl disease, PVX and CMV. The genotype Delhi Local was tolerant to leaf curl disease and TMV, also showed immune reaction to CMV and PVX (Tewari and Viswanath, 1986). The varieties namely JCA-218, JCA-248, JCA-196, NP-46, Pant C-1 and Pusa Jawala were showed resistant reaction for chilli leaf curl disease (Sanger *et al.*, 1988).

Punjab Agricultural University (PAU), Ludhiana has developed few multiple disease resistant varieties in chilli. Some of multiple virus resistant lines are Perennial, Punjab Lal, Lorai and BG-1 (Singh and Singh, 1989). These sources were used as base materials to develop high yielding hybrids (CH-1 and CH-3) with tolerance to leaf curl disease (Hundal, 1999). Recently, Dhaliwal *et al.* (2015) developed multiple disease resistant hybrid CH-27 from PAU by using nuclear male sterility. This hybrid has resistance to leaf curl virus, fruit rot, root knot nematode and sucking pests (thrips and mites).

The lines EC 7299, ED 7338, EC 6589, EC 4020, EC 9293, Puri Red and Puri Orange showed field resistance to leaf curl virus (Singh, 1973). The capsicum species *C. annuum var. angulosumn* showed tolerant reaction to leaf curl virus and CMV (Singh and Singh, 1989). Kumar *et al.* (1999) screened 37 chilli genotypes for leaf curl virus and observed that three genotypes Surya Mukhi, Loungi and Pusa Jwala showed resistant reaction. Ilyas and Khan (1996) screened 159 genotypes against leaf curl disease. Five genotypes namely LCA-135, LCA-412, Pant C-1, Cfr-10 and Puri red showed resistant or tolerant reaction to mosaic complex.

The Capsicum species, *C. frutescens* (IC 31339) and *C. angulosum* were tolerant to chilli leaf curl virus (Konai and Nariani, 1980). The variety Punjab Lal selection from Perennial × Long Red was resistant to leaf curl virus

(Singh and Kaur, 1986). In AVRDC (AVRDC, 1990) 291 *C. annuum* L. germplasm lines were screened for resistance against *Cucumber mosaic cucumovirus* (CMV) from Taiwan, *Pepper vein mottle virus* (PVMV) from England and *Chilli vein mottle virus* (CVMV) from Taiwan and Japan by using artificial inoculation method. The resistant lines were Szechuan, HAD 836 and VC 16 to PVMV; VC 41, VC 37, VC 40, VC 36 and VC 35 to CVMV; and Kunja Kea Ryong San to CMV. Albejo (1999) screened 34 pepper genotypes and found that PCBO 67 showed moderately resistant reaction. Phule Sai (GCH-8) a rainfed chilli variety was moderately resistant to leaf curl virus under field conditions (Jadhav *et al.,* 2000)

Thirty-seven chilli genotypes were screened against leaf curl virus under natural field conditions in Kerala (Jose and Khader, 2003). Eight genotypes were tolerant namely Kotti Kulam, Mangalapuram local, Chandera local, Pant C-1, Kottiyan local, Haripuram local, Neayattinkara local and Alampady local-1, twenty seven and two genotypes showed susceptible and highly susceptible reaction to the disease.

Kumar *et al.* (2006) screened 307 genotypes of chilli and sweet pepper against ChiLCV under field conditions. On the basis of CI (Coefficient of Infection) 49 genotypes were highly resistant, 40 were resistant and 19 were symptomless. Further, they selected five symptomless and three highly resistant genotypes from field screening and challenged with viruliferous white flies under glasshouse conditions. Genotypes *viz.,* GCK-29, EC-497636 and BS-35 were symptom-less under artificial whitefly mediated inoculation. The resistance reaction of these three genotypes was confirmed by graft inoculation. The viral symptoms did not observe on test plant after grafting on Pusa Jwala (susceptible rootstock).

Kumar *et al.* (2009) screened 321 chilli genotypes under field conditions in IIVR. Four genotypes *viz.,* CM-334, CV-1, Kalyanpur Chanchal and VR-339 exhibited highly tolerant reaction and two genotypes CV-2 and Punjab Lal were symptomless. These four resistant and two symptomless genotypes were subjected to artificial micro cage inoculation by using viruliferous white flies. These lines were

resistant (up to 10 days of inoculation) and the severity of the disease progressed slowly and the complete symptom appeared 18 day after inoculation, indicating highly susceptible reaction.

To identify true sources of resistance against *Pepper leaf curl virus* (PepLCV), Rai *et al.* (2014) adopted advanced microcage or individual plant cage inoculation technique and screened 22 chilli genotypes. After 7 days of inoculation, eight genotypes namely C00309, C00304, NMCA-40008, BS-35, GKC-29, IC-383072, Bhut Jolokia and Lankamura Collection were symptomless. Bhut Jolokia is considered as new source of resistance.

Sixty germplasm lines of *Capsicum annuum* L., one each of *C. chinense*, *C. chacoense* and *C. baccatum* and two of *C. frutescens* were screened against leaf curl disease under natural field conditions during summer in IARI, New Delhi (Srivastava *et al.,* 2017). Based on disease incidence and severity, none of the lines were found to be free from disease, 47 lines showed susceptible reaction, 5 showed moderate susceptible reaction and 12 genotypes were highly resistant and resistant. To identify the durability of the identified resistant lines, three more consecutive natural screening were carried out. Pusa Jwala (susceptible line) was used as an infector row at regular intervals in the field to confirm the disease severity. By the end of fourth season of natural screening they found three resistant lines *viz.,* PBC-142, WBC-Sel-5 and DLS-Sel-10.

2.4 MOLECULAR DETECTION OF GEMINIVIRUS USING DEGENERATE PRIMER

Polymerase chain reaction (PCR) is now widely followed because of smooth application, rapid, sensitivity, specificity for identification and detection of begomoviruses in epidemiological and disease management studies with minimal sample preparation.

In all begomoviruses genomes, a region with high homology is present. Universal degenerate primers are designed to anneal to these regions (Rojas *et al.,* 1993; Deng *et al.,* 1994; Wyatt and Brown, 1996). These universal primers are

identical primers with base change in one or more places. They act as universal degenerate primers which amplifies a DNA base in all begomoviruses. Nakhla *et al.* (1994), Ramos *et al.* (1996) and Martino *et al.* (1993) used PCR for confirming virus presence in the sample by using different primers.

In viral genome, universal (general) primers are used for amplification of general part. Specific (Oligonucleotide) primers which anneal to either V1 and or C1 are used for specific amplification of desired sequence in TYLCV genome. (Nakhla *et al.*, 1994). Therefore, both degenerate and specific primers can be utilize for identification and characterization of chilli infecting begomoviruses.

Detection and molecular characterization of *begomovirus* infecting tomato was studied by Gaikwad *et al.* (2011). The DNA samples from infected plants were tested for the presence of begomovirus using two universal degenerate primers (Deng *et al.*, 1994; Wyatt and Brown, 1996). Out of forty-two samples tested, twenty samples showed positive for *begomovirus.* These positive samples were subjected to begomovirus species specific primers. *Tomato leaf curl Palampur virus* (ToLCPMV) was predominant in 18 samples followed by *Tomato leaf curl New Delhi virus* (ToLCNDV) in 11 samples. In nine samples, mixed infection of ToLCNDV and ToLCPMV was found.

2.5 MEAN PERFORMANCE OF CHILLI GENOTYPES

2.5.1 Vegetative characters

Legesse *et al.* (2000) identified parental line PBC 972 with highest plant height of 56.80 cm followed by Mareko Fana (49.10 cm) and PBC 634 (50.70 cm). These lines also exhibited high GCA effects for plant height. The *per se* performance of plant height varied from 55.72 cm in the genotype Chickballapur to 33.10 in the genotype X-235 (Lohithaswa *et al.*, 2000). Rodrigues *et al.* (2012) observed the highest plant height in the parent UENF 1639 (71.82 cm) followed by UENF 1732 (68.20 cm). The superior performance for plant height was recorded in the line 38 and line 58 with 134.66 cm and 118.66 cm, respectively (do Rego *et al.*, 2009). The male parent, CA 683 (80.89 cm) and the female parent, CA 1445 (69.33 cm) showed

highest mean performance for plant height (Payakhapaab *et al.*, 2012). Singh *et al.* (2014) identified the parental line CC 141 with maximum plant height of 92.03 cm followed by SL 462 (80.40 cm) and VR 521 (79.67 cm). Bhutia *et al.* (2015) observed the range of plant height among the parents from 26.67 cm in the parent Kashi Anmol to 71.67 cm in the parent BCC-1. Marame *et al.* (2009a) observed the range of plant height from 31.63 to 62.07 cm with the overall mean of 43.83 cm.

Rohini *et al.* (2017) reported that the parent Pusa Jwala produced highest branches plant^{-1} of 9.38 followed by LCA 625 (8.95). The hybrid Arka Lohit × LCA 334 produced maximum number of branches plant^{-1} followed by the hybrid PKM 1 × Pusa Jwala (10.00). Prasath and Ponnuswami (2008) observed the overall mean of 109.12 cm for plant height in F_1 hybrids. The *per se* performance of the F_1 hybrids ranged from 75.40 to 149.35 cm for plant height. Bhutia *et al.* (2015) reported maximum number of primary branches plant^{-1} in the parent Chaitali (11.67) followed by BCC 1 (9.33) and AC-575 (9.00). Number of branches plant^{-1} varied from 3.00 to 7.75 cm with the overall mean of 4.89 cm (Marame *et al.*, 2009b).

2.5.2 Flowering characters

Geleta and Labuschagne (2006) reported early flowering in the parents, Kalocsai 'M' Cseresznye and Szegedi. Among hybrids, C00916 × Pepper 1976 was early to flower. The parental line DL 161 took 32.40 days to flower after transplanting followed by PS 403 (34.23), SD 463 (36.67) and SL 461 (36.37). The parental line CC 141 (50.23) took maximum days for flowering. The hybrids took 29.87 to 47.73 days with the overall mean of 37.51 days for early flowering (Singh *et al.*, 2014). Days to first flowering among hybrids ranges from 60.20 to 70.50 with the mean of 65.40 days (Prasath and Ponnuswami, 2008). In parents the range from 57.67 to 63.00 was observed for days to 50% flowering (Bhutia *et al.*, 2015).

Days to green fruit maturity among parents ranges from 33.17 in the parent CCA 5 to 41.37 in the parent CCA 11 (Hasanuzzaman *et al.*, 2012). The parent

AC-575 was early to 50% fruiting (102.67 days) followed by Chaitali (107.67 days) and BCCH Sel-4 (108.00 days) (Bhutia *et al.*, 2015).

5.2.3 Fruit and yield characters

Bhutia *et al.* (2015) observed the range of fruit length from 3.49 cm in the parent BCC-1 to 8.80 cm in AC-575. Butcher *et al.* (2013) reported the highest fruit length in the parent Pap2 (188.80 mm) followed by PapP30 (188.33). Naresh *et al.* (2016) observed the range of fruit length from 6.05 cm (IHR 500) to 11.92 cm (IHR 3849) in parents. In hybrids the range varied from 6.32 cm (IHR 450 × IHR 2451) to 14.20 cm (IHR 4507 × IHR 3476). Marame *et al.* (2009) observed the range of fruit length from 6.35 to 12.32 cm with the overall mean of 9.79 cm. The longest fruits were produced by the parent CCA 11 (9.35 cm) followed by CCA 15 (7.53 cm) and CCA 19 (7.40 cm) (Hasanuzzaman *et al.*, 2012). For fruit length, the superior performance was observed in three parents namely UENF 1616 (105.80 cm), UENF 1629 (91.74 cm) and UENF 1624 (82.20 cm) (Rodrigues *et al.*, 2012). Payakhapaab *et al.* (2012) observed maximum fruit length in the male parent CA 1448 (19.26 cm) and female parent CA 1450 (15.38 cm). The length of fruits in parents varied from 4.41 to 7.60 cm with overall mean of 6.04 cm whereas that of hybrids from 5.44 to 9.87 cm with overall mean of 7.40 cm (Singh *et al.*, 2014). In hybrids, Prasath and Ponnuswami (2008) observed the range from 3.08 to 6.87 cm with mean of 4.98 for fruit length. Fruit length among the parents varied from 2.3 cm (C00916) to 13.2 cm (Bakko Local), among hybrids it varied from 3.7 cm (Kalocsai 'M' Cseresznye × C00916) to 14.1 cm (Szegedi × Bakko Local) (Geleta and Labuschagne, 2006).

Geleta and Labuschagne (2006) observed the range of fruit diameter from 0.8 cm (PBC 142A) to 8.1 cm (Pepper 1976). In hybrids, it varied from 1.4 cm (Mareko Shole × PBC 142A) to 6.2 cm (Kalocsai 'M' Cseresznye × Pepper 1976). Hasanuzzaman *et al.* (2012) observed the range of fruit width from 7.45 mm (CCA 15) to 11.39 mm (CCA 11) in parents. Rodrigues *et al.* (2012) reported the range of fruit diameter from 18.73 cm (UENF 1624) to 48.66 cm (UENF 1639). Among hybrids, the fruit diameter ranged from 24.42 mm (UENF 1616 × UENF 1624) to

51.47 mm (UENF 1732 × UENF 1639). The male parent CA 1448 (3.20 cm) and the female parent CA 1450 (3.26 cm) produced maximum fruit width (Payakhapaab *et al.*, 2012). Among parental lines, the highest fruit width was observed in the parent US 501 (1.44 cm) while the lowest was in PA 401 (0.91 cm). Fruit width of hybrids varied from 0.85 to 1.43 cm, with average of 1.18 cm (Singh *et al.*, 2014). The fruit width of parents varied from 0.89 cm (Chaitali) to 1.49 cm (BCC-1) (Bhutia *et al.*, 2015). Prasath and Ponnuswami (2008) observed the fruit girth from 6.23 to 21.82 cm with mean of 11.10 cm in parents.

The fruit weight of the parents varied from 1.74 g in the parent 56 to 25.22 g in the parent 24 (do Rego *et al.*, 2009). Maximum fruit weight was recorded in the parent CA 1447 (47.50 g) to CA 683 (16.53 g) (Payakhapaab *et al.*, 2012). The fruit weight of parents and F_1 hybrids ranged from 2.35-5.61 g and 2.43-6.70 g with an average of 3.54 and 4.13 g, respectively (Singh *et al.*, 2014). The highest mean value of 19.18 g was obtained in the parent SP 128 for fruit weight (Butcher *et al.*, 2013). The fruit weight of hybrids varied from 71.50 g in the hybrid Kalocsai 'M' Cseresznye × Pepper 1976 to 6.40 g in the hybrid Kalocsai 'M' Cseresznye × PBC 142A (Geleta and Labuschagne, 2006). In parental genotypes, minimum fruit weight was recorded by CCA 15 (1.78 g) while the maximum by CCA 11 (5.95 g) (Hasanuzzaman *et al.*, 2012). The fruit weight of parental lines and hybrids varied from 9.36 g (UENF 1624) to 28.06 g (UENF 1629) and 12.85 g (UENF 1624 × UENF 1639) to 25.76 g (UENF 1624 × UENF 1639), respectively (Rodrigues *et al.*, 2012).

The fruits plant^{-1} of hybrids varied from 7 (Kalocsai 'M' Cseresznye × Pepper 1976) to 71 (C00916 × PBC 142A) whereas that of parents from 4 (Pepper 1976) to 153 (PBC 142A) (Geleta and Labuschagne, 2006). The number of fruits plant^{-1} varied from 75 (CCA 11) to 179.96 (CCA 15) (Hasanuzzaman *et al.*, 2012). Rodrigues *et al.* (2012) observed the range of number of fruit plant^{-1} from 37.64-75.52 in parents and 44.54-108.90 among hybrids. The fruits plant^{-1} in parents and hybrids ranged from 80.08-104.75 and 98.50-173.80, respectively

(Rohini *et al.*, 2017). The number of fruits produced by the hybrids and parents varied from 41.51-327.87 and 31.22-234.69, with an average of 201.14 and 124.30, respectively (Singh *et al.*, 2014). The parent CA 1445 produced maximum number of fruits plant^{-1} (28.33) followed by CA 683 (26.82) (Payakhapaab *et al.*, 2012). Number of fruits plant^{-1} varied from 47.33 in the parent BCC-1 to 114.67 in the parent BCCH Sel-4 (Bhutia *et al.*, 2015).

The fruit yield of parents varied from 117.13 to 570.33 g plant^{-1} with mean of 373.34 g plant^{-1}) whereas that of hybrids from 160.73 to 1095.80 g plant^{-1} with mean of 697.90 g plant^{-1}) (Singh *et al.*, 2014). Fruit weight plant^{-1} varied from 0.41-0.71 kg plant^{-1} and 0.53-1.06 kg plant^{-1} in parents and hybrids, respectively (Payakhapaab *et al.*, 2012). The maximum yield plant^{-1} was observed in the parent BCCH Sel-4 (277.97 g) whereas minimum was in Kashi Anmol (140.80) (Bhutia *et al.*, 2015). Geleta and Labuschagne (2006) observed the range of fruit yield from 129.60-423.70 g in parents and in hybrids from 123.40 to 538.80 g. Hasanuzzaman *et al.* (2012) reported the range of fruit yield from 189.60 g (CCA 5) to 373.30 g (CCA 19) in parental lines. The parent CA 1450 and the hybrid CA 1450 × CA 1448 produced maximum yield (Payakhapaab *et al.*, 2012).

5.2.4 Quality characters

The vitamin C content of parents varied from 79.54 to 123.41 mg/100 g whereas that of hybrids from 85.70 to 158.39 mg/100 g (Rohini *et al.*, 2017). The highest ascorbic acid content (µg g^{-1} fruit weight) was observed in the genotype Pap5 (2078.36) followed by PapP26 (1781.36), SP2 (1599.78), PapP30 (1420.81) and S48 (1492.87) (Butcher *et al.*, 2013). Bhutia *et al.* (2015) observed the parent BCC-1 with highest vitamin C content of 211.47 mg 100 g^{-1} followed by BCCH Sel-4 (129.97 mg 100 g^{-1}) and Chaitali (112.33 mg 100 g^{-1}).

The total carotenoids content (mg/100g) of the parents varied from 80.42 (IHR 3453) to 287.61 (IHR 4506) whereas that of hybrids from 79.70 (IHR 4506 × IHR 2451) to 276.31 (IHR 3476 × IHR 500) (Naresh *et al.*, 2016). The total carotenoids content of lines varied from 115.86 (LCA 615) to 419.90 mg/100 g

(LCA 355) whereas that of testers from 200.62 (LCA 315) to 250.66 mg/100 g (LCA 678). The hybrids recorded a range of 186.49 (LCA 607 × G4) to 397.32 mg/100 g (LCA 466 × LCA 453) (Maradana, 2016).

2.6 COMBINING ABILITY

The GCA variance magnitude was higher than SCA variance for fruit weight, fruit girth, yield plant^{-1} and fruits plant^{-1} suggested the involvement of additive gene effects in governing these traits (Gopalakrishnan *et al.,* 1987).

Bhagyalakshmi *et al.* (1991) observed that parents LCA 960, LCA 206 and G 4 with high GCA effects for yield attributes. The crosses LCA 206 × LCA 960 and LCA 1079 × G 4 exhibited significant negative SCA effects for fruit maturity.

The genotypes Pant C-1, PMR-52/88/K and RHRC-Cluster-Erect exhibited significant GCA effects for resistance to leaf curl complex. The magnitude of dominant variance was more than additive variance indicating the predominance of non-additive gene effects for resistance to chilli leaf curl complex (Nandadevi and Hosamani, 2003).

In a line × tester analysis Singh and Chaudhary (2005) evaluated seven parents (four lines and three testers) and their 12 F_1 hybrids to study the general and specific combining ability. Based on mean performance and GCA, the parent RHRC-CE was the best tester for yield attributes followed by IC-119797, EC-321437 and Punjab Lal. Based on *per se* performance and specific combining ability effects, the hybrids EC-321437 × RHRC-CE and IC-119367 × Punjab Lal were considered as good specific combiners for yield and its attributes.

Thirty cross combinations were developed by using six genetically diverse parental lines by Prasath and Ponnuswami (2008). The magnitude of GCA variances for vegetative, yield related traits was higher in all the crosses suggesting preponderance of additive gene action than non-additive. Based on GCA effects, parents Byadagi Kaddi and MDUY showed high GCA effects for yield traits and Arka Abhir for quality traits. Hybrids MDUY × Co 4 and MDUY × Arka Abhir showed desirable SCA effects for yield and quality traits.

Singh and Pan (2009) estimated combining ability using nine parents and their 36 F_1 hybrids. The GCA variance magnitude was greater than SCA variance, showing the involvement of additive component for days to flowering, fruit length, fruit width and number of fruits. The trait fruit yield (green) was governed by non-additive gene effects. Parents HC-7 for days to first flower, fruit width, fruit length and fruit weight, HC-51 for days to first flower, fruits number and green fruit yield were best general combiners. The cross combinations *viz.,* HC-5 1 × HC-34, HC-8 × HC-37 and HC-7 × HC-51 were the good specific combiners for fruit yield (green) and yield attributing traits.

Hasanuzzaman *et al.* (2012) reported the predominance of non-additive gene effect for all the studied traits indicated the exploitation of hybrid vigor. The parent CCA-5 showed high significant positive GCA effects for fruits plant^{-1} and yield plant^{-1}. It showed negative significant GCA effects for days to maturity which indicates early fruit maturity. Parental line CCA-19 and BARI Morich-1 showed high GCA effects for fruits plant^{-1} and yield plant^{-1}. The hybrid BARI Morich-1 × CCA-19 showed maximum significant positive SCA effects for yield plant^{-1} and it showed significant SCA effects for days to 50 per cent flowering, days to fruit maturity and fruit weight. The crosses CCA-5 × BARI Morich-1, CCA-5 × CCA-19, BARI Morich-1 × CCA-11 and CCA-11 × CCA-19 exhibited negatively significant SCA effects for days to 50 per cent flowering. Based on *per se* performance and SCA effects of hybrids BARI Morich-1 × CCA-19 and CCA-5 × BARI Morich-1 were considered as best. Parents BARI Morich-1, CCA-5 and CCA-19 were identified with high GCA effects.

Studies were conducted by Rodrigues *et al.* (2012) to estimate combining ability effects for agronomic and yield traits in chilli. The additive effects were involved on the control of plant height and mean fruit weight. Both additive and non-additive gene actions were operating in genetic control of days to fruiting, fruit length, fruit diameter, fruits plant^{-1} and yield plant^{-1}.

Chaudhary *et al.* (2013) reported the preponderance of non-additive gene action for all the traits studied except for yield per plant. The parents Pant C-1 and DC-16 were identified with high GCA effects for fruits plant^{-1}; VR-339, Kashi Sinduri and R-line for yield plant^{-1}. The cross Pant C-1 × VR-339, Kashi Sinduri × R-line and Pant C-1 × DC-16 exhibited high SCA effects for fruits plant^{-1}. Kashi Sinduri × R-line, Pusa Jwala × VR-339 and Pant C-1 × VR-339 showed high SCA for fruit weight.

Nsabiyera *et al.* (2013) revealed the predominance of non-additive gene effects for primary branches, plant height, days to 50 % flowering, fruit maturity and number of fruits. Additive gene effects were governed in the trait fruit length and fruit width. Genotypes PP9852-115, CA-UGK109-6, CA-UGK109-4 and CA-UGCE 09-3 were considered as promising general combiners. Hybrids CA-UGCE 09-3 × CA-UGKI 09-6, CA-UGKI09-6 × PP9852-115 and CA-UGCE 09-3 × PP9852-115 were the best specific combiners.

Navhale *et al.* (2014) conducted combining ability analysis by using seven parents and 42 F_1 hybrids (including reciprocals) for yield and yield attributing traits. Estimated GCA effects indicated that parent BC-28 had high GCA effects for red and green fruit yield; parent Jayanti and Konkan Kirti for fruit yield (red); and Jwala and Sel-2 for fruit yield (green). In reciprocal crosses, good specific combiners for fruit yield plant^{-1} (green) were Sel-2 × DPL-C-4, Jwala x BC-28 and Sel-2 × Konkan kirti.

do Nascimento *et al.* (2014) estimated GCA and SCA using six pepper germplasm lines; namely, UFPB 77.1, UFPB 132, UFPB 134, UFPB 77.2, UFPB 01 and UFPB 137 and their 30 F_1 hybrids, using diallel crossing system. The additive gene action is predominant in fruit length and diameter, fruit weight and vitamin C. The SCA variance magnitude was higher than GCA for all yield characteristics suggesting the involvement of non-additive gene effects, epistasis and or dominance. Estimation of GCA showed that genitors 132, 137, 77.2 and 01 had maximum GCA effects for yield and quality traits. The families namely 01 × 132, 77.2 × 137, 134 ×

77.2, 137 × 77.1, 77.1 × 01, 132 × 134 and 137 × 134 had significant SCA effects and were proceeded further for pepper breeding program with the goal of increasing fruit yield and high nutritional values.

Bhutia *et al.* (2015) crossed five genetically diverse parents in a diallel fashion to produce 10 F_1 hybrids. These hybrids were evaluated under leaf curl disease severity condition for 14 quantitative characters. The analysis of variance for combining ability revealed that mean squares due to component of GCA and SCA were highly significant for fruit yield components, fruit quality traits and leaf curl disease severity which indicated that inheritance of these traits were due to both additive and non-additive gene effects. For days to 50 per cent fruiting and fruits plant^{-1} additive gene effects were predominant. For plant height both additive and non-additive gene actions were observed. The non-additive genetic control was observed for traits viz., primary branches, days to 50 per cent flowering, fruit girth, fruit length, vitamin C, fruit yield and PDI of leaf curl virus. Two parents BCCH Sel-4 and Chaitali exhibited significant GCA effects in desirable direction for yield and quality traits and PDI of leaf curl virus. Therefore, these lines were considered as good general combiners. The cross combination BCCH Sel-4 × AC-575 showed maximum significant SCA effects for fruit yield, fruits plant^{-1}, Vitamin C and PDI for leaf curl virus in desirable direction. The hybrid BCCH Sel-4 × Chaitali exhibited significant SCA effects in desirable direction for vitamin C and PDI of leaf curl virus. The hybrid combination BCCH Sel-4 × AC-575 had maximum mean performance for fruit yield with significant SCA effects in desirable direction for horticultural traits and PDI for leaf curl virus. Therefore, this cross combination was considered as promising hybrids for certain important characters.

Kaur *et al.* (2017) observed the ratio of SCA/GCA variances with more than unity for plant height, days to flowering, fruit width, fruit length, fruit yield and early fruit yield suggesting the preponderance of non-additive gene effects. The ratio was less than one for fruit weight suggesting the predominance of additive gene action. Among parents, DL-161, MS-341, VR-521 and SL-462 identified with high GCA

effects for days to first flowering; the parent SD-463 for early and total yield; and the parent SL-461 had high GCA effects for fruit weight. The cross combinations MS-341 × DL-161 and DL-161 × SD-463 were found to be good specific combiners for early yield and total yield. These hybrids involved both the parents with positive and significant GCA effects indicating the scope of obtaining transgressive segregants with early yield and total fruit yield from these crosses

Darshan *et al.* (2017) evaluated diallel bred 30 F_1 crosses of chilli along with their parents under leaf curl disease severity conditions in Vellayani, Kerala. The non-additive gene action was predominant all the studied characters. The estimates of GCA effects revealed that the parent Pusa Sadabahar showed significant GCA effects in desirable direction for fruit yield traits and for incidence of leaf curl virus disease. The cross Vellayani Athulya × Pusa Sadabahar showed high SCA for fruit weight and yield per plot; and the cross Ujwala × Vellayani Athulya had significant and negative SCA effects for leaf curl virus disease incidence.

Rohini *et al.* (2017) observed predominance of non-additive genetic components for five quantitative and five qualitative characters in chilli. Among the parents, PKM-1, LCA-625 and K-1 were the best general combiners for most of the studied traits. The best specific combiners based on SCA effects were Pusa Jwala × PKM-1, K-1 × Arka Lohit and LCA625 × K-1 for yield components. Based on mean performance and combining ability the hybrid K-1 × Arka Lohit was considered as superior reciprocal combiner for quality traits.

Ganefianti *et al.* (2018) estimated GCA and SCA effects using seven parental lines and their 42 F_1 hybrids developed through full diallel cross. Parents G (KD-7), B (KG-2) and D (KD-4) were had high GCA effects for fruit diameter; the parent C (KG-3) for fruit length and fruit weight; and the parent F (KG-6) for fruits plant^{-1}. Cross C (KG-3) × F (KG-6) proved good combiner for fruit weight and fruits plant^{-1}; and crosses G (KG-7) × C (KG-3) and D (KG-4) × G (KG-7) for fruit length and fruit diameter.

Shumbulo *et al.* (2018) studied the gene effects and combining ability in 45 F_1 hybrids obtained from a 10 parent half-diallel cross. The additive gene action was predominant for plant height, fruit length, fruit diameter, fruit number per plant and fresh fruit yield. Among the parents, Marekofana and AVPP0514 were the best general combiners for fresh fruit yield and fruit dry weight. Among the crosses, Melkaawaze × AVPP0206, AVPP9813 × AVPP0105, Marekofana × AVPP0514 and AVPP0514 × AVPP59328 were the most promising combiners for yield and quality traits.

Singh *et al.* (2014) conducted combining ability analysis by using GMS and CGMS lines. Additive variance was important for days to flowering, fruit length, fruit width, fruit weight. Non-additive gene effects were prevalent for the trait yield plant^{-1} and plant spread. MS 341 (GMS line) had high GCA effects for fruit length, fruits plant^{-1} and early yield. The parent CC 141 (CGMS line) was good general combiner for plant spread, plant height and fruit length. The line DL 161 had high GCA effects for days to flowering and fruits plant^{-1}, SL 461 for fruit length and yield plant^{-1}, PP 402 for early yield and fruit width and SD 463 for fruit weight and pericarp thickness. The parental mean performance and general combining ability are in consonance. The highest significant positive SCA effects were showed by MS 341 × PP 402 for plant height, SD 463 × PS 403 for plant spread, EL 181 × PA 401 for fruit width and pericarp thickness, PP 402 × PS 403 for fruit weight, CC 141 × VR 521 for yield plant^{-1}.

2.7 HETEROSIS BREEDING

Heterosis is defined as "the interpretation of increased or decreased size, vigor, speed of development, fruitfulness, resistance to biotic and abiotic stresses of any kind manifested by crossbred organisms as compared with corresponding inbreds, as the specific results of unlikeness in the constitution of the uniting parental gametes" (Shull, 1908; East, 1936; Hayes, 1952).

The term 'heterosis' used when F_1 hybrid is superior or inferior to both of the parents, other phenomenon regarded as dominance or partial dominance (Powers,

1944). Extensive work on different aspects of heterosis in chilli has been carried out in recent past. However, most of these studies have been focussed in the main crop season when leaf curl virus is not a serious threat to the crop. Contrary to this, not much effort has been made to study heterosis involving leaf curl virus resistant lines and their suitability for cultivation in disease infestation conditions. The literature pertaining to heterosis in chilli has been reviewed here as under.

Geleta and Labuschagne (2004) reported that the mean values of mid-parent and standard heterosis were positive and significant for fruit diameter, plant height, fruit weight, fruits plant^{-1} and fruit yield. The magnitude of high positive heterobeltiosis was observed in plant height and yield plant^{-1}. For yield plant^{-1}, 12 hybrids showed standard heterosis, which varied from 28.00 to 68.80% and the highest standard heterosis was exhibited by the crosses Szegedi-178 × Pepper 1976, Bakko Local × Pepper 1976 and Bakko Local × Mareko Shote. The highest positive heterobeltiosis was observed in the hybrid IR × MI-2 for fruits plant^{-1} (22.59%) and total yield (113.24%) (Millawithanachchi *et al.*, 2006).

Payakhapaab *et al.* (2012) crossed three maintainers with three restorers in a testcross method to produce nine F_1 hybrids. The hybrid CA1450 × CA1447 showed better parent heterosis for average fruit weight and number of fruits plant^{-1}, 7.72% and 2.27%, respectively. The hybrid CA1450 × CA1448 showed better parent heterosis for fruits plant^{-1} and fruit weight, 6.59 and 49.25%, respectively.

Prasath and Ponnuswami (2008) evaluated 36 genotypes including six parents and their 30 F_1 hybrids. The percent of heterobeltiosis ranged from -40.35 to 126.32% for the trait dry yield ha^{-1}. Two hybrids namely Byadagi Kaddi × Arka Abir and MDU Y × Co-4 were found promising for total extractable colour, low capsaicin and also for dry yield and contributing traits.

Marame *et al.* (2009b) found the highest magnitude of standard heterosis in the cross PBC 223 × Marekoshote for number of fruits plant^{-1} (136.36%) and fruit yield plant^{-1} (92.05%). The highest magnitude of better parent heterosis was displayed by the cross PBC 223 × Marekofana for branches plant^{-1} (55.63%) and

fruit weight (50.29%), PBC 223 × Bakolocal (26.59%) for fruit length, PBC 602 × ICPN9 16 (163.80%) for yield plant^{-1} and ICPN10 5 × Bakolocal (79.61%) for fruits plant^{-1}.

To estimate heterosis and combining ability, Perez-Grajales *et al.* (2009) evaluated 15 hybrids and their six parental lines of manzano hot pepper (*Capsicum pubescens* R & P). The highest magnitude of heterobeltiosis of 51.00% was found in the hybrid Zongolica × Pueble for fruit yield.

The magnitude of highest better parent heterosis was recorded in the cross IPB C2 × IPB C15 (25.60%) for fruit weight plant^{-1} and in the cross IPB C8 × IPB C15 (63.00%) for fruits plant^{-1} (Sitaresmi *et al.,* 2010). The heterotic response of 23 single cross F_1 hybrids were studied by Shrestha *et al.* (2011). The maximum positive heterobeltiosis was showed by the cross 5AVS7 × SP32 (87.20%) and SP12 × SP38 (119.30%) for fruit number and fruit yield, respectively. The maximum positive standard heterosis for fruit yield was exhibited by the hybrids 5AVS7 × SP45, 5AVS7 × SP32, and 5AVS8 × SP48

Twenty-nine paprika and serrano pepper (*Capsicum annuum* L.) hybrids along with their 19 parents were evaluated by Butcher *et al.* (2013). The highest relative heterosis was displayed by the cross SP16 × SP57 (1289.23%) for capsaicin and the cross SP16 × SP15 (902.32%) for total capsaicinoid. The magnitude of better parent heterosis was exhibited by the cross SP41 × SP95 (75.91%) for ascorbic acid, SP15 × SP128 (24.49%) for fruit length, PapP27 × PapP67 (16.99%) for fruit diameter, SP15 × SP5 (64.96%) for fruit weight, SP16 × SP15 for capsaicin (814.95%) and total capsaicinoid (604.81%).

Chaudhary *et al.* (2013) reported the highest better parent heterosis of 161.55% in the cross Pusa Jwala × DC-16 for fruits plant^{-1}. Three hybrids namely Pant C-1 × VR-339 (239.00%), Pusa Jwala × VR-339 (220.53%) and Pusa Jwala × DC-16 (205.53%) sowed high percent of heterobeltiosis for yield plant^{-1}.

Krishnamurthy *et al.* (2013) crossed five lines with 30 testers in line × tester mating design to develop 150 F_1 hybrids and they estimated the extent of mid-parent

heterosis. For fruit yield plant^{-1} (green) seven hybrids namely CMS 8A × LCA 273, CMS 8A × Arka Suphal, CMS 2A × LAM 333, CMS 2A × CA 9, CMS 8A × Tiwari, CMS 8A × Pusa Sadabahar and CMS 8A × Vangara showed positive and significant mid-parent heterosis.

Singh *et al.* (2014) produced 66 chilli F_1 hybrids by crossing 12 genetically diverse inbred lines in a half diallel fashion. The magnitude of better parent heterosis varied from -3.11 to 32.21% for plant height, -13.77 to 20.66% for plant spread, -35.77 to -5.00% for days to flowering, -5.13 to 39.64% for fruit length, -20.60 to 10.41% for fruit width, -28.65 to 57.52 % for average fruit weight, and -71.82 to 331.11% for fruit yield plant^{-1}.

Ten F_1 hybrids were produced by crossing five genetically diverse lines in diallel mating design and these hybrids were evaluated for 14 quantitative characters. The extent of heterosis over better parent varied from -39.54 to 2.08% for plant height, -46.41 to 20.05% for primary branches, -64.66 to 6.14% for fruit length, -37.88 to 4.49% for fruit girth, -44.77 to 0.29% for fruits plant^{-1}, -69.44 to 28.93% for Vitamin C, -58.23 to 36.17% for beta-carotene, -49.45 to 71.06% for yield plant^{-1} and 157.51 to -47.61% for PDI (Percent disease index) of leaf curl virus. For yield plant^{-1} and other economic characters maximum better parent heterosis and relative heterosis was exhibited by BCCH Sel-4 × AC-575 followed by AC-575 × Chaitali (Bhutia *et al.,* 2015).

Naresh *et al.* (2016) produced 45 hybrids by crossing 10 lines in half-diallel fashion. The maximum heterosis over better parent and standard heterosis, respectively was exhibited in the cross IIHR 3453 × IHR 4507 (31.36%) and IHR 4507 × IHR 3476 (33.33%) for fruit length, IHR 3849 × IHR 2451 (15.84%) and IHR 4507 × IHR 3476 (165.00%) for fruit width.

Kaur *et al.* (2017) estimated the extent of heterobeltiosis of 28 F_1 hybrids. The magnitude of heterobeltiosis for days to flowering varied from -34.00 to 0.72%, for fruit length -24.00 to 26.05%, for fruit weight -25.12 to 31.81% and for yield plant^{-1} -23.44 to 110.62%.

Ganefianti and Fahrurrozi (2018) recorded that the magnitude of heterobeltiosis was maximum in the cross F(KG-6) × (KG-3) for fruit weight plant^{-1}, D(KG-4) × E(KG-5) for fruits plant^{-1} and D(KG-4) × G(KG-7) for fruit length and fruit diameter. Among 42 cross combinations, two crosses G(KG7) × C(KG3) and F(KG6) × C(KG3) were most promising.

In line × tester analysis, Janaki *et al.* (2018) developed 54 F_1 hybrids by crossing nine lines with six testers to identify the magnitude of combining ability and heterosis. The maximum standard heterosis (over check Tejaswini) in desirable direction was recorded in the hybrid LCA-355 × LCA-703-2 for plant height, LCA-466 × LCA-315 and LCA-466 × LCA-678 for primary branches plant^{-1} and LCA-442 × G4 for days to fruit maturity, while the high standard heterosis over check Indam-5 was observed in hybrid LCA-655 × G4 for fruits plant^{-1}, LCA-355 × LCA-315 for fruit length, LCA-466 × LCA-453 for fruit diameter, LCA-607 × LCA-453 for average dry fruit weight.

2.8 GENERATION MEAN ANALYSIS

Khereba *et al.* (1995) studied the genetic inheritance of fruit length and diameter and pericarp thickness in the cross fimentao pepper. They reported that multiple gene effects were involved in the inheritance of these traits and also partial dominance was observed for these traits. Gene actions *viz.*, additive, dominance and their interactions were involved in the inheritance of fruit length, fruit width, fruit number and yield plant^{-1} (Murthy and Deshpande, 1997).

In two intervarietal crosses Jatlong × Sampathy and Jatlong × LCA205, Sarma and Talukdar (1998) reported dominance gene action and dominance × dominance gene interaction for the inheritance of plant height, fruit length and diameter, fruits plant^{-1} and yield plant^{-1}.

In an interspecific hybrid C. *annuum* L. × C. *chinense* Jacq, Zewdie and Bosland (2000) observed the involvement of additive, dominance and their gene interactions for capsaicin, isomer of dihydrocapsaicin and dihydrocapsaicin. The growth related characters were governed by dominance and additive × additive gene

interactions and the fruit related traits were governed by additive, additive × additive gene interactions (Jagadeesha, 2000).

Dhall and Hundal (2005) reported the gene action for fruit yield and quality characters by using six cross combinations. The F_1 mean for yield (early and total) in all the hybrids were superior to their parental means indicating over dominance for these characters. Partial dominance was observed for colouring matter (red ripe fruits) and total chlorophyll content (green fruits. This suggested heterosis breeding for the improvement of yield and selection in the later generation to improve fruit colour.

Ajith and Anju (2005) reported the involvement of additive and dominance × dominance gene interaction in the cross Jwalasakhi × Ujwala and Jwalamukhi × Ujwala for fruit length, fruit girth, fruits number, fruit weight and yield plant^{-1}. For the improvement of these traits they suggested hybridization followed by selection.

Dhall and Hundal (2006) reported the involvement of epistatic interaction and higher magnitude of dominant gene effects for fruit weight and number of fruits per plant in all the six crosses except PBC 830 × Punjab Lal for fruit weight. The duplicate epistasis was exhibited in almost all the crosses. Additive gene effects had more influence which indicated that selection could be highly useful for the genetic improvement of these traits.

Kamboj *et al.* (2007) observed the importance of additive gene effects for plant height, fruits per plant and red fruit yield (dried). Dominant gene effects were high in magnitude for red fruit yield (fresh) and primary branches. For the improvement of these characters they suggested breeding strategies *viz.*, heterosis breeding, pedigree selection and reciprocal recurrent selection. The inheritance of vitamin C content in fresh green and red ripe peppers were genetically controlled by both additive and dominance gene effects (Kamboj *et al.,* 2006).

The component of additive × additive gene interaction was more predominant than other type of interactions (Somashekhar *et al.,* 2008). Jabeen *et al.* (2009) observed the high magnitude of non-additive gene effects for days to fruit set

and ripening, branches number, fruit width and fruit yield. Among gene interactions, dominance × dominance gene interactions were more common as compared to additive × additive and additive × dominance gene interactions.

The presence of transgressive segregants was observed by Marame *et al.* (2009) which indicated polygenic inheritance. The simultaneous exploitation of gene effects and genetic components could be done by adopting heterosis, backcrossing, multiple crossing and pedigree with recurrent selection.

In eight crosses, Kamboj *et al.* (2011) observed the importance of additive gene action over the dominance gene action for earliness characters and epistasis gene interactions were also involved in the inheritance of these characters.

Hasanuzzaman and Golam (2011) studied six generations of four chilli crosses for yield and yield components. The involvement of digenic type of epistasis was observed for plant height, days to first flowering, fruit width, fruit length, number of fruits, fruit weight and fruit yield. Generation mean analysis indicated that fruit number and fruit yield were controlled by dominance, additive and epistatic gene interactions. In most of the crosses, high magnitude of non-additive gene effects with complementary epistasis was noted for fruit yield, fruit number and fruit weight. This suggested the utilization of heterosis breeding for improvement of these characters.

Patil (2011) reported the importance of all forms of gene actions for the inheritance of fruit length and width and green fruit yield. They suggested heterosis breeding and transgressive segregants selection for the cultivar improvement in chillies.

Anandhi and Khader (2011) performed generation mean analysis for fruit yield trait and leaf curl virus resistance by involving two interspecific cross combinations namely Nenmara Local × Vellayani Athulya and Mavelikkara Local × Jwalasakhi. Additive gene effects were significant for all the studied traits.

The magnitude of dominance gene effect was greater and significant for many traits. In most of the crosses, dominant gene action and dominance ×

dominance interactions were in the same direction, indicating complementary epistasis. Dominance × dominance gene interaction was predominant. All three of gene actions (additive, dominance and epistasis) were significant for yield, yield traits and leaf curl virus resistance which indicated that the breeding strategies like recurrent selection and diallel selective mating system could be adopted in chilli improvement programme under leaf curl disease severity conditions. Anandhi and Khader (2014) reported predominance of dominance × dominance gene interaction component and the duplicate type of gene interaction in most of the studied cases. For yield and capsaicin content, all types of gene actions additive, dominance and epistasis were present.

The duplicate type of epistasis was observed by Patil *et al.* (2012) for fruit length and diameter and seed weight suggesting that these traits were governed by non-additive genes. For seed number per fruit both complementary and duplicate type of epistasis were seen which suggested the involvement of both additive and non-additive genes in governing these characters.

Prajapati and Agalodiya (2012) reported the involvement of dominance gene action for inheritance of number of days to flower and they recommended heterosis breeding for the varietal improvement. Prajapati *et al.* (2012) observed fixable gene effects for primary branches, fruit length and fruit number. The dry fruit weight was controlled by non-additive gene effects. Both type of gene actions (additive and non-additive) were operating in the inheritance of plant height and average fruit weight.

Silva *et al.* (2013) estimated the genetic parameters for yield by using the cross Pimenton Serrano × Aji Cayenne 958. For phenotypic expression additive, dominance and non-additive interactions components were significant. Additive × additive effects were significant for fruit weight. Recessive or double recessive epistasis was found. They suggested that recurrent selection could be used to increase the fruit yield in chillies and epistatic interaction could be effectively exploited through hybridization among promising lines.

Navhale *et al.* (2014a) observed all gene action types *i.e.* additive, dominance and their interactions for earliness, fruit yield and quality traits. They suggested reciprocal recurrent selection, reciprocal selection, diallel selective mating or bi-parental mating scheme for the improvement of these traits. The traits which expressed complex genetic behavior could be improved through modified bulk selection. Heterosis breeding was suggested for the varietal improvement of the crosses which showed complimentary epistasis. The importance of both additive and dominance gene effect was reported for days to economic fruiting period (Patel and Patel, 2015).

Manu *et al.* (2014) reported high magnitude of additive × additive gene effects for fruit length. For fruit weight, additive gene effect was observed but for fruit diameter no gene effects were observed. For improvement of these characters they recommended simple selection technique or hybridization followed by pedigree method.

Navhale *et al.* (2017) observed the importance of additive, dominant and epistatic interactions in three crosses (Jwala × DPL-C-5, Jwala × AKC-08-95-05 and Jwala × Parbhani Tejas) for plant height, days to first flowering, primary branches, fruit length, fruit diameter, fruit number and fruit yield. Duplicate epistasis was observed in majority of hybrids for many traits. Complementary epistasis was observed in the cross Jwala × DPL-C-5 for days to flowering and red fruit yield; cross Jwala × Parbhani Tejas for fruit length and fruit diameter.

The analysis of generation means in four crosses (DKC-12ms × HC-201, DKC-12ms × CW, DKC-12A × HC-201 and DKC-12A × CW) by Joshi and Nabi (2018) revealed the importance of selection in the improvement of plant height, days to 50 per cent flowering and days to first fruiting. They suggested both heterosis breeding and selection in the population for the improvement of primary branches and fruit yield in chilli. The highly heterotic cross DKC-12A × HC-201, showed complementary type of epistasis, which suggested its exploitation as F_1 hybrid. Dominance × dominance component was positively significant in the cross DKC-

12A × CW suggested the advantage of hybridization followed by selection in later generation.

Devi and Sood (2018) studied four crosses through generation mean analysis in bell pepper to identify gene action for major horticultural traits and to develop promising breeding material from the segregating generations. The magnitude of additive × additive [i] gene interactions and dominance [h] gene effects were positive and they were coupled with duplicate type of gene interaction in the cross EC 464107 × SH 1, EC 464115 × KS and EC 464107 × KS.

This indicated the exploitation of heterosis breeding along with picking up of superior segregants (pedigree method) in these crosses. For fruit yield, all four crosses showed higher values of dominance [h] gene action along with duplicate type of epistasis (low magnitude) in the cross EC 464107 × SH 1 and complementary epistasis in the cross EC 464107 × EC 464115, indicating the importance of exploiting hybrid vigour in these cross combinations.

Materials and Methods

3. MATERIALS AND METHODS

The present investigation entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" was carried out at the Department of Vegetable Science, College of Agriculture, Kerala Agricultural University, Vellayani, during 2015-2018. The study aimed at identification of sources of leaf curl virus resistance, to estimate the heterosis, general combining ability (GCA) of parents and specific combining ability (SCA) of the crosses for yield and quality traits and to study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and leaf curl virus resistance in chilli.

Experimental Site

The experimental site was located at 8.50° North-latitude and 76.90° East-longitude, at an altitude of 29.00 m above mean sea level. Predominant soil type of the experimental site was red loam to Vellayani series, texturally classified as sandy clay loam (Appendix I). The region appreciates a warm humid tropical climate.

The present study consisted of the following experiments.

3.1 EXPERIMENT I (a): EVALUATION OF CHILLI GENOTYPES FOR YIELD AND QUALITY

3.1.1 Materials

Seventy chilli genotypes had been collected from numerous sources. The list of genotypes and their source of origin is given in Table 1.

3.1.2 Methods

3.1.2.1 Design and Layout

Seventy chilli genotypes were evaluated for yield and quality attributes during summer (2016). The crop was raised according to the package of practices

suggestions of Kerala Agricultural University (KAU, 2016). Field view of the experiment is given in the plate 1.

The experiment was laid out as follows:

Design : RBD
Treatments : 70 genotypes
Replications : 3
Spacing : 45 × 45 cm
Plot size : 3.6 × 1.8 m
Season : Summer (2016)

3.1.1 EXPERIMENT I (b): FIELD SCREENING OF GENOTYPES FOR ChiLCV RESISTANCE

3.1.1.1 Materials

The same 70 chilli genotypes (Table 1) used for Experiment I (a) were used for field screening against ChiLCV resistance under natural epiphytotic conditions during summer (2016).

3.1.1.2 Methods

The field screening was undertaken when the natural ChiLCV pressure was at its peak because of high whitefly population. No plant protection measures were provided. The visual observation on appearance of ChiLCV symptom was noted at fortnightly periods after transplanting. Field view of the experiment is given in the plate 2.

3.1.1.2.1 Design and Layout

The experiment was laid out as follows:

Design : RBD
Treatments : 70 genotypes
Replications : 3
Spacing : 45 × 45 cm
Plot size : 3.6 × 1.8 m
Season : Summer (2016)

Plate 1: General view of experimental field (experiment I (a))

Plate 2: General view of experimental field (experiment I (b))

3.2 EXPERIMENT II (a): ARTIFICIAL SCREENING FOR ChiLCV RESISTANCE

3.2.1 Whitefly Mediated Inoculation

3.2.1.1 Materials

Ten symptomless and five highly resistant genotypes identified under natural field conditions in Experiment I (b) were subjected to screening under artificial inoculation condition by whitefly mediated inoculation and graft inoculation against leaf curl virus isolate. The genotypes used for artificial screening were presented in the Table 2.

3.2.2.1 Methods

3.2.2.2 Maintenance of ChiLCV *Inoculum*

Based on the previous experiment I (b), the susceptible chilli plants affected with ChiLCV were selected and replanted in clay pot and they were kept in insect proof cage at Research Farm, Department of Vegetable Science, KAU. The same plants were used as source of inoculums for whitefly mediated inoculation.

3.2.2.3 Raising of Healthy Chilli Seedling

The chilli seeds were sown in the plug trays filled with vermicompost and cocopeat in 1:1 proportion. The trays were kept in insect proof cage. Twenty day after sowing the seedlings were gently removed and transplanted into plastic pot of size 14 × 10 × 13.5 cm filled with soil mixture with vermicompost and kept in insect proof cage for inoculation (Plate 3a (C)).

3.2.2.4 Maintenance of Vector

Whiteflies (*Bemisia tabaci* Genn.) originally collected from the Research Farm, Department of Vegetable Science, KAU were multiplied and maintained on brinjal plants grown in clay pots (12 × 8 cm) and they were kept in insect proof cage for virus free whitefly culture.

Table 1: List of 70 genotypes used for the study

Treatments	Accessions/ Genotypes	Source	Treatments	Accessions/ Genotypes	Source
T_1	Sel-1	AVRDC, Taiwan	T_{36}	Pant C 1	GBPUAT, Pantnagar
T_2	Sel-3	AVRDC, Taiwan	T_{37}	Punjab Surkh	PAU, Ludhiana
T_3	Sel-4	AVRDC, Taiwan	T_{38}	Kashi Anmol	IIVR, Varanasi
T_4	Sel-5	AVRDC, Taiwan	T_{39}	DCL 524	HRS, Deihosur
T_5	Sel-6	AVRDC, Taiwan	T_{40}	C-31-1	HRS, Deihosur
T_6	Punjab Lal	PAU, Ludhiana	T_{41}	ACC-2-1	HRS, Deihosur
T_7	Punjab Tej	PAU, Ludhiana	T_{42}	I-1	HRS, Deihosur
T_8	Punjab Sindhuri	PAU, Ludhiana	T_{43}	I-2	HRS, Deihosur
T_9	Punjab Guchhader	PAU, Ludhiana	T_{44}	I-3	HRS, Deihosur
T_{10}	Vellayani Athulya	KAU	T_{45}	I-4	HRS, Deihosur
T_{11}	Ujwala	KAU	T_{46}	CHIVAR-1	IIVR, Varanasi
T_{12}	DCA 268	HRS, Devihosur	T_{47}	CHIHYB-2	IIVR, Varanasi
T_{13}	DCA 167	HRS, Devihosur	T_{48}	CHIVAR-3	IIVR, Varanasi
T_{14}	DCA 157	HRS, Devihosur	T_{49}	CHIHYB-3	IIVR, Varanasi
T_{15}	DCA 142	HRS, Devihosur	T_{50}	CHIVAR-2	IIVR, Varanasi
T_{16}	PS 1	HRS, Devihosur	T_{51}	CHIVAR-4	IIVR, Varanasi
T_{17}	Byadagi Dabbi	HRS, Devihosur	T_{52}	CHIVAR-6	IIVR, Varanasi
T_{18}	Byadagi Kaddi	HRS, Devihosur	T_{53}	CHIVAR-7	IIVR, Varanasi
T_{19}	Jwalasakhi	NBPGR, New Delhi	T_{54}	LCA-334	HRS, Devihosur
T_{20}	EC 354890	NBPGR, New Delhi	T_{55}	KA-2	HRS, Devihosur
T_{21}	EC 599958	NBPGR, New Delhi	T_{56}	CHIVAR-10	IIVR, Varanasi
T_{22}	IC 572483	NBPGR, New Delhi	T_{57}	CHIVAR-8	IIVR, Varanasi
T_{23}	EC 599960	NBPGR, New Delhi	T_{58}	CHIVAR-9	IIVR, Varanasi
T_{24}	IC 572468	NBPGR, New Delhi	T_{59}	CHIVAR-5	IIVR, Varanasi
T_{25}	Nagachilli	N-E region	T_{60}	Japani Longi	PAU, Ludhiana
T_{26}	Arka Lohith	IIHR, Bengaluru	T_{61}	Perennial	PAU, Ludhiana
T_{27}	Anugraha	KAU	T_{62}	VS-7	PAU, Ludhiana
T_{28}	CA-3 (EC-391083)	NBPGR, New Delhi	T_{63}	VS-9	PAU, Ludhiana
T_{29}	CA-5 (EC-596920)	NBPGR, New Delhi	T_{64}	S-217621	PAU, Ludhiana
T_{30}	CA-6 (EC-596940)	NBPGR, New Delhi	T_{65}	Sel. 40	PAU, Ludhiana
T_{31}	CA-8 (EC-599969)	NBPGR, New Delhi	T_{66}	Sel.7-1	PAU, Ludhiana
T_{32}	CA-32 (DWD-2)	NBPGR, New Delhi	T_{67}	Sel. 36-1	PAU, Ludhiana
T_{33}	Jwalamukhi	KAU	T_{68}	PLS-3-1	PAU, Ludhiana
T_{34}	Keerthi	KAU	T_{69}	Sel. 20-1	PAU, Ludhiana
T_{35}	Pusa Jwala	IARI, New Delhi	T_{70}	ms-12	PAU, Ludhiana

Table 2: List of genotypes used in artificial screening

Treatments	Genotypes	Reaction under field conditions
T_2	**Sel-3**	Symptomless
T_3	**Sel-4**	Symptomless
T_5	**Sel-6**	Symptomless
T_{46}	**CHIVAR-1**	Symptomless
T_{50}	**CHIVAR-2**	Symptomless
T_{57}	**CHIVAR-8**	Symptomless
T_{63}	**VS-9**	Symptomless
T_{65}	**Sel-40**	Symptomless
T_{66}	**Sel-7-1**	Symptomless
T_{67}	**Sel-36-1**	Symptomless
T_{51}	**CHIVAR-4**	Highly resistant
T_{60}	**Japani Longi**	Highly resistant
T_{61}	**Perennial**	Highly resistant
T_{68}	**PLS-3-1**	Highly resistant
T_{69}	**Sel-20-1**	Highly resistant

3.2.2.5 Whiteflies collection

Whiteflies were collected by using aspirator (90 ml test tube entomological aspirator). With the help of suction pipe, the flies were collected from under side of the leaves (Plate 3a (A & B)).

3.2.2.6 Acquisition of Virus from ChiLCV *infected plant*

The acquisition cage cum collection bottle was prepared by using two liters plastic bottles. The lower end of the bottles were removed and covered with muslin cloth and the upper ends were closed with the help of cotton plugs. For acquisition of virus, ChiLCV infected plant branches were inserted inside the bottles which contain non viruliferous whiteflies. These flies were allowed to feed on the ChiLCV infected branches for 24 hours (Acquisition period). The viruliferous whiteflies were removed from the bottle and were used for artificial whitefly inoculation of genotypes (Plate 3a (D & E)).

3.2.2.7 Inoculation of Virus

The inoculation cages were prepared by using glossy photo sheets (21 × 29.7 cm). These sheets were rolled and stapled to form open cylinder. The one end of cylinder was covered with muslin cloth which avoids excess moisture accumulation inside cylinder and also it avoids the escape of flies from the cylinder. The viruliferous whiteflies (10 whiteflies per seedling) were released inside the cylinder which contains young test plant seedlings (Plate 3a (G & H)). After inoculation feeding period (24 hours) the caged test plant seedlings were treated with insecticide Imidacloprid 17.8 % SL @ 0.10 % to kill all the whiteflies inside the cylinder.

3.2.2.8 Artificial Screening of Genotypes

The healthy chilli seedlings (resistant lines) were inoculated at two-true leaf stage. Cage or single plant inoculation technique was followed for artificial whitefly inoculation. Every test plant seedlings were exposed to viruliferous whiteflies (10 numbers). The inoculated test plant seedlings were kept in insect proof cage and the observations were noted (Plate 3a (I)).

3.2.2.9 Design and Layout

The inoculated plants were observed regularly for incidence and intensity of the disease from inoculation upto a period of six week based on Coefficient of Infection (CI).

The experiment was laid out as follows:

Design	:	CRD
Treatments	:	10 symptomless and 5 highly resistant genotypes from field screening
Replications	:	3
Season	:	July- September (2016)

3.2.2 Graft Inoculation

3.2.2.1 Materials

The materials used for graft inoculation was as mentioned vide 3.2.1.1

(A)

(B)

(C)

(D)

(E)

Plate 3 (a): Steps of artificial whitefly mediated inoculation technique

(F)

(G)

(H)

(I)

Plate 3 (a) continued: Steps of artificial whitefly mediated inoculation technique

(A) & (B) Collection of whiteflies from brinjal plants

(C) Healthy test plants under insect proof cage

(D) & (E) Acquisition of virus by whiteflies from ChiLCV infected plant (AAP: 24 hours)

(F) Viruliferous whiteflies transfered inside individual plant cage

(G) & (H) Single plants of chilli inoculated by viruliferous whiteflies (IAP: 24 hours)

(I) General view of experiment II (a)

3.2.2.2 Methods

The healthy test plants were grown in pots under insect proof cage (Plate 4a (D & E)). Small branches (10-15 cm) were selected from 70-80 days old test plants and were used for preparing the scions. For rootstock purpose the ChiLCV infected plants from the previous experiment I (b) were uprooted and transplanted into clay pots and kept under greenhouse conditions (Plate 4a (B & C)). The presence of ChiLCV from the infected plants was confirmed by Polymerase chain reaction (PCR) by using degenerate primers (Wyatt and Brown, 1996). The infected plants which showed positive for virus were used as rootstock in graft inoculation.

The base of the scions were trimmed to a wedge shape and inserted into a cleft made on the stem of the infected chilli rootstock plant. The graft was then tied firmly using a para film strip. To increase grafting success the plastic zip lock pouch bags (10" × 12" inch) were covered over grafted plants (Plate 4a (H & I)). The grafted plants were kept under observation for the development of systemic symptoms in test scions.

3.2.2.3 Design and Layout

The experiment was conducted as follows:

Design : CRD

Treatments : 10 SL and 5 HR genotypes from field screening

Replications : 3

Season : July- September (2016)

3.2.1 EXPERIMENT II (b): MOLECULAR DETECTION OF ChiLCV IN AFTIFICIALLY INOCULATED PLANTS

The resistant genotypes identified under artificial condition in Experiment II (a) were assessed for presence/absence of viral nucleic acid by Polymerase Chain Reaction (PCR) using universal degenerate primer (AV494/AC1048) for identification of Geminivirus isolates (subgroup III) (Wyatt and Brown, 1996).

(A)

(B)

(C)

(D)

(E)

Plate 4 (a): Graft inoculation technique

(F)

(G)

(H)

(I)

(J)

(K)

Plate 4 (a) continued: Graft inoculation technique

(A) General view of experiment
(B) & (C) Susceptible rootstocks
(D) & (E) Healthy seedling for scions preparation
(F) Rootstock preparation
(G) Grafted plant (test plant scion on infected rootstock)
(H) & (I) Placing the healing graft inside a sealed plastic bag

3.2.1.1 Materials

The genotypes used for molecular detection of ChiLCV are T_2 (Sel-3), T_3 (Sel-4), T_5 (Sel-6), T_{46} (CHIVAR-1), T_{50} (CHIVAR-2), T_{57} (CHIVAR-8), T_{63} (VS-9), T_{65} (Sel-40), T_{66} (Sel-7-1) and T_{67} (Sel-36-1).

3.2.1.2 Methods

3.2.1.2.1 Extraction of DNA from Chilli Leaf Samples

The ChiLCV symptomatic samples were collected from whitefly and graft inoculated plants. From these samples the genomic DNA was extracted following CTAB method with slight modifications. The brief procedure is as follows;

Protocol for CTAB (Cetyl Trimethyl Ammonium Bromide) Method

1. Two to three leaves which showed typical ChiLCV symptoms after whitefly and graft inoculation were collected and they were crushed with the help of pestle and mortar using liquid nitrogen at frequent intervals. The ground powder was transferred to centrifuge tubes (2.0 ml).
2. Pre heated (65°C) CTAB buffer (900-1000µl) was added to the ground powder and shaked thoroughly.
3. At 65°C these tubes were incubated for 50 minutes. For every 10 minutes these tubes were shaked thoroughly.
4. After incubation, each tube was added with 700 µl of chloroform: isoamylalcohol (24:1) and mixed gently by inverting the tubes to form an emulsion. All the tubes were on gyratory shaker for 15-20 minutes.
5. At 10,000 rpm the mixture was centrifuged for 10-15 minutes using Eppendrof 5820R.
6. The upper layer of supernatant layer was pipetted and transferred to a micro centrifuge tube (1.5 ml).
7. Ice cold Isopropanal (600-700 µl) was added to supernatant and mixed thoroughly. For DNA precipitation, these tubes were kept in freezer at -20 °C (20 minutes).

8. After DNA precipitation the tubes were centrifuged (10,000 rpm) for 10 minutes. The supernatant was discarded and the pellets remained in the bottom of the tube. These pellets were washed with ethanol (70 %) and air dried for few hours.
9. The pellets were resuspended in 70 µl of tris extraction (1XTE) buffer (pH 8.3).

3.2.1.2.2 Viral Diagnostic PCR Primers

Presence of virus was confirmed using universal degenerate primers basically designed to detect whitefly transmitted begomoviruses. (Primer AV 496: 5'GCC(CT)AT(GA)TA(TC)AG(AG)AAGCC(AC)AG 3' and Primer AC 1048: 5' GG(AG)TT(AGT)GA(GA)GCATG(TAC)GTACATG 3') (Wyatt and Brown, 1996).

3.2.1.2.3 Polymerase Chain Reaction (PCR)

The extracted DNA was used as template for PCR reaction. For PCR the reaction mixture (25µl) was prepared as follows;

PCR Master Mix

Component (Concentration)	Concentration used	Volume
PCR buffer 5X	1X	5.0 µl
2mM dNTPs	2mM	0.5 µl
25 mM $MgCl_2$	1.5mM	1.5 µl
Forward primer (100 pmol/ µl)	20 pmol/ µl	1.0 µl
Reverse Primer (100 pmol/ml)	20 pmol/ µl	1.0 µl
Taq DNA polymerase (3U/ µl)		0.3 µl
DNA sample template (450ng/ µl)		2.0 µl
Nuclease free water		13.7 µl
Total volume		25.0 µl

AV 496/ AC 1048 forward and reverse primers were used in PCR reaction. PCR tubes were spun briefly in centrifuge. In thermal cycler the PCR amplification was performed with initial denaturation at 94 °C (1 minute), annealing at 52 °C (1 minute) and the extension at 72 °C (2 minutes) followed by 35 cycles each consisting of denaturation at 94 °C (50 seconds), annealing at 52 °C (45 seconds) followed by extension at 72 °C (1:30 minutes). After PCR completion, the PCR product was stored at -20 °C before gel electrophoresis.

3.2.1.2.4 PCR Amplified Products analysis

a) The PCR products were analysed using gel electrophoresis unit.

b) Agarose gel (1.00%) was prepared by mixing 1.00 g agarose in 100 ml 1X TBE by boiling.

c) 5µl/100 ml ethidium bromide was added in the molten gel. The molten agarose was cool down to 50-60 °C, and poured into the mould and comb was inserted. The gel was allowed to set for 30 minutes. The tray was filled with 1 X TBE and the comb was removed gently.

d) The wells were loaded carefully with 5 µl of the PCR product in the respective well. The marker of 100 bp and positive control were also loaded.

e) The gel was subjected to 100 V/40 mA for 1 hour and then analysed using UV transilluminator system (Bio-Rad). The PCR prosuct for ChiLCV with degenerate universal primers is ~560 bp in length. The results were verified against positive control and DNA marker.

3.2.1.2.5 Interpretation of PCR Test Result:

The test is negative if the characterised ~560 bp fragment (ChiLCV) or the virus is not detected. It is positive if the ~560 bp fragment (ChiLCV) was detected and the fragment should be identical to positive control and compare with marker.

3.2.2 Molecular Characterization of Virus

Molecular diagnosis of ChiLCV was carried out in four chilli samples showing leaf curl disease symptoms in the field conditions. The method used for detection is as mentioned vide 3.2.1.2.

3.2.2.1 Characterization of Sequence

The amplicon of viral DNA detected vide 3.2.2 was sequenced at SciGenom Lab, Cochin.

3.2.2.2 Sequence Analysis

The sequences were analysed using bioinformatics tools. The homology

check was carried out using BLASTn. The nucleotide sequences based on the coat protein region of begomovirus virus pertaining to various geographical locations were retrieved from NCBI data base and phylogeny related studies were carried out using multiple sequence alignment tool Clustal Omega.

3.3 EXPERIMENT III (a): LINE × TESTER ANALYSIS

3.3.1 Materials

The material for this experiment comprised of seven genotypes with high yield and quality and four resistant genotypes. Seven genotypes with high yield and quality *viz.*, L1 (CHIVAR-3), L2 (CHIVAR-7), L3 (CHIVAR-6), L4 (CA-32), L5 (Vellayani Athulya), L6 (Keerthi) and L7 (CHIVAR-10) were selected based on selection indices from Experiment I (a). Four highly resistant genotypes (confirmed from graft inoculation) *viz.,* T1 (Sel-3), T2 (Sel-4), T3 (Sel-6) and T4 (CHIVAR-1) were selected from Experiment II (b) (Plate 5).

3.3.2 Methods

The selected seven superior genotypes (lines) and four highly resistant genotypes (testers) were raised in a crossing block in the polyhouse and were crossed in a line × tester mating design to produce 28 F_1 hybrids (Plate 6 (A & B)).

3.3.2.1 Crossing and Selfing Technique

In chilli, anthesis occurs between 8.00 to 11.00 a.m. Hence, well developed flower-buds likely to open next morning were emasculated during evening hours and bagged. The anthesis in chilli starts from 8.00 am and continues up to 11.00 am. For crossing purpose, well matured flower buds which are likely to anthesis next morning were selected and were carefully emasculated during evening time by using forceps and closed with butter paper bags. These emasculated flower buds acts as female parent. The pollens were collected from male parent of fully matured flowers. On next morning between 8.00 am to 10.00 am, the emasculated flower buds were pollinated by using male pollens and they were again covered with butter paper bags and labeled. The seeds were collected separately from successfully crossed red ripe

(A)

(B)

(C)

(D)

(E)

(F)

(G)

(H)

(I)

(J)

(K)

Plate 5 : Parents used for line × tester analysis in experiment III (a)

(A) L-1 (CHIVAR-3) (B) L-2 (CHIVAR-7) (C) L-3 (CHIVAR-6)
(D) L-4 (CA-32) (E) L-5 (Vellayani Athulya) (F) L-6 (Keerthi)
(G) L-7 (CHIVAR-10) (H) T-1 (Sel-3) (I) T-2 (Sel-4)
(J) T-3 (Sel-6) (K) T-4 (CHIVAR-1)

fruits. To get selfed seeds of parental lines, individual mature flower buds from all parents were covered with butter paper bags, after 2 to 3 days bags were removed and later the seeds were collected from full red ripen fruits

3.3.1 EXPERIMENT III (b): EVALUATION OF F_1 HYBRIDS

3.3.1.1 Materials

The 28 F_1 hybrids derived from the Line × Tester mating will be evaluated along with the 11 parents and two check hybrids CH-27 F_1 and Arka Harita for yield and quality attributes and ChiLCV resistance.

3.3.1.2 Methods

The seeds were sown in portrays by using potting mixture. The portrays were kept in insect proof cage to avoid the contact of sucking pests. During summer season thirty day old healthy seedlings (8-10 cm height) were transplanted into well prepared main field during summer season. The crop was raised according to the package of practices suggestions of Kerala Agricultural University (KAU, 2016). However, to facilitate the attack of leaf curl virus disease in the experiment, plant protection measures were not used for proliferation of the vector whitefly. Data were noted from five randomly selected plants, two border plants were excluded, one on each side. Field view of the experiment is given in Plate 6 (E).

3.3.1.3 Design and Layout

The experiment was laid out as follows:

Design : RBD

Treatments : 41 (28 F_1 hybrids + 11 Parents + 2 Checks)

Replications : 3

Spacing : 45 × 45 cm

Plot size : 3.6 × 1.8 m

Season : Summer (2017)

(A)

(B)

(C)

(D)

(E)

Plate 6: Production and evaluation of F_1 hybrids in experiment III (a) & (b)

(A): Hybridization block of female parents (lines), (B): Hybridization block of male parents (testers), (C) & (D): Fruit set after hybridization, (E): Experimental field for F_1 hybrid evaluation

3.4 EXPERIMENT IV: GENERATION MEAN ANALYSIS

3.4.1 Materials

3.4.1.1 Building up of Six Generations

Three superior (performing) F_1 hybrids *viz.*, L1 × T1 (CHIVAR-3 × Sel-3), L3 × T2 (CHIVAR-6 × Sel-4) and L7 × T1 (CHIVAR-10 × Sel-3) were selected from Experiment III (b). These F_1 hybrids were back crossed to both of their respective parents (P_1 and P_2) by taking F_1 as female parent to generate BC_1 and BC_2 generations. The F_1's will be selfed to produce F_2 (Plate 7 (A & B)).

3.4.2 Methods

3.4.2.1 Evaluation of Six Generations

The seedlings of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three crosses were raised and transplanted in the field. All three crosses were evaluated in replicated field experiment [(Plate 7 (C)].

3.4.2.2 Design and Layout

The experiment was laid out as follows:

Design : RBD

Treatment : 18 (P_1, P_2, F_1, F_2, BC_1 and BC_2)

Replication : 3

Spacing : 45 cm × 45 cm

Season : Summer (2018)

3.5 MAIN ITEMS OF OBSERVATIONS

3.5.1 Recorded Observations in Respect of the Following Characters from Experiment I (a), III (b) and IV

3.5.1.1 Vegetative Characters

(A) (B)

(C)

Plate 7: Production and evaluation of six generations of three crosses in experiment IV

(A) & (B): Hybridization block for production of six generations of three crosses

(C): Experimental field of six generations of three crosses

3.5.1.1.1 Plant Height (cm)

The measurement of plant height was done at the time of final harvest using meter scale (cm) from ground level to the highest bud tip. Five plants were selected randomly from each genotype in each replication. The mean values were worked out.

3.5.1.1.2 Primary Branches Plant[1]

At the end of final harvest, the primary branches emerging from main stem were recorded.

3.5.1.2 Flowering Characters

3.5.1.2.1 Days to First Flowering

From five randomly selected plants, the duration (days) taken to first flower opening from the date of transplanting were calculated and the mean worked out.

3.5.1.2.2 Days to First Harvest

The days taken from the date of transplanting to the first fruit harvest from five randomly plants were noted and the mean worked out.

3.5.1.3 Fruit and Yield Characters

3.5.1.3.1 Fruit Length (cm)

Ten matured green fruits were randomly selected from each tagged plant in third harvest. The fruit length (cm) was measured from pedicel attachment of the fruit to its tip end and the mean was worked out.

3.5.1.3.2 Fruit Girth (cm)

The girth of fruit was noted from the central or middle portion of the mature fruit by using twine and scale. The same fruits which were used to measure length of fruit was used to measure fruit girth and the average girth was noted.

3.5.1.3.3 Fruits Plant^{-1}

The mature fruits number from each harvest were counted and recorded. Counted fruits were added and the average number of fruits per plant was worked out.

3.5.1.3.4 Fruit Weight (g)

The average weight of fruits was measured from 10 randomly picked fruits from third picking. The weight of fruits was measured on electronic balance.

3.5.1.3.5 Yield Plant^{-1} (g)

Yield plant^{-1} was computed by adding the mature green fruit weight from every harvest and dividing by number of randomly selected plants (five), the mean weight is expressed in grams.

3.5.1.3.6 Yield Plot^{-1} (kg/6.48m^2)

From each plot harvested weight of fruits was calculated and expressed in kilograms.

3.5.1.4 Quality Characters

3.5.1.4.1 Vitamin C (mg 100 g^{-1} fresh fruit weight)

To estimate the vitamin C content from green fruits 2,6-dichloro phenol indophenol dye procedure method was followed (Sadasivam and Manickam, 1992)

Reagents

1. Four per cent Oxalic acid
2. Preparation of ascorbic acid standard: 100 mg of ascorbic acid is dissolved in 100 ml of oxalic acid (4 %), from this 10 ml of stock solution was diluted to 10 ml to get working standard solution.
3. 2,6-dichlorophenol indophenol dye: Sodium bicarbonate (42 mg) was dissolved in little quantity of distilled water and 2,6-dichloro phenol indophenol (52 mg) was added in to this solution. The final volume was made up to 200 ml with distilled water.

4. Working standard solution: The stock solution (10 ml) was diluted to 100 ml oxalic acid (4 %) and the stock solution concentration was 100 mg ml^{-1}.

Procedure followed:

The working standard solution (5 ml) was pippeted in to a conical flask (100 ml) and for this 10 ml oxalic acid (4 %) was added. This solution was titrated against the dye (V_1 ml). The appearance of pink color (persisted for 5 seconds) was regarded as end point. From red ripe fruit, five grams of fruit was crushed in oxalic acid (4 %) and the juice was extracted and final volume was made up to 100 ml by using oxalic acid. From this solution five milliliter of aliquoet was taken and added with 10 ml of oxalic acid (4 %). Finally, this solution was titrated against dye and the end point was recorded (V_2 ml).

Sample ascorbic acid concentration was identified using the formula

$$\text{Ascorbic acid (mg } 100^{-1} \text{ g of fresh weight)} = \frac{0.5 \times V_2 \times 100 \times 100}{V_1 \times 5 \times \text{Weight of sample}}$$

3.5.1.4.2 Carotenoids (mg 100 g^{-1})

Two groups (isochromic families) of carotenoid pigments are present in chilli *viz.,* yellow fractions and red fractions. These fractions were detected using UV-visible spectrophotometric measurements at two characteristic wavelengths and application of Lambert-Beer law for multi-component mixtures according to procedure developed by Hornero-Mendez and Minguez-Mosquera (2001).

Procedure:

The dried red ripe fruits were selected and were ground into fine powder. This powder (100 mg) was extracted with acetone (25 ml). This extract was transferred to volumetric flask and the volume was made up to 50 ml by adding acetone. By using acetone as blank, the absorbance of the sample was recorded at two wavelengths (472 nm and 508 nm).

The red (C^R) and yellow (C^Y) fractions were calculated using the following formulae.

$$C^R\ (\mu g/ml) = \frac{A_{508} \times 2144 - A_{472} \times 403.3}{270.9}$$

$$C^Y\ (\mu g/ml) = \frac{A_{472} \times 1724.3 - A_{508} \times 2450.1}{270.9}$$

$$C^T\ (\mu g/ml) = C^R + C^Y$$

µg/ml values were converted into percentage on dry weight basis.

3.5.1.5 Incidence of Pests and Diseases

3.5.1.5.1 Leaf Curl Disease

Leaf curl incidence (%) was first recorded 15 days after transplanting. Subsequent observations were recorded at fortnightly intervals as described by Muniyappa *et al* (1991).

3.5.1.5.2 White Fly

Five plants were randomly selected from each treatment, from those plants adult whitefly population was counted from two leaves each from lower and upper canopy. Both upper and lower surface of leaves were examined for adult whitefly population. The observation was taken at 30^{th}, 60^{th} and 90^{th} days after transplanting (DAT).

3.5.1.5.3 Thrips

From five randomly selected plants, three leaves (top, middle and lower part) from the selected plant were examined for presence of nymphs and adults of thrips using magnifying hand lens (10 X). Mean pest population was worked out.

3.5.1.5.4 Mites

The mites population (nymphs and adults) were recorded form five randomly tagged plants. Four leaves from each tagged plant (two each from lower and upper canopy) were plucked and collected in polythene bag. These leaves were examined for the presence of nymphs and adults in laboratory under stereo binocular microscope. The observation was taken at 30^{th}, 60^{th} and 90^{th} DAT.

3.5.1.5.5 Fruit Rot

The characteristic symptoms were observed from five randomly tagged plants from each genotype. Per cent disease incidence from each observational plant was recorded using the formula.

$$\text{Per cent disease incidence} = \frac{\text{No. fruits affected by fruit rot in a plant}}{\text{Total number of fruits in the same plant}} \times 100$$

3.5.1.5.6 Bacterial Wilt (BW)

Bacterial wilt incidence (%) among the selected plants was calculated out by using formula.

$$\text{Bacterial wilt incidence (\%)} = \frac{\text{Number of plants affected by bacterial wilt}}{\text{Total number of plant}} \times 100$$

3.5.2 Observations Recorded from Experiment I (b) and II (a)

Chilli genotypes and hybrids were screened for ChiLCV resistance during summer. On each genotype the severity of symptom was noted on the basis of severity scale 0-6 (Banerjee and Kalloo, 1987). The specific disease reaction was assigned for all the genotypes based on Coefficient of Infection (CI) as suggested by Kumar *et al.* (2006) (Table 3).

Table 3. An arbitrary scale employed for scoring ChiLCV reaction

Symptom	Severity grade	Coefficient of infection (CI)	Disease reaction (DR)
Absence of visual symptom	0	0	Symptomless – SL
Clearing and curling of top leaves, 0-5 % curling	1	0.1 – 5	Highly Resistant – HR
Clearing of leaves and veins swelling, 6-25 % curling	2	5.1 – 10	Resistant – R
Yellowing and puckering of leaves and veins swelling, 26-50% % leaf curling	3	10.1 – 20	Moderately resistant – MR
Curling of leaves, internodes blistered and stunted plant growth, 51-75 % leaf curling	4	20.1 – 40	Moderately susceptible – MS
Small deformed leaves, overall stunted plant growth with very few or no flowers and fruits, > 75 % leaf curling	5	40.1 – 70	Susceptible – S
Deformed very small leaves, severely stunted plant growth. The flowers and fruits were completely absent.	6	70.1 – 100	Highly susceptible – HS

The degree of resistance was measured by individual plant score or individual plant belongs to each class of score (0-6) (Plate 8). DSI (Disease severity index) gives the representative measure of disease reaction on an individual plant basis (Pyne, 2015).

$$\text{Coefficient of Infection (CI) (\%)} = \frac{\text{DSI (Disease Severity Index)} \times \text{DI (Disease Incidence)}}{100}$$

$$\text{Disease severity index (DSI) (\%)} = \frac{\sum \text{Infected plants in each class}}{\text{Total number of plants} \times \text{Max. disease score}} \times 100$$

$$\text{Disease Incidence (DI) (\%)} = \frac{\text{Total infected plant number}}{\text{Total number of plants}} \times 100$$

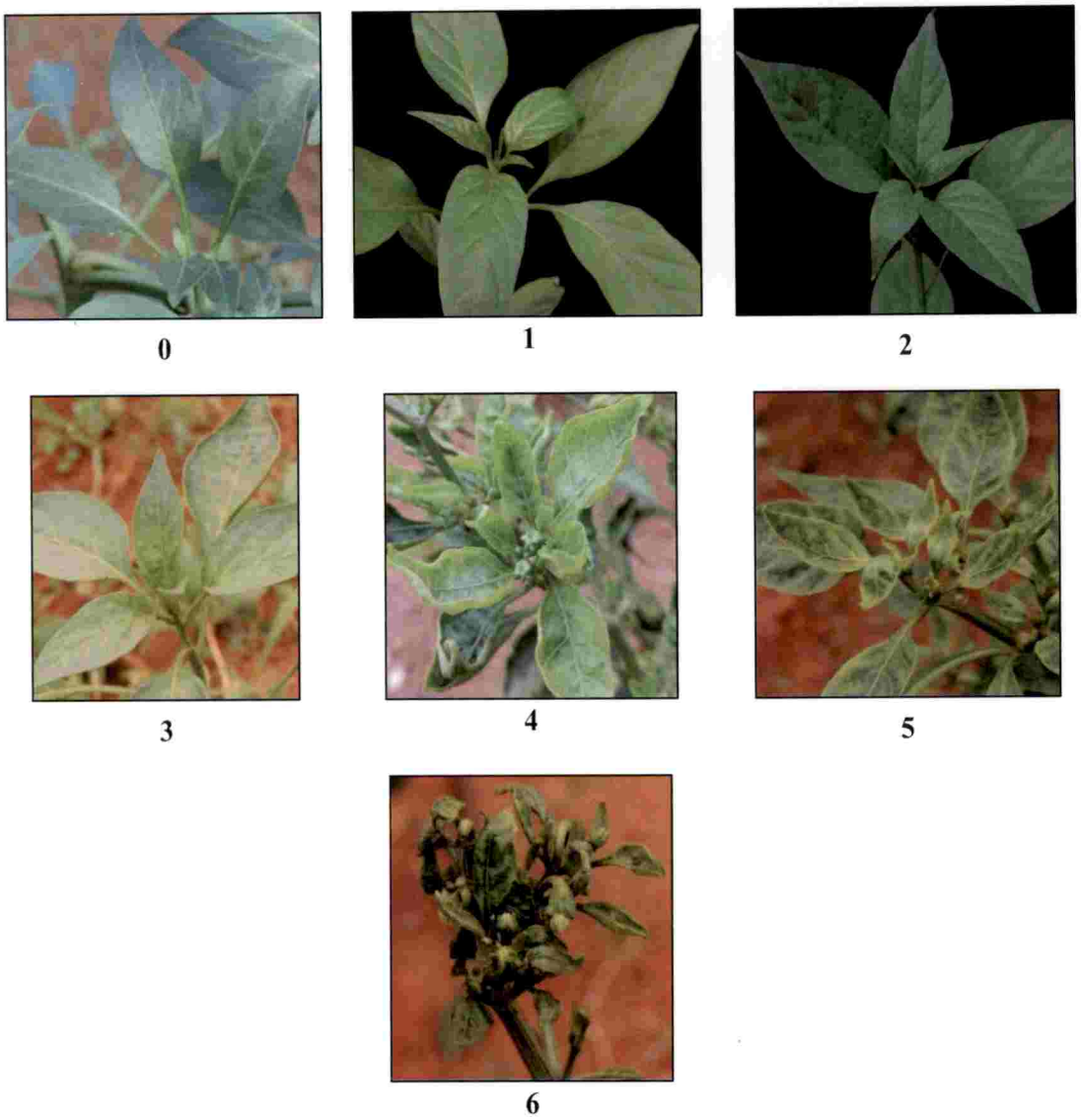

Plate 8: Scoring scale based on severity (0-6) of leaf curl virus disease

3.5.3 Observations Recorded from Experiment II (b)

The presence/ absence of ChiLCV specific PCR band will be observed based on expected size apmlicon (~560 bp).

3.5.4 STATISTICAL ANALYSIS

The experiment data from all experiments were analyzed by using computer software 'PBTools' (PBTools-1.4, 2014).

3.5.4.1 Selection Index

To discriminate genotypes based on all the characters selection index was employed in experiment I (a). The selection index is described by the function, $I = b_1x_1 + b_2x_2 + \ldots\ldots\ldots + b_kx_k$ and the merit of a plant is described by the function, $H=a_1G_1 + a_2G_2 + \ldots\ldots + a_KG_K$ where $x_1, x_2 \ldots x_k$ are the phenotypic values and $G_1, G_2 \ldots\ldots\ldots G_k$ are the genotypic values of the plants with respect to the characters $x_1, x_2 \ldots\ldots x_k$ and H is the genetic worth of the plant. It is assumed that economic weight assigned to each characters is equal to unity i.e. $a_1, a_2, \ldots\ldots\ldots\ldots + a_k = 1$ and b (regression) coefficients are determined such that correlation between H and I is maximum. The procedure will reduce to an equation of the form $b = P^{-1}Ga$ where P and G are the phenotypic and genotypic variance covariance matrices respectively from which the b_i values are estimated. Based on the 'b' estimates and the mean values for the 12 characters with respect to each genotype, scores were calculated and the genotypes were ranked.

3.5.4.2 Analysis of Variance (ANOVA) for Experimental Design

To test the significant of differences among progenies (parents and hybrids) for different characters, the data were analyzed on the basis of following model:

$$p_{ij} = m + g_i + b_j + e_{ij}$$

Where,

p_{ij}= Phenotypic value of i^{th} genotype grown in j^{th} block

m = General mean

g_i= Effect of i^{th} genotype

b_j= Effect of j^{th} block

e_{ij}= Error associated with ij^{th} observation

Total variation among the progenies was partitioned into blocks and genotypes as per the following expectations;

Source of Variation	**d.f.**	**Sum of Squares**	**Mean Squares**	
			Observed	**Expected**
Replications	(r-1)	$Sr = \frac{\sum x^2.j}{g} - \frac{\sum x^2}{N}$	Mr = Sr / (r-1)	Ve + gVr
Genotypes	(g-1)	$Sg = \frac{\sum xi^2}{r} - \frac{\sum x^2}{N}$	Mg = Sg / (g-1)	Ve + rVg
Error	(r-1) (g-1)	*Se* =St-Sr-Sg	Me = Se / (r-1)(g-1)	Ve

Where,

r = replications numbers

g = genotype numbers

N = Total number of observations

Se = Error sum of squares

St = Total sum of squares

Vr = Replication variance

Vg = Genotype variance

Ve = Error variance

The progeny variance was tested against error variance by 'F' test at (g-1), (r-1) (g-1) degree of freedom. Similarly block variance was compared against error variance at (r-1), (r-1) (g-1) degree of freedom.

3.5.4.3 ANOVA for Combining Ability

The data recorded was statistically analyzed following standard procedures for the estimation of components of genetic variation. Combining ability analysis was done in the line × tester fashion, as given by Kempthorne (1957).

To identify differences among genotypes *viz.*, parents, their F_1 hybrids and parents vs. hybrids, the recorded data from randomized block design (RBD) was analyzed on the basis of mathematical model: $Y_{ik}= \mu+ g_i+ r_k +e_{ik}$

Where,

Y_{ik} is the phenotype of the i^{th}genotype grown in the k^{th}replication

μ is the general mean

g_i is the effect of i^{th} genotype

r_k is the effect of k^{th} replication

e_{ik} is the error component associated with the i^{th} genotype and k^{th} replication

In the above model the effects were assumed to be unknown parameters fixed except e_{ik} which was assumed to be normally and independently distributed with mean zero and common variance (σ^2). The ANOVA based on this model as follows:

Where,

r - Replications number

g - Total genotypes number (lines + testers + hybrids)

p - Parents number (testers + lines)

f - Number of female parents

m - Number of male parents

Y_k - total of k^{th} replication over genotypes

G_i - total of i^{th} genotype over replication

P_i - total of i^{th} parents over replication

F_i - total of i^{th} female parents over replication

M_i - total of i^{th} male parents over replication

C_i - total of i^{th} hybrid over replication

The standard error of difference (SE_d) between the genotypic means and critical difference (CD) were calculated as follows,

$SE_d= \pm (2\ EMS/r)^{0.5}$

Source of Variance	d.f.	Sum of Square
Replication	r-1	$\sum_{k=1}^{r} \frac{Y^2_k}{g} - \frac{(Y_k)^2}{g.r.}$ ---------- (1)
Genotype	g-1	$\sum_{i=1}^{g} \frac{G^2_i}{g} - \frac{(G_i)^2}{g.r.}$ ----------(2)
Parents	p-1	$\sum_{i=1}^{p} \frac{P^2_i}{r} - \frac{(P_i)^2}{p.r.}$ ----------(3)
Female (lines)	f-1	$\sum_{i=1}^{f} \frac{F^2_i}{r} - \frac{(F_i)^2}{f.r.}$ ----------(4)
Male (tester)	m-1	$\sum_{i=1}^{m} \frac{M^2_i}{r} - \frac{(M_i)^2}{m.r.}$ ----------(5)
Line vs tester	1	(3) - (4) - (5) ---------- (6)
Hybrids	mf-1	$\sum_{i=1}^{mf} \frac{C^2_i}{r} - \frac{(C_i)^2}{m.f.r.}$ ----------(7)
Parents vs Hybrids	1	(2) – (3) – (7) ----------(8)
Error	(r-1) (g-1)	TSS – (1) – (2) ----------(9)
Total	(gr-1)	$\sum_{i=1}^{g}\sum_{k=1}^{r} Y^2k - (\sum_{i=1}^{g}\sum_{k=1}^{r} Y^2k)^2/ gr$ ----------(10)

Where:

EMS = Error mean square

r = Number of replication

CD = $t_{(g-1)(r-1)} \times S.E._d$

Where, $t_{(g-1)(r-1)}$ is the t value at (g-1) (r-1) degrees of freedom

If the differences among the hybrids were found significant, only then combining the analysis of combining ability was done.

3.5.4.3.1 Combining Ability Analysis

Based on the mathematical model suggested by Kempthorne (1957), the combining ability analysis for different traits was carried out.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

Y_{ijk} = Performance of $(i \times j)^{th}$ hybrid in k^{th} replication

μ = Population mean

g_i = *gca* effect of i^{th} parent

g_j = *gca* effect of j^{th} parent

s_{ij} = *sca* effect of $(i \times j)^{th}$ cross

r_k = effect of k^{th} replication

e_{ijk} = Random experimental error associated with ijk^{th} observation in k^{th} replication

i = Number of parents (female)

j = Number of parents (male)

k = Number of replications

The effects in the above model were assumed to be fixed unknown parameters except e_{ijk} which was assumed to be normally and independently distributed with mean zero and common variance (σ^2). The ANOVA based on this model as follows:

Source of Variations	**d.f.**	**M.S.S.**	**Expectations of Mean Square**
Replication	r-1	-	
Hybrids	fm - 1	-	
Lines	(f-1)	fhM	σ^2 e + r[Cov(FS)] - 2Cov(HS)] + rm [Cov (HS)]
Testers	(m-1)	MhMS	Cov FS-2Cov(HS) + rfCov(HS)
Lines × testers	(m-1) (f-1)	FmhMS	σ^2 e + r [Cov (FS) - 2Cov (HS)]
Error	(r-1) (mf-1)	EMS	σ^2e
Total	mf r - 1		

The different sum of squares was computed based on formula:

$CF = (Y..)^2 / mfr$

$TSS = \sum_i \sum_j \sum_k (Y_{ijk})^2 - CF$

$fhSS = [\sum_i (Y_{i..})^2 / mr] - CF$

$mhSS = [\sum_i (Y._{j.})^2 / fr] - CF$

$fmhSS = [\sum_i \sum_j (Y_{ij.})^2 / r] - CF - fhSS - mhSS$

$ESS = TSS - [\sum_k (Y..{}_k)^2 / fm - CF] - [\sum_i \sum_j (Y_{ij.})^2 / r - CF]$

Where,

$Y..$ = Total number of all hybrids over all replication

$Y_{i..}$ = i^{th} total number of female parents

$Y_{.j.}$ = j^{th} total number of male parents

$Y_{ij.}$ = $(i \times j)^{th}$ total number of hybrids

$Y..{}_k$ = k^{th} total replications

$Cov\ (HS) = (mh\ MS + fh\ MS - 2fmh\ MS) / r\ (m + f)$

$Cov\ (FS) = [mh\ MS + fh\ MS + fmh\ MS - 3e\ MS + 6r\ Cov\ (HS) - r\ (m + f).Cov(HS)] / 3r$

The mean sum of squares was calculated by dividing sum of squares with their respective degree of freedom.

First, fmhMS was tested against eMS. If it is found significant then both fhMS and mhMS were tested against fmhMS. On the contrary, if fmhMS found non-significant, then both fhMS and mhMS were tested against eMS.

The general combining ability variance ($\sigma^2 gca$) and specific combining ability variance ($\sigma^2 sca$) were worked out as followes:

$\sigma^2 gca = Cov\ (HS)$

$\sigma^2 sca = Cov\ (FS) - 2\ Cov\ (HS)$

Degrees of dominance were identified as below:

$\sigma^2_A = \sigma^2 gca / [(1 + F)/4] = 4\sigma^2 gca$

$\sigma^2_D = \sigma^2 sca / [(1 + F)/2] = 2\sigma^2 sca$

Degree of dominance = $(2\sigma^2_D / \sigma^2_A)^{0.5}$

3.5.4.3.2 General Combining Ability Effects and Specific Combining Ability Effects

The GCA effects of parents (testers and lines) and SCA effects of each cross combination were identified using mean value as,

(a) *GCA* effect of i^{th} line (gi) = $(Y_{i..} / mr) - (Y.. / mfr)$

$$\sum_{i=1}^{f} g_i = 0$$

(b) *GCA* effect of j^{th} tester (gj) = $(Y_{.j.} / fr) - (Y.. / mfr)$

$$\sum_{j=1}^{m} g_j = 0$$

(c) *SCA* effect of $(i \times j)^{th}$ crosses $(s_{ij}) = (Y_{ij.} / r) - (Y... / mfr) - g_s - g_j$

$$\sum_{i=1}^{f} \sum_{j=1}^{m} s_{ij} = 0$$

Where,

$Y..$ = the total of all hybrids over replications

$Y_{i..}$ = total of hybrids involving ith female over all replication

$Y_{.j.}$ = total of hybrids involving jth male over all replication

$Y_{ij.}$ = total of $(i \times j)^{th}$ hybrids over all replications

(d) Testing the significance of *gca* and *sca* effects, the standard error (S.E.) were estimated as follows:

S.E. (gi) = $[(f-1)\ eMS / mfr\ ]^{0.5}$

S.E. (gj) = $[(m-1)\ eMS / mfr\ ]^{0.5}$

S.E. (gij) = $[(f-1)\ (m-1) eMS / mfr\ ]^{0.5}$

3.5.4.3.3 Estimation of Proportional Contribution of Testers, Lines, their Interactions

The proportional contribution was calculated as:

i) Contribution of lines (%) = $\frac{SS\ (lines)}{SS\ (Crosses)} \times 100$

ii) Contribution of testers (%) $= \frac{\text{SS (testers)}}{\text{SS (Crosses)}} \times 100$

iii) Contribution of (l x t) (%) $= \frac{\text{SS (l x t)}}{\text{SS (Crosses)}} \times 100$

Where,

SS (lines) = Sum of squares due to lines

SS (testers) = Sum of squares due to testers

SS (l x t) = Sum of squares due to lines × testers

SS (Crosses) = Sum of squares due to cross combinations

3.5.4.4 Estimation of Heterosis

The heterosis magnitude was identified in relation to mid-parent, better parent and standard check. It was calculated based on per cent decrease or increase of F_1 hybrids over mid-parent (MP), better parent (BP) and standard check (SC) following the methods described by Turner (1953) and Hayes (1952).

Heterosis was expressed as per cent deviation of F_1 hybrid performance from the better parent, mid-parent and standard check

$$\% \text{ Heterosis better parent} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where, $\overline{F_1}$ and $\overline{BP}$ are mean values of F_1 hybrids and better parent, respectively.

$$\% \text{ Heterosis mid parent} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where, $\overline{F_1}$ and $\overline{MP}$ are mean values of F_1 hybrids and better parent, respectively.

$$\% \text{ Heterosis over standard check} = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

Where, $\overline{F_1}$ and $\overline{SC}$ are mean values of F_1 hybrids and standard check, respectively.

3.5.4.4.1 Test of Significance for Heterosis Over Better Parent (BP), Mid-Parent (MP) and Standard Check (SC):

To test the significant of extent of heterosis, standard errors (S.E.) and the critical difference (C.D.) were identified as under:

CD = S.E. (d) × t value

Where,

$$SE\ (d) = SD_d = \pm\sqrt{2\frac{MSE}{r}}$$

MSE = error mean square as calculated in RBD using parents, F_1 hybrids and standard checks

r = number of replication

The critical difference (C.D.) was calculated by multiplying the SD_d with t-value (at both error df $P \leq 0.05$ and $P \leq 0.01$ level of significance)

3.5.5 Observations Recorded from Experiment II (b)

3.5.5.1 Generation Mean Analysis

The statistical analysis for generation mean analysis was carried out by using 'PBTools' software programme developed by 'IRRI'.

3.5.5.1.1 Computation of Generation Means

From individual plant data, means of all generations were computed:

$$\mathbf{x} = \frac{\sum x_i}{n}$$

Where:

$\bar{x}$ = generation mean

$\sum x_i$ = grand total

x_i = i^{th} observation in a particular generation

n = number of plants

3.5.5.1.2 Variance of Generation Means ($V_{\bar{x}}$)

Within each generation individual variance was identified replication wise and pooled. The variance of generation means ($V_{\bar{x}}$) was calculated by dividing the variance within generation (V x) with the no. of individuals within generations.

$$V_{\bar{x}} = \frac{V_x}{n}$$

Where,

$V\bar{x}$ = Variance of generation mean

Vx = Variance among individuals with in generation

n = number of observations within generation

The value thus obtained was utilized for further analysis.

3.5.5.2 Genetic Analysis

3.5.5.2.1 Detection of Genetic Effects

Digenic interaction components were detected by using scaling tests as given by Mather (1949) and Hayman and Mather (1955). The gene effects estimates were derived from the generation mean analysis of joint scaling tests (Cavalli, 1952) and perfect fit solution of Hayman (1958).

3.5.5.2.2 Simple Scaling Test

The adequacy of additive-dominance model was tested by scaling tests (Mather, 1949; Hayman and Mather, 1955).

$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$

$B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$

$D = 2\bar{F}_2 - \bar{B}_1 - \bar{B}_2$

The variance of A, B, C and D were calculated as follows:

$V_A = 4V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)$

$V_B = 4V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)$

$V_C = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$

$V_D = 4V(\bar{F}_2) + V(\bar{B}_1) + V(\bar{B}_2)$

Then standard error of A, B, C and D is worked out by taking square root of respective variance and *t* values are calculated by dividing the effects of A, B, C and D by their respective error.

The calculated *t* values of these tests are compared against 1.96, which is the table value of *t* at 5% level of significance. The significance of any of these four scales indicates the presence of epistasis.

The type of epistasis is revealed by the significant of specific scale as given below,

a) The significance of A and B scales indicates the presence of all the three types of non-allelic gene interaction, *viz.*, additive × additive [i], additive × dominance [j] and dominance × dominance [l].
b) The significance of C scale suggests dominance × dominance [l] type of non-allelic gene interactions
c) The significance of D scale reveals additive × additive [i] type of gene interaction,
d) Significance of C and D scales indicates additive × additive [i] and dominance × dominance [l] type gene interactions.

3.5.5.2.3 Estimation of Genetic Effects and Joint Scaling Test

The main drawback of scaling test is that out of six populations only three or four are included in the test at a time. In order to overcome this problem another test, known as joint scaling test has been developed, which permits any combination of the six populations at a time. Estimation of various genic effects and test of fitness of appropriate genetic model was done according to joint scaling test of Cavalli (1952), as described in detail by Mather and Jinks (1982). Joint scaling test in general consists of estimating genetic parameters [m], [d] and [h] by weighted least square technique followed by comparison of observed means with their expected values

derived from the estimates of the parameters. The observed and expected generation means were compared by Chi-square test with the degree of freedom equals to number of generations (n) minus the number of parameters (p) estimated.

In the present study, the estimation of genic effects and chi-square test of goodness of fit were carried out using three-parameter and six-parameter models. In three-parameter model (additive-dominance model or non-epistatic model), the following genic effects were estimated:

[m] = Inbred population mean = $1/2\bar{P}_1 + 1/2\bar{P}_2 + 4\bar{F}_2 - 2\bar{B}_1 - 2\bar{B}_2$

[d] = additive gene effects = $1/2\bar{P}_1 - 1/2\bar{P}_2$

[h] = dominance gene effects = $6\bar{B}_1 + 6\bar{B}_2 - 8\,\bar{F}_2 - \bar{F}_1 - 3/2\bar{P}_1 - 3/2\bar{P}_2$

3.5.5.2.4 Digenic Epistatic Model

When simple additive-dominance model was inadequate, a weighted six-parameter model which included digenic epistatic effects was fitted. An exact fit solution was employed by Hayman (1958), who gave the following formulae:

m = Mean effects = $\bar{F}_2$

[d] = additive effects = $\bar{B}_1 - \bar{B}_2$

[h] = dominance effect = $\bar{F}_1 - 4\bar{F}_2 - 1/2\bar{P}_1 - 1/2\bar{P}_2 + 2\bar{B}_1 + 2\bar{B}_2$

[i] = additive × additive interaction = $2\bar{B}_1 + 2\bar{B}_2 - 4\bar{F}_2$

[j] = additive × dominance interaction = $\bar{B}_1 - 1/2\,\bar{P}_1 - \bar{B}_1 + 1/2\bar{P}_2$

[l] = dominance × dominance interaction = $\bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\,\bar{B}_1 - 4\bar{B}_2$

Where,

$\bar{P}_1, \bar{P}_2, \bar{F}_1, \bar{F}_2, \bar{B}_1$ and $\bar{B}_2$ are the mean values over replication for the character in $\bar{P}_1, \bar{P}_2, \bar{F}_1, \bar{F}_2, \bar{B}_1$ and $\bar{B}_2$ populations, respectively. The variance for the above gene effects are obtained as follows:

Vm = V ($\bar{F}_2$)

Vd = V ($\bar{B}_1$) + V ($\bar{B}_2$)

Vh = V ($\bar{F}_1$) +16V ($\bar{F}_2$) + ¼V ($\bar{P}_1$) + ¼V ($\bar{P}_2$) +4V ($\bar{B}_1$) + 4V ($\bar{B}_2$)

Vi = V ($\bar{B}_1$) + ¼V ($\bar{B}_2$) + 16V ($\bar{F}_2$)

Vj = V ($\bar{B}_1$) + ¼V ($\bar{P}_1$) + V ($\bar{B}_2$) + ¼V ($\bar{P}_2$)

$Vl = V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)$

Since the number of estimated parameters is equal to the number of generation used, no degree of freedom left for testing adequacy of the model. However, standard errors of the parameters were obtained by usual ways as suggested by Mather and Jinks (1971). The standard error was calculated as follows:

$SE(m) = V(\bar{F}_2)^{1/2}$

$SE(d) = [V(\bar{B}_1) + V(\bar{B}_2)]^{1/2}$

$SE(h) = [V(\bar{F}_1) + 16V(\bar{F}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2) + 4V(\bar{B}_1) + 4V(\bar{B}_2)]^{1/2}$

$SE(i) = [V(\bar{B}_1) + \frac{1}{4}V(\bar{B}_2) + 16V(\bar{F}_2)]^{1/2}$

$SE(j) = [V(\bar{B}_1) + \frac{1}{4}V(\bar{P}_1) + V(\bar{B}_2) + \frac{1}{4}V(\bar{P}_2)]^{1/2}$

$SE(l) = [V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)]^{1/2}$

The significance of the gene effects can be tested by 't' test:

$t(m) = [m]/ SE[m]$

$t(d) = [d]/ SE[d]$

$t(h) = [h]/ SE[h]$

$t(i) = [i]/ SE[i]$

$t(j) = [j]/ SE[j]$

$t(l) = [l]/ SE[l]$

The calculated value of the *t* is compared with 1.96, which is the table value of the *t* at 5% level of significance. If the calculated value is greater than 1.96 (table value), it is considered as significant and vice versa.

Results

4. RESULTS

The present study entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" was carried out at the Department of Vegetable Science, College of Agriculture, Vellayani, during 2015-2018.

The study was conducted to identify the sources for ChiLCV resistance in a collection of germplasm through natural and artificial screening; to identify potential parents for ChiLCV resistant hybrid breeding based on mean performance and general combining ability (GCA) effects; to identify superior performing ChiLCV resistant hybrids on the basis of expressed heterosis and specific combining ability (SCA) effects; and to study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and for ChiLCV resistance using generation mean analysis. Experimental data from all the experiments were subjected to statistical analysis and the results are reported under the following sub-heads:

4.1 EVALUATION OF CHILLI GENOTYPES FOR YIELD AND QUALITY

4.1.1 Analysis of Variance (ANOVA) for the Experimental Design

The results pertaining to the ANOVA for the experimental design indicated that the mean squares (MS) due to genotypes were highly significant at $P \leq 0.01$ for all the 12 characters *viz.,* plant height, primary branches plant^{-1}, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection (Table 4).

4.1.2 Mean Performance of Chilli Genotypes for Vegetative, Flowering, Fruit Yield and Quality Characters

The mean performance of 70 genotypes for various characters under study were recorded from experiment I (a) and are presented in Tables 5a to 5c.

Table 4. Analysis of variance for various characters in 70 genotypes of chilli

Source of variation	Replication	Genotypes	Error
df	2	69	138
Plant height (cm)	2.33	248.41**	9.74
Primary branches plant^{-1}	0.48	1.05**	0.08
Days to first flower	0.22	18.24**	1.00
Days to first harvest	1.62	26.52**	1.94
Fruit length (cm)	0.59	4.80**	0.09
Fruit girth (cm)	0.004	1.03**	0.01
Fruit weight (g)	0.05	2.78**	0.01
Fruits plant^{-1}	7.56	155.42**	9.69
Yield plant^{-1} (g)	165.69	33944.85**	56.76
Yield plot^{-1} (kg)	0.93	30.67**	0.50
Vitamin C (mg100^{-1} g)	4.01	202.51**	3.70
Carotenoids (mg100^{-1} g)	13.83	3550.70**	4.89
Coefficient of infection (%)	1.42	1896.46**	2.90

Data represent mean sum of squares; *significant at $P \leq 0.05$; **significant at $P \leq 0.01$

4.1.2.1 Vegetative Characters

4.1.2.1.1 Plant Height (cm)

The genotype T_{58} was the tallest (73.33 cm) which was on par with T_{31} (71.93 cm). The mean performance for plant height in genotypes ranged from 31.33 cm in T_{22} to 73.33 cm in T_{58}, with the overall mean of 46.59 cm among 70 genotypes (Table 5a).

4.1.2.1.2 Primary Branches Plant^{-1}

Among genotypes, the primary branches plant^{-1} ranged from 2.07 in T_{16} to 4.77 in T_{51}, with the overall mean of 3.27 (Table 5a). The genotype T_{51} had maximum number of primary branches (4.77) which was on par with T_{25} (4.63) and T_{11} (4.50).

4.1.2.2 Flowering Characters

4.1.2.2.1 Days to First Flower

The genotype T_{10} (26.94) and T_{32} (28.26) were at par for early flowering. The genotype T_{61} was late to flower (38.70) which was on par with T_{25} (38.02), T_{60} (37.88), T_{54} (37.78), T_{49} (37.71), T_{37} (37.33) and T_9 (37.23). Among genotypes, the overall mean for days to first flower was 34.52 (Table 5a).

4.1.2.2.2 Days to First Harvest

Among genotypes, T_{19} required less number of days for first harvest (42.00) followed by T_{32} (48) and T_{10} (48). The genotype T_{11} required maximum number of days for first harvest (61.76). The overall mean performance for days to first harvest among genotypes was 55.16 (Table 5a).

4.1.2.3 Fruit and Yield Characters

4.1.2.3.1 Fruit Length (cm)

The genotype T_{10} exhibited maximum fruit length (8.50 cm) which was on par with T_{31} (8.28 cm) and T_{28} (8.10 cm). The genotypes T_{38} and T_{70} exhibited minimum fruit length (3.2 cm) and they were at par with T_{36} (3.44cm), T_{21} (3.47

Table 5a. Mean performance of genotypes for plant height, primary branches plant^{-1}, days to first flower and days to first harvest

Treatments	Genotypes	Plant height (cm)	Primary branches plant^{-1}	Days to first flower	Days to first harvest
T_1	Sel-1	46.37	3.47	37.01	57.00
T_2	Sel-3	56.67	4.33	35.02	56.67
T_3	Sel-4	43.00	2.67	34.03	57.67
T_4	Sel-5	53.67	2.73	35.97	56.00
T_5	Sel-6	42.33	4.07	33.25	54.04
T_6	Punjab Lal	58.53	3.30	36.13	57.00
T_7	Punjab Tej	46.07	3.47	37.07	58.00
T_8	Punjab Sindhuri	45.67	3.33	37.00	58.00
T_9	Punjab Guchhader	48.00	4.20	37.23	58.00
T_{10}	Vellayani Athulya	47.67	3.73	26.94	48.00
T_{11}	Ujwala	59.13	4.50	35.33	61.76
T_{12}	DCA 268	34.73	2.67	35.90	57.00
T_{13}	DCA 167	44.00	3.27	33.30	54.00
T_{14}	DCA 157	43.73	3.67	34.30	55.00
T_{15}	DCA 142	38.33	2.47	35.70	56.00
T_{16}	PS 1	46.87	2.07	33.93	54.00
T_{17}	Byadagi Dabbi	43.60	3.83	34.93	55.00
T_{18}	Byadagi Kaddi	39.67	4.07	34.92	55.00
T_{19}	Jwalasakhi	33.67	4.00	29.84	42.00
T_{20}	EC 354890	38.00	3.20	31.93	53.00
T_{21}	EC 599958	34.90	3.00	33.99	54.00
T_{22}	IC 572483	31.33	4.27	32.93	53.00
T_{23}	EC 599960	34.47	3.80	35.92	56.00
T_{24}	IC 572468	37.03	3.00	35.91	57.00
T_{25}	Nagachilli	52.45	4.63	38.02	59.00
T_{26}	Arka Lohith	48.47	3.33	34.92	56.00
T_{27}	Anugraha	46.33	3.53	30.72	52.00
T_{28}	CA-3 (EC-391083)	53.33	3.53	29.89	50.00
T_{29}	CA-5 (EC-596920)	57.80	3.47	30.88	52.00
T_{30}	CA-6 (EC-596940)	58.67	3.20	32.17	52.00
T_{31}	CA-8 (EC-599969)	71.93	3.60	30.02	50.00
T_{32}	CA-32 (DWD-2)	44.33	2.80	28.26	48.00
T_{33}	Jwalamukhi	43.27	3.13	33.84	55.00
T_{34}	Keerthi	55.67	4.17	31.53	51.67
T_{35}	Pusa Jwala	45.00	3.07	35.80	56.00
T_{36}	Pant C 1	50.67	2.40	35.30	55.00
T_{37}	Punjab Surkh	39.33	2.80	37.33	58.00

cm) and T_{65} (3.70 cm). The overall mean performance of genotypes for fruit length was 5.35 cm (Table 5b).

4.1.2.3.2 Fruit Girth (cm)

The genotype T_{10} exhibited maximum fruit girth of 4.78 cm followed by T_{29} (4.25 cm). The lower fruit girth was exhibited in T_{38} (1.98 cm) which was on par with the genotype T_{41} (1.99 cm) (Table 5b).

4.1.2.3.3 Fruit Weight (g)

Fruit weight exhibited a wide variation range among genotypes from 7.57 g (T_{10}) to 2.20 g (T_{65}), with an overall mean of 3.91 g. Fruits of T_{10} recorded maximum weight of 7.57 g followed by T_{58} (6.23 g) and T_{31} (6.10 g) (Table 5b).

4.1.2.3.4 Fruits Plant^{-1}

A wide range of variation was noticed for fruits plant^{-1}. Among genotypes fruits plant^{-1} ranged from 137.33 (T_{53}) to 49.33 (T_{35}), with an overall mean of 90.46. The genotype T_{53} produced the higher number of fruits plant^{-1} and was on par with T_{34} (136), T_6 (132) and T_{22} (132) (Table 5b). The genotype T_{35} (49.33) produced lower number of fruits plant^{-1} and it was on par with T_{18} (51.67).

4.1.2.3.5 Yield Plant^{-1} (g)

The genotype T_{32} produced the maximum fruit yield plant^{-1} of 587.33 g followed by T_{34} (547.67 g), T_{52} (546.67 g), T_{56} (521.00 g), T_{53} (513.33 g), T_{48} (490.33 g) and T_{10} (455.00 g). The genotype T_{35} produced the minimum fruit yield of 125.33 g. The genotypes registered an overall mean of 322.80 g (Table 5c).

4.1.2.3.6 Yield Plot^{-1} (kg/6.48 m^2)

The genotype T_{32} recorded highest yield plot^{-1} of 16.10 kg/6.48 m^2 which was on par with T_{48} (16.06 kg/6.48 m^2). The genotype T_{35} recorded the lowest yield plot^{-1} (3.2 kg/6.48 m^2). The overall mean of genotypes for yield plot^{-1} was 8.85 kg/6.48 m^2 (Table 5c).

Table 5a. continued

Treatments	Genotypes	Plant height (cm)	Primary branches plant^{-1}	Days to first flower	Days to first harvest
T_{38}	Kashi Anmol	34.00	2.47	34.77	55.00
T_{39}	DCL 524	35.27	3.00	36.33	57.00
T_{40}	C-31-1	33.33	2.60	35.93	57.00
T_{41}	ACC-2-1	43.87	2.80	36.81	57.00
T_{42}	I-1	61.67	3.20	33.83	54.00
T_{43}	I-2	60.53	2.73	34.90	55.00
T_{44}	I-3	44.33	2.73	36.86	57.00
T_{45}	I-4	54.33	3.27	32.80	54.00
T_{46}	CHIVAR-1	48.67	3.33	36.33	56.33
T_{47}	CHIHYB-2	50.00	3.27	32.92	54.00
T_{48}	CHIVAR-3	43.33	2.67	30.00	51.67
T_{49}	CHIHYB-3	62.10	3.13	37.71	58.00
T_{50}	CHIVAR-2	45.67	2.83	34.17	55.00
T_{51}	CHIVAR-4	38.50	4.77	33.70	55.00
T_{52}	CHIVAR-6	42.33	3.47	36.00	56.55
T_{53}	CHIVAR-7	52.33	2.59	34.70	56.82
T_{54}	LCA-334	38.27	2.47	37.78	58.00
T_{55}	KA-2	42.00	2.33	33.72	55.00
T_{56}	CHIVAR-10	53.33	3.33	31.67	52.33
T_{57}	CHIVAR-8	49.67	3.67	35.71	56.02
T_{58}	CHIVAR-9	73.33	3.00	36.70	57.00
T_{59}	CHIVAR-5	57.00	3.80	35.75	56.00
T_{60}	Japani Longi	44.00	2.82	37.88	58.00
T_{61}	Perennial	59.33	3.50	38.70	59.00
T_{62}	VS-7	45.33	2.37	34.10	55.00
T_{63}	VS-9	47.67	2.77	34.89	56.00
T_{64}	S-217621	39.00	3.17	33.98	56.00
T_{65}	Sel. 40	35.33	3.83	36.88	57.00
T_{66}	Sel.7-1	39.33	3.17	32.86	54.00
T_{67}	Sel. 36-1	42.67	2.83	35.84	57.00
T_{68}	PLS-3-1	52.00	3.57	36.93	57.00
T_{69}	Sel. 20-1	55.00	2.97	33.93	55.00
T_{70}	ms-12	36.67	3.57	36.33	57.87
Mean		46.59	3.27	34.52	55.16
CD 5%		5.04	0.47	1.60	2.26
SE (m)		1.80	0.17	0.57	0.81

Table 5b. Mean performance of genotypes for fruit length, fruit girth, fruits plant^{-1} and fruit weight

Treatments	Genotypes	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}
T_1	Sel-1	6.39	2.91	4.14	99.33
T_2	Sel-3	4.57	2.56	3.60	84.67
T_3	Sel-4	5.47	3.63	4.53	70.33
T_4	Sel-5	5.40	2.30	3.30	99.00
T_5	Sel-6	6.27	3.13	4.28	97.00
T_6	Punjab Lal	4.46	2.82	3.13	132.00
T_7	Punjab Tej	5.17	2.31	3.19	105.00
T_8	Punjab Sindhuri	5.53	3.12	3.40	124.00
T_9	Punjab Guchhader	4.17	3.55	4.11	111.00
T_{10}	Vellayani Athulya	8.50	4.78	7.57	64.67
T_{11}	Ujwala	4.93	2.65	3.25	125.33
T_{12}	DCA 268	4.17	3.83	4.00	97.00
T_{13}	DCA 167	5.23	3.42	3.95	102.00
T_{14}	DCA 157	4.66	2.49	3.80	112.00
T_{15}	DCA 142	6.57	2.46	4.30	79.00
T_{16}	PS 1	4.56	2.16	3.90	112.00
T_{17}	Byadagi Dabbi	4.80	2.28	3.31	62.00
T_{18}	Byadagi Kaddi	6.87	2.34	4.15	51.67
T_{19}	Jwalasakhi	5.23	2.61	5.17	57.67
T_{20}	EC 354890	3.85	2.55	2.80	94.00
T_{21}	EC 599958	3.47	2.39	3.10	120.00
T_{22}	IC 572483	3.90	2.11	2.40	132.00
T_{23}	EC 599960	3.79	2.51	2.80	122.00
T_{24}	IC 572468	4.37	2.01	3.16	98.00
T_{25}	Nagachilli	4.77	2.56	4.20	84.00
T_{26}	Arka Lohith	5.82	3.60	4.25	98.00
T_{27}	Anugraha	5.80	2.66	3.90	109.00
T_{28}	CA-3 (EC-391083)	8.10	3.83	5.32	82.00
T_{29}	CA-5 (EC-596920)	7.23	4.25	4.50	60.00
T_{30}	CA-6 (EC-596940)	6.93	3.21	5.10	87.00
T_{31}	CA-8 (EC-599969)	8.28	3.71	6.10	62.00
T_{32}	CA-32 (DWD-2)	6.53	3.20	4.73	130.67
T_{33}	Jwalamukhi	6.30	2.95	4.17	65.67
T_{34}	Keerthi	4.20	3.37	4.07	136.00
T_{35}	Pusa Jwala	4.57	2.09	3.20	49.33
T_{36}	Pant C 1	3.44	2.03	3.10	69.33
T_{37}	Punjab Surkh	5.32	2.97	4.12	99.00

Table 5b. continued

Treatments	Genotypes	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}
T_{38}	Kashi Anmol	3.20	1.98	2.80	59.00
T_{39}	DCL 524	5.43	2.57	3.32	78.00
T_{40}	C-31-1	5.13	2.24	4.30	82.00
T_{41}	ACC-2-1	4.47	1.99	3.90	74.00
T_{42}	I-1	7.03	2.63	3.90	114.00
T_{43}	I-2	6.77	2.65	4.20	103.00
T_{44}	I-3	6.03	2.75	3.40	89.00
T_{45}	I-4	6.30	2.53	3.70	81.00
T_{46}	CHIVAR-1	3.80	3.07	3.65	79.33
T_{47}	CHIHYB-2	7.07	3.45	5.80	81.00
T_{48}	CHIVAR-3	4.57	3.03	3.90	127.33
T_{49}	CHIHYB-3	7.00	3.29	5.33	75.67
T_{50}	CHIVAR-2	7.93	3.69	4.60	92.00
T_{51}	CHIVAR-4	5.47	2.89	4.80	82.00
T_{52}	CHIVAR-6	5.97	3.04	4.67	122.33
T_{53}	CHIVAR-7	6.07	2.57	3.94	137.33
T_{54}	LCA-334	4.47	2.24	3.20	68.00
T_{55}	KA-2	4.43	2.12	2.95	74.00
T_{56}	CHIVAR-10	5.60	3.62	5.17	99.00
T_{57}	CHIVAR-8	5.60	2.97	4.20	99.00
T_{58}	CHIVAR-9	6.90	3.47	6.23	58.00
T_{59}	CHIVAR-5	6.60	3.38	5.03	65.67
T_{60}	Japani Longi	4.93	2.84	3.40	89.00
T_{61}	Perennial	4.80	3.35	3.10	81.00
T_{62}	VS-7	3.87	2.34	2.80	78.00
T_{63}	VS-9	4.77	2.84	3.10	71.00
T_{64}	S-217621	4.83	2.86	3.50	71.00
T_{65}	Sel. 40	3.70	2.07	2.20	82.00
T_{66}	Sel.7-1	5.03	2.45	3.10	92.00
T_{67}	Sel. 36-1	5.57	2.81	3.30	97.00
T_{68}	PLS-3-1	4.80	2.94	2.90	94.00
T_{69}	Sel. 20-1	3.93	2.68	2.95	91.00
T_{70}	ms-12	3.20	3.53	3.07	68.00
Mean		5.35	2.84	3.91	90.46
CD 5%		0.49	0.21	0.18	5.03
SE (m)		0.17	0.07	0.66	1.79

Table 5c. Mean performance of genotypes for yield plant^{-1}, yield plot^{-1}, vitamin C and carotenoids

Treatments	Genotypes	Yield plant^{-1} (g)	Yield plot^{-1} (kg)	Vitamin C (mg100^{-1} g)	Carotenoids (mg100^{-1} g)
T_1	Sel-1	411.33	10.87	81.00	197.35
T_2	Sel-3	303.00	8.23	72.33	158.00
T_3	Sel-4	308.33	8.40	74.00	134.33
T_4	Sel-5	304.00	8.07	68.67	228.67
T_5	Sel-6	352.67	9.48	88.67	204.00
T_6	Punjab Lal	385.00	9.67	119.33	233.00
T_7	Punjab Tej	305.00	7.79	97.33	239.67
T_8	Punjab Sindhuri	404.00	10.43	120.33	207.67
T_9	Punjab Guchhader	428.00	10.80	100.00	212.67
T_{10}	Vellayani Athulya	455.00	12.30	95.67	221.00
T_{11}	Ujwala	415.33	12.43	91.33	245.00
T_{12}	DCA 268	349.00	9.03	68.33	196.33
T_{13}	DCA 167	378.00	10.55	74.50	208.67
T_{14}	DCA 157	392.00	10.29	73.33	219.67
T_{15}	DCA 142	305.00	8.10	79.33	242.33
T_{16}	PS 1	410.00	11.10	80.67	174.33
T_{17}	Byadagi Dabbi	178.00	4.53	88.00	327.33
T_{18}	Byadagi Kaddi	166.00	4.27	84.33	331.33
T_{19}	Jwalasakhi	279.00	7.67	86.67	195.67
T_{20}	EC 354890	232.00	6.43	64.00	178.67
T_{21}	EC 599958	356.00	8.81	56.67	193.67
T_{22}	IC 572483	285.00	7.34	47.67	207.67
T_{23}	EC 599960	299.00	7.70	43.00	211.33
T_{24}	IC 572468	276.00	6.79	58.33	186.67
T_{25}	Nagachilli	325.00	8.69	83.00	226.67
T_{26}	Arka Lohith	385.00	9.93	93.00	220.00
T_{27}	Anugraha	396.00	10.23	85.67	196.67
T_{28}	CA-3 (EC-391083)	434.33	12.10	91.33	279.67
T_{29}	CA-5 (EC-596920)	242.00	6.22	87.33	275.67
T_{30}	CA-6 (EC-596940)	405.00	11.24	85.67	260.33
T_{31}	CA-8 (EC-599969)	342.00	9.53	91.33	245.67
T_{32}	CA-32 (DWD-2)	587.33	16.10	100.33	262.81
T_{33}	Jwalamukhi	229.00	6.33	85.33	210.00
T_{34}	Keerthi	547.67	14.97	96.33	205.67
T_{35}	Pusa Jwala	125.33	3.20	76.33	193.33
T_{36}	Pant C 1	168.00	4.23	77.67	197.67
T_{37}	Punjab Surkh	365.00	9.43	94.00	231.33

Table 5c. continued

Treatments	Genotypes	Yield plant^{-1} (g)	Yield plot^{-1} (kg)	Vitamin C (mg100^{-1} g)	Carotenoids (mg100^{-1} g)
T_{38}	Kashi Anmol	141.00	5.90	68.33	191.33
T_{39}	DCL 524	222.00	6.13	59.00	226.67
T_{40}	C-31-1	321.00	8.94	62.33	211.67
T_{41}	ACC-2-1	249.00	6.93	71.33	226.67
T_{42}	I-1	405.00	11.21	79.33	194.33
T_{43}	I-2	399.00	11.17	74.67	184.67
T_{44}	I-3	276.00	7.65	71.67	179.00
T_{45}	I-4	271.00	7.53	84.33	213.67
T_{46}	CHIVAR-1	263.67	7.10	93.00	223.00
T_{47}	CHIHYB-2	432.00	12.03	93.00	274.33
T_{48}	CHIVAR-3	490.33	16.06	103.33	215.33
T_{49}	CHIHYB-3	396.33	13.77	92.67	222.67
T_{50}	CHIVAR-2	420.00	14.03	75.33	205.00
T_{51}	CHIVAR-4	361.00	10.02	68.00	229.00
T_{52}	CHIVAR-6	546.67	15.12	113.67	227.67
T_{53}	CHIVAR-7	513.33	14.00	105.33	272.41
T_{54}	LCA-334	184.00	4.52	66.00	194.67
T_{55}	KA-2	201.00	5.30	73.67	187.67
T_{56}	CHIVAR-10	521.00	14.20	112.67	255.33
T_{57}	CHIVAR-8	389.67	10.03	94.00	221.33
T_{58}	CHIVAR-9	364.67	11.44	109.33	262.00
T_{59}	CHIVAR-5	327.67	12.87	92.33	206.03
T_{60}	Japani Longi	266.00	7.33	62.67	195.00
T_{61}	Perennial	205.00	5.64	81.33	208.33
T_{62}	VS-7	178.00	4.87	73.67	208.67
T_{63}	VS-9	185.00	5.13	72.00	207.67
T_{64}	S-217621	222.00	5.54	66.00	225.00
T_{65}	Sel. 40	159.00	4.12	76.00	195.33
T_{66}	Sel.7-1	268.00	7.01	75.67	184.33
T_{67}	Sel. 36-1	295.00	7.59	73.33	209.00
T_{68}	PLS-3-1	251.00	6.72	67.67	244.67
T_{69}	Sel. 20-1	249.00	6.40	74.33	166.67
T_{70}	ms-12	196.00	5.13	86.00	173.67
Mean		322.80	8.85	81.52	217.42
CD 5%		12.13	1.03	3.11	3.56
SE (m)		4.33	0.36	1.11	1.27

4.1.2.4 Quality Characters

4.1.2.4.1 Vitamin C (mg 100 g^{-1})

The vitamin C content among the genotypes ranged from 43.00 mg 100 g^{-1} (T_{23}) to 120.33 mg 100 g^{-1} (T_8). The genotype T_8 had highest content of vitamin C (120.33 mg 100 g^{-1}) and was on par with T_6 (119.33 mg 100 g^{-1}). The average mean of genotypes was 81.52 mg 100 g^{-1} (Table 5c).

4.1.2.4.2 Carotenoids (mg 100 g^{-1})

The genotype T_{18} had highest quantity of carotenoids (331.33 mg 100 g^{-1}) and was at par with the genotype T_{17} (327.33 mg 100 g^{-1}). The carotenoids among the genotypes ranged from 331.33 mg 100 g^{-1} (T_{18}) to 134.33 mg 100 g^{-1} (T_3), with an overall mean of 217.42 mg 100 g^{-1} (Table 5c).

4.1.3 Selection Index

Selection indices were computed for 70 genotypes based on the twelve characters *viz.*, plant height, primary branches $plant^{-1}$, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits $plant^{-1}$, yield $plant^{-1}$, yield $plot^{-1}$, vitamin C and carotenoids. The index value of each genotype was determined and they were ranked. The score obtained for the genotypes based on the selection index are given in Table 6.

Among the genotypes, T_{32} (CA-32) ranked first with the highest index value of 1227.35, followed by T_{53} (CHIVAR-7), T_{52} (CHIVAR-6), T_{56} (CHIVAR-10), T_{34} (Keerthi), T_{48} (CHIVAR-3) and T_{10} (Vellayani Athulya) ranked next position. The minimum scores were obtained for T_{35} (Pusa Jwala) followed by T_{38} (Kashi Anmol) with an index of 590.16 and 591.03, respectively. The top ranking seven genotypes redesignated as L1: CHIVAR-3, L2: CHIVAR-7, L3: CHIVAR-6, L4: CA-32, L5: Vellayani Athulya, L6: Keerthi and L7: CHIVAR-10 and were used as female parent (lines) in line × tester hybridization programme.

Table 6. Chilli genotypes ranked according to selection index

Treatments	Genotypes	Index	Ranks in ascending order
T_{32}	CA-32 (DWD-2)	1227.35	1
T_{53}	CHIVAR-7	1191.34	2
T_{52}	CHIVAR-6	1170.09	3
T_{56}	CHIVAR-10	1146.83	4
T_{34}	Keerthi	1146.18	5
T_{48}	CHIVAR-3	1088.57	6
T_{10}	Vellayani Athulya	1050.70	7
T_{28}	CA-3 (EC-391083)	1044.59	8
T_{47}	CHIHYB-2	1040.59	9
T_{6}	Punjab Lal	1036.81	10
T_{8}	Punjab Sindhuri	1016.61	11
T_{9}	Punjab Guchhader	1011.41	12
T_{30}	CA-6 (EC-596940)	1001.26	13
T_{11}	Ujwala	989.79	14
T_{58}	CHIVAR-9	983.56	15
T_{49}	CHIHYB-3	971.34	16
T_{57}	CHIVAR-8	962.71	17
T_{42}	I-1	961.23	18
T_{50}	CHIVAR-2	955.11	19
T_{26}	Arka Lohith	953.25	20
T_{1}	Sel-1	947.47	21
T_{14}	DCA 157	946.07	22
T_{37}	Punjab Surkh	941.53	23
T_{27}	Anugraha	934.67	24
T_{43}	I-2	929.70	25
T_{16}	PS-1	927.73	26
T_{31}	CA-8 (EC-599969)	915.40	27
T_{13}	DCA 167	912.83	28
T_{7}	Punjab Tej	903.32	29
T_{5}	Sel-6	893.46	30
T_{51}	CHIVAR-4	886.95	31
T_{25}	Nagachilli	882.82	32
T_{59}	CHIVAR-5	869.07	33
T_{31}	EC 599969	861.50	34
T_{4}	Sel-5	858.33	35
T_{12}	DCA 268	853.35	36
T_{15}	DCA 142	853.28	37

Table 6. continued

Treatments	Genotypes	Index	Rank in ascending order
T_{67}	Sel. 36-1	824.02	38
T_{29}	CA-5 (EC-596920)	822.43	39
T_{40}	C-31-1	819.42	40
T_{23}	EC 599960	814.88	41
T_{68}	PLS-3-1	814.74	42
T_{46}	CHIVAR-1	813.41	43
T_{45}	I-4	807.05	44
T_{22}	IC 572483	804.79	45
T_{17}	Byadagi Dabbi	800.26	46
T_{18}	Byadagi Kaddi	779.47	47
T_{2}	Sel-3	778.69	48
T_{41}	ACC-2-1	771.41	49
T_{44}	I-3	769.60	50
T_{60}	Japani Longi	765.89	51
T_{66}	Sel-7-1	760.59	52
T_{24}	IC 572468	760.19	53
T_{19}	Jwalasakhi	747.96	54
T_{61}	Perennial	744.11	55
T_{33}	Jwalamukhi	739.71	56
T_{3}	Sel-4	737.58	57
T_{69}	Sel-20-1	734.47	58
T_{39}	DCL 524	728.12	59
T_{64}	S-217621	724.33	60
T_{20}	EC 354890	704.68	61
T_{63}	VS-9	685.22	62
T_{62}	VS-7	682.39	63
T_{55}	KA-2	677.16	64
T_{70}	ms-12	665.72	65
T_{36}	Pant C 1	661.23	66
T_{54}	LCA-334	656.05	67
T_{65}	Sel-40	652.01	68
T_{38}	Kashi Anmol	591.03	69
T_{35}	Pusa Jwala	590.16	70

4.1.4 Field Screening of Chilli Genotypes for ChiLCV Resistance

The field screening was undertaken in experiment I (b) to evaluate 70 chilli germplasm against chilli leaf curl disease. The genotypes / accessions were evaluated based on severity scale 0-6 (Banerjee and Kalloo, 1987). The symptom severity on individual plant basis was noted to calculate disease severity index (DSI). The DSI was multiplied by disease incidence (DI) and divided by 100 to get Coefficient of Infection (CI). All the genotypes were assigned specific disease reaction based on CI (Kumar *et al.*, 2006). The reactions of 70 chilli genotypes to ChiLCV under natural field conditions are presented in Table 7.

Days taken for first appearance of the symptoms of the disease on the genotypes screened is given in Table 8. Out of 70 genotypes screened, ten genotypes were found to be completely free (symptomless) from ChiLCV infection, and were, therefore regarded as symptomless genotypes. The genotype which showed symptomless reaction to ChiLCV included T_2, T_3, T_5, T_{46}, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67} (Table 7)

Out of the remaining 60 genotypes, five genotypes showed highly resistant reaction and they were T_{51}, T_{60}, T_{61}, T_{68} and T_{69}. The first disease symptom appearance was delayed upto 45 days after transplanting (DAT) in genotype T_{51}, whereas, in genotypes T_{60}, T_{61}, T_{68} and T_{69} it was delayed up to 60 DAT (Table 8).

Out of the remaining 55 genotypes, six genotypes showed resistant reaction with CI ranging from 5 to 10. The genotypes which showed resistant reaction to ChiLCV included T_4, T_6, T_{23}, T_{28}, T_{58} and T_{64} (Table 7). Among six genotypes, T_6 had early disease appearance (within 15 DAT). Remaining five genotypes expressed delayed symptom development and first symptoms were visible 30 DAT in T_{23}; 45 DAT in T_4, T_{28} and T_{58}; and 60 DAT in T_{64} (Table 8).

Twelve genotypes were moderately resistant with CI ranged from 10 to 20. The genotypes which showed moderate resistant reaction to ChiLCV included T_1, T_8, T_{21}, T_{25}, T_{29}, T_{31}, T_{32}, T_{42}, T_{48}, T_{59}, T_{62} and T_{70}. Four genotypes (T_8, T_{21}, T_{42} and

Table 7. Screening of 70 chilli genotypes against ChiLCV disease under field conditions

Treatments	Genotypes	No of plants screened per replication	Mean number of infected plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease Reaction[4]
			0	1	2	3	4	5	6				
T_1	Sel-1	20	3.33	9.00	3.67	4.00	0.00	0.00	0.00	23.61	83.33	19.68	MR
T_2	Sel-3	20	20.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_3	Sel-4	20	20.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_4	Sel-5	20	6.33	9.67	4.00	0.00	0.00	0.00	0.00	14.72	68.33	10.07	R
T_5	Sel-6	20	20.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_6	Punjab Lal	20	7.33	6.33	6.33	0.00	0.00	0.00	0.00	15.83	63.33	9.97	R
T_7	Punjab Tej	20	1.00	2.67	5.67	5.00	5.67	0.00	0.00	43.06	95.00	40.90	MS
T_8	Punjab Sindhuri	20	3.67	8.67	3.00	4.67	0.00	0.00	0.00	23.89	81.67	19.47	MR
T_9	Punjab Guchhader	20	1.00	5.33	2.67	5.00	6.00	0.00	0.00	41.39	95.00	39.35	MS
T_{10}	Vellayani Athulya	20	1.67	3.67	2.33	5.67	6.67	0.00	0.00	43.33	91.67	39.75	MS
T_{11}	Ujwala	20	1.67	2.33	5.67	4.33	6.00	0.00	0.00	42.22	91.67	38.71	MS
T_{12}	DCA 268	20	0.00	0.00	1.67	5.67	3.67	9.00	0.00	66.67	100.00	66.67	S
T_{13}	DCA 167	20	3.00	0.33	3.67	4.00	9.00	0.00	0.00	46.39	85.00	39.43	MS
T_{14}	DCA 157	20	0.00	0.00	0.00	6.33	5.33	8.33	0.00	68.33	100.00	68.33	S
T_{15}	DCA 142	20	0.00	0.00	0.67	3.33	6.33	9.67	0.00	70.83	100.00	70.83	S
T_{16}	PS 1	20	2.67	2.33	1.33	4.00	9.67	0.00	0.00	46.39	86.67	40.22	MS
T_{17}	Byadagi Dabbi	20	0.00	1.00	0.00	4.33	3.67	11.00	0.00	69.72	100.00	69.72	S
T_{18}	Byadagi Kaddi	20	0.00	0.67	0.33	3.33	5.67	10.00	0.00	70.00	100.00	70.00	S
T_{19}	Jwalasakhi	20	2.33	0.67	4.67	6.33	6.00	0.00	0.00	44.17	88.33	39.01	MS
T_{20}	EC 354890	20	0.00	0.00	1.00	4.67	6.67	7.67	0.00	67.50	100.00	67.50	S
T_{21}	EC 599969	20	5.67	4.00	3.33	5.33	1.67	0.00	0.00	27.78	71.67	19.83	MR
T_{22}	IC 572483	20	2.00	1.33	5.00	5.33	6.33	0.00	0.00	43.89	90.00	39.47	MS
T_{23}	EC 599960	20	8.33	2.67	9.00	0.00	0.00	0.00	0.00	17.22	58.33	10.04	R

Table 7. continued

Treatments	Genotypes	No of plants screened per replication	Mean number of infected plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease Reaction[4]
			0	1	2	3	4	5	6				
T_{24}	IC 572468	20	1.00	2.00	8.00	4.33	4.67	0.00	0.00	41.39	95.00	39.36	MS
T_{25}	Nagachilli	20	4.33	6.67	4.00	5.00	0.00	0.00	0.00	24.72	78.33	19.33	MR
T_{26}	Arka Lohith	20	0.67	2.00	8.67	4.33	4.33	0.00	0.00	41.39	96.67	40.00	MS
T_{27}	Anugraha	20	2.00	1.00	5.67	4.67	6.67	0.00	0.00	44.17	90.00	39.75	MS
T_{28}	CA-3 (EC-391083)	20	6.67	9.00	4.33	0.00	0.00	0.00	0.00	14.72	66.67	9.82	R
T_{29}	CA-5 (EC-596920)	20	4.00	8.00	3.33	4.67	0.00	0.00	0.00	23.89	80.00	19.10	MR
T_{30}	CA-6 (EC-596940)	20	1.00	1.33	9.00	4.67	4.00	0.00	0.00	41.11	95.00	39.06	MS
T_{31}	CA-8 (EC-599969)	20	3.67	7.33	5.33	3.67	0.00	0.00	0.00	24.17	81.67	19.72	MR
T_{32}	CA-32 (DWD-2)	20	2.33	12.00	2.67	3.00	0.00	0.00	0.00	21.94	88.33	19.39	MR
T_{33}	Jwalamukhi	20	0.67	5.00	5.00	3.33	6.00	0.00	0.00	40.83	96.67	39.43	MS
T_{34}	Keerthi	20	1.67	2.33	5.00	5.00	6.00	0.00	0.00	42.78	91.67	39.21	MS
T_{35}	Pusa Jwala	20	0.00	0.00	0.00	0.33	5.00	4.33	10.33	87.22	100.00	87.22	HS
T_{36}	Pant C 1	20	0.00	0.00	1.33	4.33	4.00	10.33	0.00	69.44	100.00	69.44	S
T_{37}	Punjab Surkh	20	0.33	4.67	5.33	5.33	4.33	0.00	0.00	40.56	98.33	39.86	MS
T_{38}	Kashi Anmol	20	0.00	0.00	0.00	0.00	0.00	6.67	13.33	94.44	100.00	94.44	HS
T_{39}	DCL 524	20	0.00	0.33	1.67	3.33	3.33	11.33	0.00	69.72	100.00	69.72	S
T_{40}	C-31-1	20	2.00	1.00	5.33	5.00	6.67	0.00	0.00	44.44	90.00	39.96	MS
T_{41}	ACC-2-1	20	2.33	1.33	2.33	7.67	6.33	0.00	0.00	45.28	88.33	39.99	MS
T_{42}	I-1	20	5.33	3.33	5.33	6.00	0.00	0.00	0.00	26.67	73.33	19.57	MR
T_{43}	I-2	20	2.00	1.67	3.33	6.00	7.00	0.00	0.00	45.28	90.00	40.64	MS
T_{44}	I-3	20	0.00	1.00	0.67	2.67	4.67	11.00	0.00	70.00	100.00	70.00	S
T_{45}	I-4	20	0.00	0.00	0.00	6.67	3.67	9.67	0.00	69.17	100.00	69.17	S
T_{46}	CHIVAR-1	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{47}	CHIHYB-2	20	0.67	4.67	3.67	7.00	4.00	0.00	0.00	40.83	96.67	39.43	MS
T_{48}	CHIVAR-3	20	5.00	4.33	4.33	6.33	0.00	0.00	0.00	26.67	75.00	19.94	MR
T_{49}	CHIHYB-3	20	0.33	4.67	5.33	5.33	4.33	0.00	0.00	40.56	98.33	39.85	MS

Table 7. continued

Treatments	Genotypes	No of plants screened per replication	Mean number of infected plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease Reaction[4]
			0	1	2	3	4	5	6				
T_{50}	CHIVAR-2	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{51}	CHIVAR-4	20	9.33	10.67	0.00	0.00	0.00	0.00	0.00	8.89	53.33	4.75	HR
T_{52}	CHIVAR-6	20	1.00	3.67	4.33	6.00	5.00	0.00	0.00	41.94	95.00	39.76	MS
T_{53}	CHIVAR-7	20	1.33	4.00	3.00	6.33	5.33	0.00	0.00	41.94	93.33	39.11	MS
T_{54}	LCA-334	20	0.00	0.00	2.33	3.67	5.33	8.67	0.00	66.94	100.00	66.94	S
T_{55}	KA-2	20	0.00	0.00	1.00	4.00	5.00	10.00	0.00	70.00	100.00	70.00	S
T_{56}	CHIVAR-10	20	1.33	4.00	3.33	6.00	5.33	0.00	0.00	41.67	93.33	38.86	MS
T_{57}	CHIVAR-8	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{58}	CHIVAR-9	20	7.33	6.67	6.00	0.00	0.00	0.00	0.00	15.56	63.33	9.85	R
T_{59}	CHIVAR-5	20	6.00	2.00	3.67	8.33	0.00	0.00	0.00	28.61	70.00	20.03	MR
T_{60}	Japani Longi	20	10.33	9.67	0.00	0.00	0.00	0.00	0.00	8.06	48.33	3.96	HR
T_{61}	Perennial	20	9.67	10.33	0.00	0.00	0.00	0.00	0.00	8.61	51.67	4.51	HR
T_{62}	VS-7	20	6.00	3.33	2.67	8.00	0.00	0.00	0.00	27.22	70.00	19.07	MR
T_{63}	VS-9	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{64}	S-217621	20	7.67	6.33	6.00	0.00	0.00	0.00	0.00	15.28	61.67	9.46	R
T_{65}	Sel. 40	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{66}	Sel.7-1	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{67}	Sel. 36-1	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
T_{68}	PLS-3-1	20	10.33	9.67	0.00	0.00	0.00	0.00	0.00	8.06	48.33	3.93	HR
T_{69}	Sel. 20-1	20	9.33	10.33	0.00	0.00	0.00	0.00	0.00	8.61	51.67	4.57	HR
T_{70}	Ms-12	20	5.00	4.67	4.00	6.33	0.00	0.00	0.00	26.39	75.00	19.76	MR
Mean		20	3.44	3.28	2.86	3.41	2.85	1.82	0.34	34.80	72.79	31.96	
CD 5%										2.68	5.78	2.72	
CD 1%										3.52	7.60	3.58	

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

Table 8. Days taken to first ChiLCV symptom expression in 70 genotypes under natural field conditions

Sl No.	Genotypes	Severity grade					Final severity grade	Coefficient of infection	Disease reaction*
		Days after transplanting (DAT)							
		15 DAT	30 DAT	45 DAT	60 DAT	75 DAT			
1	Sel-1	0.00	0.66	2.30	3.33	3.33	3.33	19.68	MR
2	Sel-3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
3	Sel-4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
4	Sel-5	0.00	0.00	0.66	1.00	2.00	2.00	10.07	R
5	Sel-6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
6	Punjab Lal	0.66	0.66	1.66	1.66	1.66	2.00	9.97	R
7	Punjab Tej	1.00	1.66	1.66	4.00	4.00	4.00	40.90	MS
8	Punjab Sindhuri	0.66	1.00	2.00	3.00	3.00	3.00	19.47	MR
9	Punjab Guchhader	0.00	1.00	2.33	4.00	4.00	4.00	39.35	MS
10	Vellayani Athulya	1.00	1.66	3.33	3.33	3.66	4.00	39.75	MS
11	Ujwala	0.66	1.66	1.66	2.66	3.66	4.00	38.71	MS
12	DCA 268	1.00	2.33	3.33	4.00	5.00	5.00	66.67	S
13	DCA 167	1.66	2.33	3.00	4.00	4.00	4.00	39.43	MS
14	DCA 157	1.00	2.00	2.33	4.33	5.00	5.00	68.33	S
15	DCA 142	0.66	0.66	2.66	4.66	5.00	5.00	70.83	S
16	PS 1	1.66	2.00	2.00	4.33	4.33	4.00	40.22	MS
17	Byadagi Dabbi	2.66	3.33	3.66	3.66	5.00	5.00	69.72	S
18	Byadagi Kaddi	2.66	3.00	4.00	4.00	5.33	5.00	70.00	S
19	Jwalasakhi	1.66	1.66	2.66	2.66	4.00	4.00	39.01	MS
20	EC 354890	1.00	1.66	3.66	4.66	5.33	5.00	67.50	S
21	EC 599969	1.66	2.00	2.00	2.00	3.00	3.00	19.83	MR
22	IC 572483	1.66	1.66	3.00	3.66	3.66	4.00	39.47	MS
23	EC 599960	0.00	1.33	2.33	2.33	2.33	2.00	10.04	R
24	IC 572468	1.33	2.66	2.66	3.66	3.66	4.00	39.36	MS

*SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

Table 8. continued

Sl No.	Genotypes	Severity grade					Final severity grade	Coefficient of infection	Disease reaction*
		Days after transplanting (DAT)							
		15 DAT	30 DAT	45 DAT	60 DAT	75 DAT			
25	Nagachilli	0.00	1.00	2.00	2.00	3.33	3.00	19.33	MR
26	Arka Lohith	1.33	1.66	1.66	4.00	4.00	4.00	40.00	MS
27	Anugraha	1.66	2.33	3.33	3.33	4.33	4.00	39.75	MS
28	CA-3 (EC-391083)	0.00	0.00	0.66	2.00	2.00	2.00	9.82	R
29	CA-5 (EC-596920)	0.00	0.00	0.66	2.00	3.00	3.00	19.10	MR
30	CA-6 (EC-596940)	0.00	0.00	1.00	3.00	4.00	4.00	39.06	MS
31	CA-8 (EC-599969)	0.00	0.00	0.66	2.00	3.00	3.00	19.72	MR
32	CA-32 (DWD-2)	0.00	0.00	1.00	2.00	3.00	3.00	19.39	MR
33	Jwalamukhi	1.66	2.00	3.33	3.33	4.00	4.00	39.43	MS
34	Keerthi	1.00	2.33	2.33	4.00	4.00	4.00	39.21	MS
35	Pusa Jwala	3.66	4.33	4.33	6.00	6.00	6.00	87.22	HS
36	Pant C 1	3.00	3.33	3.66	5.00	5.00	5.00	69.44	S
37	Punjab Surkh	1.66	2.33	2.66	3.66	3.66	4.00	39.86	MS
38	Kashi Anmol	3.66	3.66	4.66	6.00	6.00	6.00	94.44	HS
39	DCL 524	1.66	1.66	3.00	4.00	4.00	5.00	69.72	S
40	C-31-1	0.66	2.00	3.00	34.33	4.33	4.00	39.96	MS
41	ACC-2-1	0.66	1.66	1.66	3.00	4.00	4.00	39.99	MS
42	I-1	0.66	2.00	2.00	3.00	3.00	3.00	19.57	MR
43	I-2	1.00	1.66	1.66	2.66	3.66	4.00	40.64	MS
44	I-3	0.66	2.00	2.00	4.00	5.00	5.00	70.00	S
45	I-4	1.66	2.33	4.33	5.00	5.00	5.00	69.17	S
46	CHIVAR-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
47	CHIHYB-2	0.00	0.00	2.66	3.66	3.66	4.00	39.43	MS
48	CHIVAR-3	0.00	0.00	2.00	3.00	3.00	3.00	19.94	MR

*SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

Table 8. continued

Sl No.	Genotypes	Severity grade					Final severity grade	Coefficient of infection	Disease reaction*
		Days after transplanting (DAT)							
		15 DAT	30 DAT	45 DAT	60 DAT	75 DAT			
49	CHIHYB-3	0.00	0.00	2.66	3.66	4.33	4.00	39.85	MS
50	CHIVAR-2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
51	CHIVAR-4	0.00	0.00	1.00	1.00	1.00	1.00	4.75	HR
52	CHIVAR-6	0.00	0.00	1.00	2.66	3.66	4.00	39.76	MS
53	CHIVAR-7	0.00	0.00	2.66	3.66	4.33	4.00	39.11	MS
54	LCA-334	2.33	4.33	4.33	5.00	5.00	5.00	66.94	S
55	KA-2	0.66	1.66	2.33	4.33	5.33	5.00	70.00	S
56	CHIVAR-10	1.00	1.66	2.33	3.66	4.00	4.00	38.86	MS
57	CHIVAR-8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
58	CHIVAR-9	0.00	0.00	1.66	1.66	1.66	2.00	9.85	R
59	CHIVAR-5	0.00	0.00	0.00	2.00	3.00	3.00	20.03	MR
60	Japani Longi	0.00	0.00	0.00	1.00	1.00	1.00	3.96	HR
61	Perennial	0.00	0.00	0.00	1.00	1.00	1.00	4.51	HR
62	VS-7	0.00	0.00	2.00	2.00	3.00	3.00	19.07	MR
63	VS-9	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
64	S-217621	0.00	0.00	0.00	1.00	1.00	1.00	9.46	R
65	Sel. 40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
66	Sel.7-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
67	Sel. 36-1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
68	PLS-3-1	0.00	0.00	0.00	1.00	1.00	1.00	3.93	HR
69	Sel. 20-1	0.00	0.00	0.00	1.00	1.00	1.00	4.57	HR
70	ms-12	0.00	1.00	1.00	2.33	3.33	3.00	19.76	MR

*SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

T_{70}) showed disease infection within 15 DAT; T_1 and T_{25} in 30 DAT; T_{29}, T_{31}, T_{32}, T_{48} and T_{62} in 45 DAT; and T_{59} in 60 DAT.

Twenty three genotypes were found to be moderately susceptible with CI ranging from 20 to 40. The genotypes which showed moderate susceptible reaction were T_7, T_9, T_{10}, T_{11}, T_{13}, T_{16}, T_{19}, T_{22}, T_{24}, T_{26}, T_{27}, T_{30}, T_{33}, T_{34}, T_{37}, T_{40}, T_{41}, T_{43}, T_{47}, T_{49}, T_{52}, T_{53} and T_{56} (Table 7). In the genotype, T_9 the first disease symptom appeared 30 DAT. Five genotypes (T_{30}, T_{47}, T_{49}, T_{52} and T_{53}) were free from infection upto 45 DAT (Table 8). Twelve genotypes *viz.*, T_{12}, T_{14}, T_{15}, T_{17}, T_{18}, T_{20}, T_{36}, T_{39}, T_{44}, T_{45}, T_{54} and T_{55} showed susceptible reaction. Two genotypes T_{35} and T_{38} showed highly susceptible reaction (Table 7).

Based on the Coefficient of Infection (CI) and disease reaction under field conditions (Table 7), it was found that greater number of genotypes were moderately susceptible (MS) (23), followed by moderately resistant (MR) (12), susceptible (S) (12), symptomless (SL) (10), resistant (R) (6), highly resistant (HR) (5) and highly susceptible (HS) (2).

4.1.5 Incidence of other Pests and Diseases

4.1.5.1 Incidence of Whiteflies, Thrips and Mites

Incidence of whiteflies, thrips and mites were found to be negligible. The mean number of whitefly, thrips and mites population per leaf at 30, 60 and 90 DAT is given in the Table 9.

4.1.5.2 Incidence of Bacterial Wilt and Fruit Rot

Bacterial wilt and fruit rot incidence was found to be negligible (Table 10).

4.2 ARTIFICIAL SCREENING FOR ChiLCV RESISTANCE

Selfed progenies of 10 symptomless (SL) genotypes (T_2, T_3, T_5, T_{46}, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67}) and five highly resistant (HR) genotypes (T_{51}, T_{60}, T_{61}, T_{68} and T_{69}) under field conditions were raised under insect proof cage. These genotypes (SL, HR) were subjected to artificial screening by using whitefly

Table 9. Mean population of whitefly, thrips and mites in 70 chilli genotypes under field conditions

Sl. No.	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
1	Sel-1	2.20	2.50	2.70	0.00	0.00	0.00	0.00	0.31	0.45
2	Sel-3	0.65	0.80	0.98	0.00	0.00	0.00	0.00	0.00	0.00
3	Sel-4	0.79	0.88	0.56	0.00	0.00	0.00	0.10	0.32	0.48
4	Sel-5	0.95	0.89	0.65	0.00	0.00	0.00	0.00	0.00	0.00
5	Sel-6	0.98	1.12	1.13	0.00	0.00	0.00	0.00	0.00	0.00
6	Punjab Lal	0.85	1.10	0.85	0.00	0.00	0.20	0.20	0.64	0.54
7	Punjab Tej	1.21	1.89	2.10	0.32	0.56	0.41	0.19	0.54	0.20
8	Punjab Sindhuri	0.90	1.40	1.52	0.18	0.27	0.39	0.20	0.42	0.25
9	Punjab Guchhader	1.12	2.10	1.98	0.24	0.29	0.80	0.00	0.00	0.00
10	Vellayani Athulya	1.95	2.10	1.99	0.55	0.53	0.72	0.15	0.87	0.45
11	Ujwala	1.56	1.98	1.85	0.48	0.58	0.52	0.21	0.78	0.35
12	DCA 268	1.12	2.10	1.90	0.39	0.36	0.41	0.29	0.70	0.56
13	DCA 167	1.74	2.10	2.10	0.42	0.24	0.30	0.22	0.98	0.62
14	DCA 157	1.50	2.30	2.10	0.52	0.50	0.54	0.00	0.85	0.76
15	DCA 142	0.89	1.87	1.75	0.58	0.59	0.63	0.00	0.64	0.67
16	PS 1	1.10	2.10	1.95	0.52	0.52	0.60	0.00	0.95	0.86
17	Byadagi Dabbi	1.90	2.30	2.80	0.51	0.42	0.80	0.52	1.31	1.21
18	Byadagi Kaddi	1.30	1.98	2.50	0.53	0.71	0.46	0.42	1.28	1.32
19	Jwalasakhi	1.59	2.60	2.70	0.45	0.22	0.48	0.21	1.15	0.96
20	EC 354890	1.95	2.50	2.80	0.47	0.54	0.61	0.25	1.12	1.07
21	EC 599958	1.20	2.10	1.95	0.45	0.35	0.47	0.10	0.75	0.57
22	IC 572483	1.54	2.40	2.30	0.36	0.50	0.43	0.00	0.98	0.88
23	EC 599960	0.98	1.50	1.90	0.45	0.34	0.37	0.18	0.33	0.24
24	IC 572468	1.24	2.90	2.40	0.45	0.43	0.37	0.00	0.48	0.39
25	Nagachilli	2.34	2.958	2.60	0.21	0.45	0.29	0.00	0.31	0.21
26	Arka Lohith	1.98	2.80	3.00	0.52	0.80	0.67	0.30	0.00	0.39
27	Anugraha	2.80	2.50	3.10	0.64	0.08	0.21	0.31	0.41	0.27
28	CA-3 (EC-391083)	1.23	1.65	1.71	0.00	0.00	0.00	0.00	0.00	0.00

DAT- Days after transplanting

Table 9. continued

Sl. No.	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
29	CA-5 (EC-596920)	1.78	1.97	1.81	0.00	0.08	0.00	0.00	0.00	0.00
30	CA-6 (EC-596940)	1.12	1.45	1.69	0.00	0.00	0.00	0.00	0.00	0.00
31	CA-8 (EC-599969)	1.32	1.81	1.67	0.00	0.00	0.00	0.00	0.00	0.00
32	CA-32 (DWD-2)	0.89	1.20	1.15	0.00	0.00	0.00	0.00	0.00	0.00
33	Jwalamukhi	1.78	1.98	1.99	0.25	0.50	0.39	0.29	0.21	0.46
34	Keerthi	1.21	1.35	1.21	0.26	0.42	0.23	0.23	0.55	0.35
35	Pusa Jwala	1.48	3.20	3.00	0.21	0.62	0.45	0.75	1.39	0.89
36	Pant C 1	1.81	3.20	3.40	0.72	0.61	0.64	0.38	0.95	0.85
37	Punjab Surkh	1.56	2.30	2.50	0.23	0.32	0.00	0.00	0.71	0.60
38	Kashi Anmol	1.12	3.80	3.10	0.52	0.71	0.24	0.89	0.58	0.89
39	DCL 524	2.58	3.00	2.80	0.41	0.52	0.23	0.21	0.14	0.24
40	C-31-1	1.12	2.35	2.41	0.32	0.41	0.21	0.25	0.28	0.35
41	ACC-2-1	0.85	1.20	1.10	0.41	0.39	0.00	0.20	0.20	0.36
42	I-1	1.89	2.67	2.70	0.26	0.23	0.00	0.00	0.33	0.00
43	I-2	1.42	2.34	2.45	0.72	0.44	0.32	0.00	0.33	0.23
44	I-3	1.64	2.90	3.10	0.32	0.50	0.54	0.00	0.56	0.41
45	I-4	1.45	3.10	2.80	0.89	0.96	0.81	0.00	0.69	0.52
46	CHIVAR-1	0.59	0.89	0.54	0.00	0.00	0.00	0.00	0.00	0.00
47	CHIHYB-2	1.00	0.97	0.99	0.32	0.26	0.38	0.33	0.81	0.55
48	CHIVAR-3	0.40	0.20	0.30	0.00	0.00	0.07	0.00	0.45	0.34
49	CHIHYB-3	1.23	2.045	2.015	0.23	0.25	0.36	0.00	0.72	0.52
50	CHIVAR-2	0.59	0.64	0.89	0.00	0.00	0.00	0.00	0.00	0.00
51	CHIVAR-4	0.20	0.25	0.4	0.00	0.00	0.00	0.00	0.00	0.00
52	CHIVAR-6	0.65	0.81	0.75	0.00	0.00	0.21	0.00	0.00	0.00
53	CHIVAR-7	1.24	1.84	1.75	0.00	0.54	0.39	0.00	0.00	0.00
54	LCA-334	1.87	3.10	2.9	0.32	0.41	0.40	0.23	0.47	0.43
55	KA-2	1.13	2.94	2.9	0.22	0.32	0.47	0.23	0.57	0.35
56	CHIVAR-10	1.38	1.71	1.64	0.00	0.00	0.00	0.00	0.00	0.69
57	CHIVAR-8	0.25	0.24	0.42	0.00	0.00	0.00	0.00	0.00	0.00

DAT- Days after transplanting

Table 9. continued

Sl. No.	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
58	CHIVAR-9	0.95	0.87	0.78	0.00	0.00	0.00	0.00	0.35	0.21
59	CHIVAR-5	0.28	0.39	0.78	0.00	0.29	0.19	0.00	0.28	0.32
60	Japani Longi	0.54	0.62	0.41	0.00	0.25	0.24	0.00	0.00	0.00
61	Perennial	0.45	0.59	0.65	0.25	0.19	0.28	0.00	0.00	0.00
62	VS-7	1.12	1.85	1.95	0.00	0.26	0.36	0.25	0.45	0.26
63	VS-9	0.98	0.49	0.85	0.00	0.00	0.00	0.21	0.48	0.35
64	S-217621	0.25	0.34	0.52	0.20	0.14	0.19	0.23	0.64	0.56
65	Sel. 40	0.95	2.24	2.00	0.44	0.52	0.36	0.00	0.36	0.25
66	Sel.7-1	0.69	0.89	0.87	0.00	0.07	0.07	0.12	0.74	0.68
67	Sel. 36-1	0.61	0.62	0.57	0.00	0.23	0.19	0.23	0.63	0.43
68	PLS-3-1	0.95	2.00	1.85	0.13	0.18	0.39	0.00	0.42	0.35
69	Sel. 20-1	0.89	1.87	2.10	0.19	0.41	0.46	0.00	0.33	0.23
70	ms-12	0.74	2.90	2.50	0.39	0.46	0.42	0.14	0.61	0.48
CD		0.053	0.090	0.080	0.017	0.037	0.038	0.025	0.025	0.052
SE (m)		0.019	0.032	0.029	0.006	0.013	0.013	0.009	0.009	0.019
SE (d)		0.027	0.045	0.040	0.009	0.019	0.019	0.012	0.013	0.026

DAT- Days after transplanting

Table 10. Mean per cent incidence of bacterial wilt and fruit rot in 70 chilli genotypes under field conditions

Sl. No.	Genotypes	Mean per cent incidence	
		Bacterial wilt	Fruit rot
T_1	Sel-1	11.90	0.82
T_2	Sel-3	10.12	0.45
T_3	Sel-4	5.36	0.00
T_4	Sel-5	14.29	0.00
T_5	Sel-6	10.71	0.14
T_6	Punjab Lal	11.90	0.34
T_7	Punjab Tej	5.36	0.90
T_8	Punjab Sindhuri	10.12	0.32
T_9	Punjab Guchhader	13.10	0.27
T_{10}	Vellayani Athulya	8.93	0.19
T_{11}	Ujwala	0.00	0.37
T_{12}	DCA 268	2.38	0.72
T_{13}	DCA 167	0.00	0.65
T_{14}	DCA 157	10.71	0.72
T_{15}	DCA 142	1.79	0.89
T_{16}	PS 1	0.00	0.17
T_{17}	Byadagi Dabbi	5.36	1.82
T_{18}	Byadagi Kaddi	0.00	0.78
T_{19}	Jwalasakhi	0.00	0.53
T_{20}	EC 354890	0.00	1.48
T_{21}	EC 599958	8.33	0.00
T_{22}	IC 572483	6.55	1.25
T_{23}	EC 599960	2.38	1.13
T_{24}	IC 572468	10.71	1.63
T_{25}	Nagachilli	2.38	0.40
T_{26}	Arka Lohith	7.14	0.49
T_{27}	Anugraha	6.55	0.27
T_{28}	CA-3 (EC-391083)	2.38	1.02
T_{29}	CA-5 (EC-596920)	5.95	1.27
T_{30}	CA-6 (EC-596940)	0.00	0.98
T_{31}	CA-8 (EC-599969)	0.00	0.77
T_{32}	CA-32 (DWD-2)	0.00	0.00
T_{33}	Jwalamukhi	0.00	2.78
T_{34}	Keerthi	0.00	0.21
T_{35}	Pusa Jwala	5.36	1.70
T_{36}	Pant C 1	5.36	1.55

Table 10. continued

Sl. No.	Genotypes	Mean per cent incidence	
		Bacterial wilt	Fruit rot
T_{37}	Punjab Surkh	7.14	0.92
T_{38}	Kashi Anmol	6.55	2.17
T_{39}	DCL 524	0.00	1.62
T_{40}	C-31-1	0.00	0.58
T_{41}	ACC-2-1	0.00	2.36
T_{42}	I-1	0.00	0.77
T_{43}	I-2	0.00	0.39
T_{44}	I-3	0.00	0.87
T_{45}	I-4	0.00	0.66
T_{46}	CHIVAR-1	0.00	0.63
T_{47}	CHIHYB-2	0.00	0.78
T_{48}	CHIVAR-3	0.00	0.70
T_{49}	CHIHYB-3	0.00	0.75
T_{50}	CHIVAR-2	0.00	0.55
T_{51}	CHIVAR-4	0.00	0.37
T_{52}	CHIVAR-6	0.00	0.00
T_{53}	CHIVAR-7	0.00	0.21
T_{54}	LCA-334	8.93	2.36
T_{55}	KA-2	4.76	1.48
T_{56}	CHIVAR-10	4.17	0.21
T_{57}	CHIVAR-8	8.33	0.60
T_{58}	CHIVAR-9	7.14	0.60
T_{59}	CHIVAR-5	0.00	0.71
T_{60}	Japani Longi	0.00	1.19
T_{61}	Perennial	0.00	1.20
T_{62}	VS-7	0.00	0.00
T_{63}	VS-9	0.00	5.20
T_{64}	S-217621	9.52	0.71
T_{65}	Sel. 40	6.55	2.60
T_{66}	Sel.7-1	7.14	1.04
T_{67}	Sel. 36-1	5.95	1.19
T_{68}	PLS-3-1	3.57	1.21
T_{69}	Sel. 20-1	5.95	1.41
T_{70}	ms-12	4.87	1.02
CD 5%		2.69	0.66
SE (m)		0.96	0.23
SE (d)		1.36	0.33

mediated inoculation and graft inoculation under greenhouse conditions in experiment II (a).

4.2.1 Whitefly Mediated Inoculation under Insect Proof Cage

Out of 10 symptomless genotypes, six genotypes *viz.*, T_2, T_3, T_5, T_{46}, T_{50} and T_{57} remained symptomless under artificial whitefly mediated conditions (Table 11). Two genotypes namely T_{63} and T_{67} were found resistant, and the first disease symptoms appeared on 23.67 and 22.33 days after inoculation, respectively. The genotype T_{65} and T_{66} were found highly resistant, and the first symptom development started 26.67 and 27.67 days after inoculation, respectively.

Out of five highly resistant genotypes, T_{60}, T_{61} and T_{69} expressed resistant reaction under whitefly mediated inoculation. The symptom development started from 22.33, 22.67 and 19.33 days after inoculation in genotypes T_{60}, T_{61} and T_{69}, respectively. Two genotypes namely T_{51} and T_{68} showed moderate resistant reaction and the symptom development started from 20.00 and 21.00 days after inoculation, respectively (Table 12).

4.2.2 Graft Inoculation Under Greenhouse Conditions

Out of 10 symptomless genotypes under field conditions, none were completely free from ChiLCV infection. Four genotypes showed highly resistant reaction and six showed moderately resistant reaction under graft inoculation. The four highly resistant genotypes include T_2, T_3, T_5 and T_{46} and the first disease symptoms appeared 32.00, 34.33, 33.33 and 34.33 days after graft inoculation, respectively. The genotypes *viz.*, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67} showed moderate resistant reaction. In these genotypes, the days to first appearance of disease ranged from 25.67 in genotype T_{50} to 27.33 in T_{67} (Table 12).

The genotypes which showed highly resistant reaction under field conditions were moderately susceptible under artificial graft inoculation. The genotypes which showed moderately susceptible reaction were T_{51}, T_{60}, T_{61}, T_{68},

Table 11. Reaction of symptomless and highly resistant genotypes (under field conditions) against ChiLCV under whitefly mediated inoculation

Treatments	Genotypes	Reaction under field conditions	Appearance of symptom after inoculation (days)	Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]	Virus presence by PCR[5]
T_2	Sel-3	Symptomless	0.00	0.00	0.00	0.00	SL	-
T_3	Sel-4	Symptomless	0.00	0.00	0.00	0.00	SL	-
T_5	Sel-6	Symptomless	0.00	0.00	0.00	0.00	SL	-
T_{46}	CHIVAR-1	Symptomless	0.00	0.00	0.00	0.00	SL	-
T_{50}	CHIVAR-2	Symptomless	0.00	0.00	0.00	0.00	SL	+
T_{57}	CHIVAR-8	Symptomless	0.00	0.00	0.00	0.00	SL	+
T_{63}	VS-9	Symptomless	23.67	15.56	60.00	9.33	R	+
T_{65}	Sel-40	Symptomless	26.67	6.67	40.00	2.67	HR	+
T_{66}	Sel-7-1	Symptomless	27.67	7.78	46.67	3.78	HR	+
T_{67}	Sel-36-1	Symptomless	22.33	14.44	60.00	8.67	R	+
T_{51}	CHIVAR-4	Highly resistant	20.00	23.33	86.67	20.22	MR	Not tested
T_{60}	Japani Longi	Highly resistant	22.33	15.56	60.00	9.33	R	Not tested
T_{61}	Perennial	Highly resistant	22.67	14.44	60.00	8.67	R	Not tested
T_{68}	PLS-3-1	Highly resistant	21.00	25.56	80.00	20.44	MR	Not tested
T_{69}	Sel-20-1	Highly resistant	19.33	15.56	60.00	9.33	R	Not tested
	Mean		13.71	9.26	36.89	6.16		
	CD 5%		0.99	2.20	7.06	1.93		
	SE(m)		0.34	0.760	2.43	0.66		
	SE(d)		0.48	1.075	3.44	0.94		

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible.

[5]- : absence, +: presence of 550bp viral genome

Table 12. Reaction of symptom-less and highly resistant genotypes (under field conditions) against ChiLCV by graft inoculation under greenhouse conditions

Treatments	Genotypes	Reaction under field conditions	Appearance of symptom after grafting (days)	Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]	Virus presence by PCR[5]
T_2	Sel-3	Symptomless	32.00	8.89	40.00	3.56	HR	+
T_3	Sel-4	Symptomless	34.33	8.89	53.33	4.89	HR	+
T_5	Sel-6	Symptomless	33.33	7.78	40.00	3.11	HR	+
T_{46}	CHIVAR-1	Symptomless	34.33	7.78	40.00	3.11	HR	+
T_{50}	CHIVAR-2	Symptomless	25.67	22.22	73.33	16.44	MR	+
T_{57}	CHIVAR-8	Symptomless	26.00	20.00	80.00	16.00	MR	+
T_{63}	VS-9	Symptomless	26.33	23.33	80.00	18.67	MR	+
T_{65}	Sel-40	Symptomless	26.67	21.11	66.67	14.22	MR	+
T_{66}	Sel-7-1	Symptomless	26.33	20.00	80.00	16.00	MR	+
T_{67}	Sel-36-1	Symptomless	27.33	24.44	80.00	19.56	MR	+
T_{51}	CHIVAR-4	Highly resistant	22.33	35.56	100.00	35.56	MS	Not tested
T_{60}	Japani Longi	Highly resistant	22.00	37.78	100.00	37.78	MS	Not tested
T_{61}	Perennial	Highly resistant	21.67	36.67	100.00	36.67	MS	Not tested
T_{68}	PLS-3-1	Highly resistant	21.67	35.56	106.67	37.78	MS	Not tested
T_{69}	Sel-20-1	Highly resistant	22.67	36.67	106.67	39.11	MS	Not tested
	Mean		26.84	21.67	71.67	18.90		
	CD 5%		1.22	3.90	11.17	4.55		
	SE(m)		0.42	1.34	3.84	1.57		
	SE(d)		0.59	1.90	5.44	2.22		

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible.

[5]- : absence, +: presence of 550bp viral genome

and T_{69} (Table 12). Days to first symptom appearance in these genotypes ranged from 22.00 (T_{60}) to 22.67 (T_{69}).

4.2.3 Molecular Detection of ChiLCV by Polymerase Chain Reaction (PCR)

In order to confirm the presence of virus from artificially inoculated plants, the DNA from the top young leaves of the artificially inoculated plants were subjected to Polymerase Chain Reaction (PCR) using geminivirus universal primers (AV494/AC1048) for confirmation of ChiLCV (Wyatt and Brown, 1996) in experiment II (b).

After whitefly inoculation, six genotypes (T_2, T_3, T_5, T_{46}, T_{50} and T_{57}) were symptomless, two (T_{65} and T_{66}) were highly resistant and two (T_{63} and T_{67}) were resistant. Out of six symptomless genotypes, four genotypes namely T_2, T_3, T_5 and T_{46} did not show virus specific amplification, which confirms the absence of viral genome in the inoculated plants (Table 11). However, two symptomless genotypes (T_{50} and T_{57}), two highly resistant (T_{65} and T_{66}) and two resistant genotypes (T_{63} and T_{67}) showed amplification of 560 bp DNA fragment specific to viral genome indicating the presence of viral genomes in the plants (Plate 9).

Under graft inoculation, all tested genotypes (4 highly resistant and 6 moderately resistant) showed presence of virus (Table 12) by amplification of 560 bp DNA fragment specific to viral genome (Plate 10).

4.2.4 Molecular Characterization of Virus

The four samples collected from field showing symptoms resembling to chilli leaf curl disease (Plate 11) were subjected to PCR using geminivirus universal primers (AV494/AC1048) for detection of ChiLCV (Wyatt and Brown, 1996). Molecular detection of ChiLCV showed an amplicon of size 560 bp in all the four samples (Plate 12). The virus specific amplicon was sequenced and is represented in FASTA format (Figure 1).

Homology analysis of the generated sequence showed 93 % similarity with *Tomato leaf curl Karnataka virus.* The sequence generated mentioned vide 4.2.4

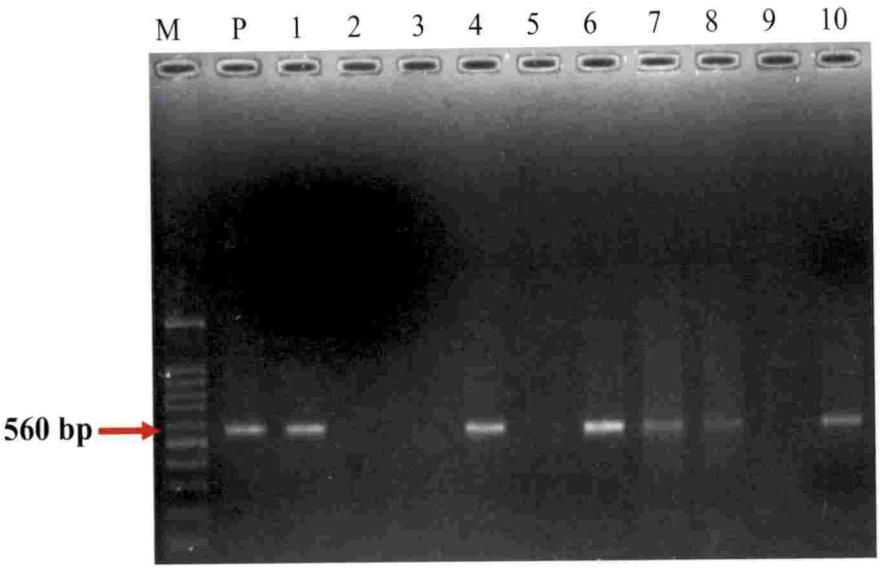

Plate 9: Detection of begomovirus in white fly inoculated plants

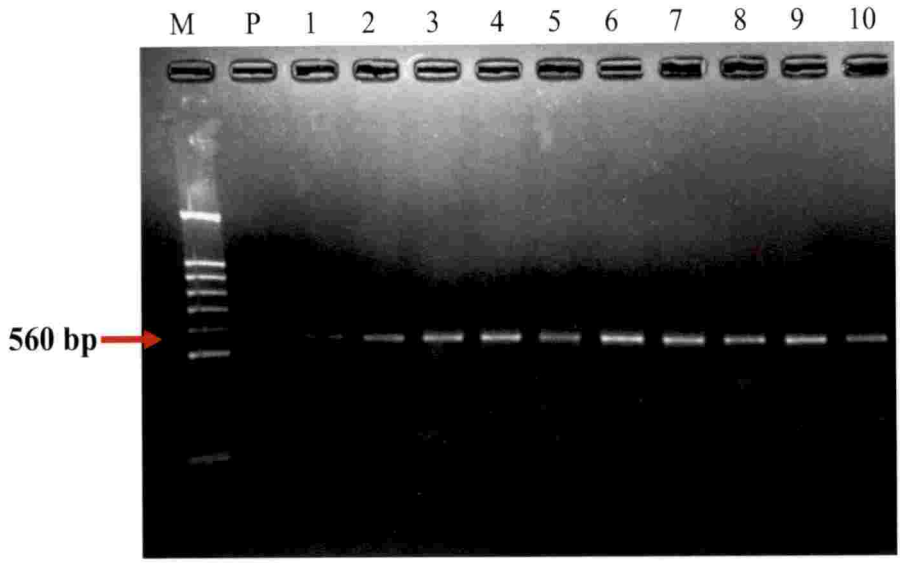

Plate 10: Detection of begomovirus in graft inoculated plants

Lane M: 100 bp DNA marker, Lane P: Positive sample with ChiLCV infection , Lane 1: Sel-7-1, Lane 2: Sel-3, Lane 3: Sel-4, Lane 4: Sel-36-1, Lane 5: Sel-6, Lane 6: Sel-40, Lane 7: VS-9, Lane 8: CHIVAR-8, Lane 9: CHIVAR-1 and Lane 10: CHIVAR-2

(A) (B)

(C) (D)

Plate 11: ChiLCV symptomatic chilli samples (A, B, C & D) collected under natural field conditions

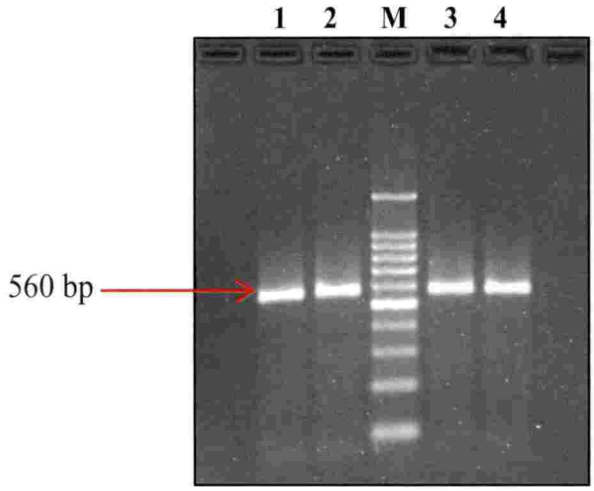

Plate 12: Molecular detection of ChiLCV from four symptomatic chilli samples (A, B, C & D)

Lane M: 100 bp DNA marker, Lane 1: sample (A), Lane 2: sample (B), Lane 3: sample (C) , Lane 4: sample (D)

>5_AC-Reverse_5684-4_P0768,Raw Sequence(560 bp)
CCACCCCGGGTAACTCATAGGATGCATTCTCTGGAGTTCTCATACTTACCAGCTTCCTGC
TGGTTATAAATTACATAATTGTTAACTCTAACAAACTTCCTAACTAATGCTTGCTCCTTT
GATGCGTATTGACCACCAGTCACAGTTGCATGCCATTTCCTTAGAACCTGATATCTGTCA
CGATGTACGTTCTTCACGGTTGCGGTACTGGGTTCATTATCAAACATGTTGAACACCTCA
CCAAAATCTTGGGGTCTATCAACGGGCCTTCGATCACGGACAAGGAAAAACATAACACTG
TTAGTGTGGTTCTTCGTCTTGATGTTCTCATCCATCCAAATCTTGCCCAACACATAAACG
GACTTAACACAAAAACGTTTACCTACTCTATGGGTCAGCCCATTACCTCGTGTAACATCA
CTAATACACATGACCTTACCAACATGGGTCACGTCATGTCTGGACTCAAAAGACTGGACC
TTACATGGGCCTTCACATCCCCGTGGAACATCTGGGCTTCTGTACATCCTGTACATCCTG
GGCTTCCTGAACATGGACAA

Figure 1. FASTA format of 560 bp sequence of *Tomato leaf curl Karnataka virus*

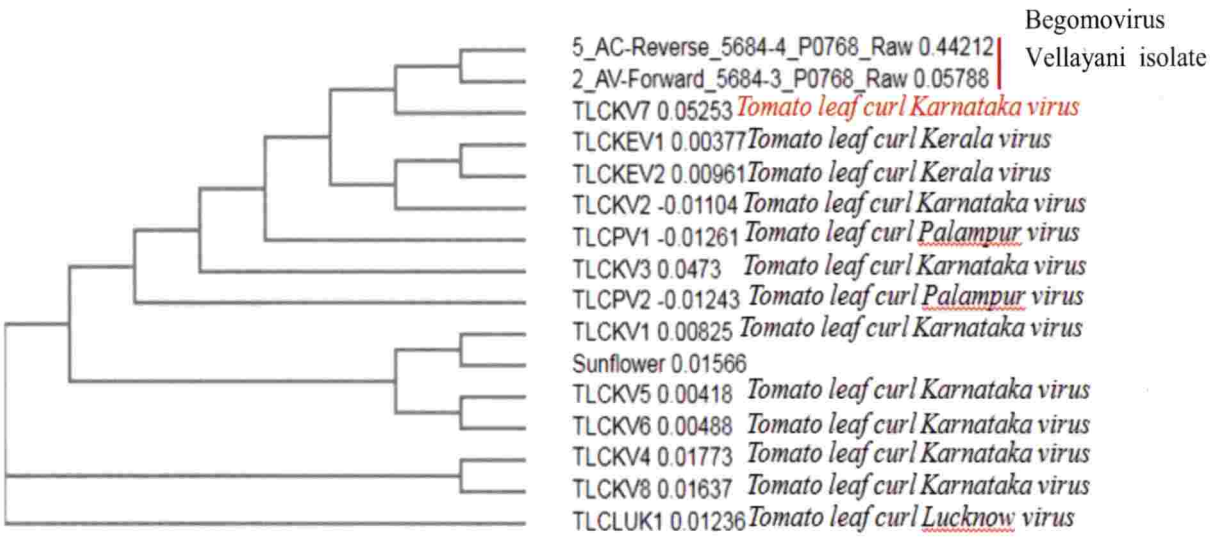

Figure 2. Phylogenetic Tree showing relationship of chilli begomovirus from Vellayani, Thiruvananthapuram with other related sequences from NCBI

(Begomovirus Vellayani isolate) was aligned and compared with the sequence of begomovirus pertaining to other geographical locations obtained from NCBI. Multiple sequence alignment study using Clustal Omega indicated that the isolate under study is in the same cluster as that of *Tomato leaf curl Karnataka virus.*

4.3 EVALUATION OF CHILLI F_1 HYBRIDS

Seven genotypes with high yield and quality *viz.*, L1 (CHIVAR-3), L2 (CHIVAR-7), L3 (CHIVAR-6), L4 (CA-32), L5 (Vellayani Athulya), L6 (Keerthi) and L7 (CHIVAR-10) were selected from result 4.1.3 based on selection indices (Table 6) and these seven genotypes were used as lines (female parent) in hybridization program. The genotypes which showed highly resistant reaction after graft inoculation *viz.*, T1 (Sel-3), T2 (Sel-4), T3 (Sel-6) and T4 (CHIVAR-1) were used as testers (male parent) in hybridization program.

Seven genotypes (lines) with high yield and quality were crossed with four highly resistant genotypes (testers) in line × tester mating design to produce 28 one-way F_1 hybrids in experiment III (a). These hybrids and their parents and two checks (CH-27 and Arka Harita) were evaluated for vegetative, flowering, fruit and yield, quality traits and ChiLCV resistance in experiment III (b).

4.3.1 Mean Performance of Parents and Hybrids

The mean performance of parents and standard checks (Table 13), and F_1 hybrids (Tables 14a to 14c) are presented character wise as under:

4.3.1.1 Plant Height (cm)

The plant height in lines ranged from 42 cm (L1) to 56 cm (L6). For testers, the range varied from 42.93 cm (T3) to 55.03 cm (T1). The average plant height in parents was 47.63 cm. The check hybrids CH-27 and Arka Harita had a plant height of 57.71 and 54.56 cm, respectively (Table 13). Among 28 hybrids, the hybrid L7 × T3 was the tallest with 70.70 cm and the hybrid L1 × T4 was the shortest (41.82 cm). The average plant height in hybrids was 56.07 cm (Table 14a).

Table 13. Mean performance of female parents, male parents and standard checks for various characters in chilli

Source	Plant height (cm)	Primary branches plant^{-1}	Days to first flower	Days to first harvest	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48m^2)	Vitamin C (mg100g^{-1})	Carotenoids (mg100 g^{-1})
Female parents (Lines)												
L1	42.00	2.56	30.33	51.00	4.60	2.95	3.70	148.00	580.22	16.05	103.00	214.33
L2	51.76	2.56	35.44	57.00	5.97	2.56	3.95	132.00	510.75	14.10	105.33	272.00
L3	42.76	3.52	36.74	56.00	5.83	2.95	4.50	116.00	545.00	15.06	114.67	227.67
L4	44.79	2.67	28.74	48.00	6.35	3.12	4.60	123.00	584.15	16.16	99.33	263.00
L5	47.84	3.80	26.79	48.00	8.43	4.12	7.45	57.00	449.00	12.37	94.33	221.00
L6	56.00	4.33	31.82	52.50	3.72	3.30	4.20	133.00	544.50	15.05	95.75	205.00
L7	48.00	3.30	32.00	52.67	5.43	3.42	5.10	93.00	514.90	14.22	112.00	250.67
Mean	47.00	3.25	31.70	52.17	5.76	3.20	4.79	114.57	532.65	14.71	103.24	236.24
SE (m)	0.68	0.25	0.54	0.60	0.11	0.09	0.07	0.56	5.97	0.21	0.85	1.03
CD 5%	2.13	0.79	1.68	1.87	0.36	0.29	0.23	1.75	18.62	0.67	2.66	3.20
Male parents (Testers)												
T1	55.03	4.22	35.74	57.00	4.30	2.64	3.55	81.00	300.67	8.22	71.00	155.00
T2	44.82	2.56	34.32	58.00	5.52	3.64	4.40	63.00	307.88	8.42	75.00	131.00
T3	42.93	4.11	33.27	54.00	6.10	3.11	4.25	84.00	349.67	9.50	87.33	202.67
T4	48.02	3.45	36.12	56.00	3.47	3.00	3.55	73.00	260.67	7.10	93.67	222.67
Mean	47.70	3.59	34.86	56.25	4.85	3.10	3.94	75.25	304.72	8.31	81.75	177.83
SE (m)	0.84	0.21	0.29	0.76	0.08	0.10	0.05	2.15	6.95	0.10	1.02	1.26
CD 5%	2.96	0.74	1.02	2.68	0.31	0.38	0.19	7.61	24.51	0.38	3.60	4.45
Overall mean (Lines + Testers)	47.63	3.37	32.85	53.65	5.43	3.17	4.48	100.27	449.76	12.39	95.58	215.00
Commercial checks												
CH-27 F_1*	57.71	3.13	35.84	54.00	4.33	3.34	3.40	105.33	342.43	9.39	98.80	236.67
Arka Harita F_1	54.56	3.22	33.15	53.00	5.67	2.98	3.53	99.33	341.07	9.35	106.00	217.33

* Resistant check

The hybrid L1 × T4 was the shortest with 41.82 cm followed by L1 × T3 (44.78 cm).

4.3.1.2 Primary Branches Plant^{-1}

Primary branches plant^{-1} ranged from 2.56 (L1, L2 and T2) to 4.33 (L6) in parents, with average of 3.37. Among the lines, primary branches plant^{-1} ranged from 2.56 (L1 and L2) to 4.33 (L6), and it varied from 2.56 (T2) to 4.22 (T1) among testers. The checks CH-27 and Arka Harita recorded a mean of 3.13 and 3.22, respectively. Among hybrids, primary branches plant^{-1} varied from 2.44 (L4 × T4) to 5.31 (L4 × T2), with overall mean of 3.88 (Table 14a).

4.3.1.3 Days to First Flower

The parental line L5 (26.79) was earliest to flower and L3 (36.74) exhibited maximum delay for first flowering. Testers took 33.27 (T3) to 36.12 (T4) days to produce first flower. The overall mean for days to first flower in parents was 32.85 (Table 13). The standard check CH-27 and Arka Harita recorded 35.84 and 33.15 for days to first flower, respectively. Among the F_1 hybrids, the hybrid L1 × T4 (25.69) was the earliest. The second early flowering hybrid was L5 × T1 (27.02) which was on par with L3 × T2 (27.12), L4 × T1 (27.83), L5 × T2 (28.05), L3 × T4 (28.07) and L4 × T3 (28.17). The hybrids L7 × T4 (36.80) and L6 × T4 (35.97) exhibited maximum days for first flower.

4.3.1.4 Days to First Harvest

The data revealed that days to first harvest in parents ranged from 48.00 (L4 and L5) to 58 days (T2). Among lines, L4 and L5 (48) were early to harvest whereas, L2 (57) was late to first harvest. The testers took 54 (T3) to 58 (T2) days to first harvest. The standard check CH-27 and Arka Harita recorded 54 and 53 days to first harvest, respectively. Among 28 hybrids, L1 × T4 (46), L3 × T2 (46) and L5 × T1 (46) were earliest for first harvest and they were at par with L5 × T2 (47), L4 × T3 (47), L5 × T4 (48), L5 × T3 (48) and L4 × T1 (48). The hybrids L1 × T1 (55) and L7 × T4 (55) recorded maximum days for first harvest.

4.3.1.5 Fruit Length (cm)

The parents recorded an average fruit length ranging from 3.47 cm (T4) to 8.43 cm (L5) with the overall mean of 5.43 cm. Among lines, fruit length varied from 3.72 cm (L6) to 8.43 cm (L5) whereas, for testers it ranged from 3.47 cm (T4) to 6.10 cm (T3). Among hybrids, it ranged from 5.07 cm (L2 × T4) to 10.40 cm (L4 × T2) as compared to standard checks CH-27 (4.33 cm) and Arka Harita (5.67 cm).

4.3.1.6 Fruit Girth (cm)

Among lines, the data on fruit girth indicated a range of 2.56 cm (L2) to 4.12 cm (L5). In testers, it ranged from 2.64 cm (T1) to 3.64 cm (T2). The standard check CH-27 and Arka Harita recorded 3.34 cm and 2.98 cm for fruit girth, respectively. The fruit girth of hybrids varied from 2.73 cm (L2 × T4) to 4.33 cm (L5 × T3). The hybrid L5 × T3 exhibited maximum fruit girth of 4.33 cm which was at par with hybrids L4 × T3 (4.29 cm), L6 × T3 (4.22 cm), L5 × T4 (4.13 cm), L2 × T3 (4.12 cm) and L4 × T2 (4.06 cm) (Table 14a).

4.3.1.7 Fruit Weight (g)

Fruit weight among parents varied from 3.55 g (T1 and T4) to 7.45 g (L5). The range was from 3.70 g (L1) to 7.45 g (L5) in lines and from 3.55 g (T1 and T4) to 4.40 g (T2) in testers. The standard check CH-27 and Arka Harita showed 3.40 g and 3.53 g for weight, respectively. Among hybrids, the fruit weight varied from 3.70 g (L2 × T3) to 6.90 g (L1 × T2) (Table 14b). Hybrids which showed superior *per se* performance were L1 × T2 (6.90 g), L7 × T1 (6.00 g) and L5 × T2 (5.78 g).

4.3.1.8 Fruits Plant^{-1}

It is evident from data that the mean fruits plant^{-1} of parents and hybrids ranged from 57.00 (L5) to 148.00 (L1) and 68.33 (L5 × T1) to 189.33 (L6 × T1), respectively. The fruits plant^{-1} in lines varied from 57.00 (L5) to 148.00 (L1) and among testers it varied from 63.00 (T2) to 84.00 (T3) (Table 13). In standard check CH-27 and Arka Harita, the mean fruits plant^{-1} was 105.33 and 99.33, respectively.

Table 14a. Mean performance of F_1 hybrids for plant height, primary branches plant^{-1}, days to first flower, days to first harvest, fruit length and fruit girth

Hybrids	Plant height (cm)	Primary branches plant^{-1}	Days to first flower	Days to first harvest	Fruit length (cm)	Fruit girth (cm)
L1 × T1	59.69	4.11	30.33	55.00	6.45	3.56
L1 × T2	58.91	3.32	33.81	53.00	9.17	3.60
L1 × T3	44.78	3.23	30.80	50.83	6.18	3.52
L1 × T4	41.82	3.34	25.69	46.00	6.81	3.47
L2 × T1	60.64	3.86	33.73	53.00	6.67	3.16
L2 × T2	57.66	3.30	33.36	54.00	7.60	3.45
L2 × T3	64.56	3.67	32.71	53.00	5.60	4.12
L2 × T4	58.68	3.51	34.26	53.00	5.07	2.73
L3 × T1	59.03	4.75	30.58	50.00	6.27	3.67
L3 × T2	47.50	5.25	27.12	46.00	6.53	3.26
L3 × T3	46.92	4.31	34.52	53.00	7.53	3.29
L3 × T4	52.71	2.56	28.07	49.00	6.62	3.14
L4 × T1	48.92	4.18	27.83	48.00	9.37	3.86
L4 × T2	51.90	5.31	29.62	49.00	10.40	4.06
L4 × T3	50.81	4.36	28.17	47.00	8.63	4.29
L4 × T4	54.66	2.44	30.83	50.00	9.20	3.76
L5 × T1	52.81	4.03	27.02	46.00	6.40	3.81
L5 × T2	49.74	2.88	28.05	47.00	8.33	3.28
L5 × T3	48.57	4.00	28.50	48.00	7.67	4.33
L5 × T4	51.95	3.56	28.81	48.00	7.53	4.13
L6 × T1	60.63	5.22	29.96	50.00	5.73	3.90
L6 × T2	59.82	2.55	29.39	49.00	5.13	3.96
L6 × T3	58.54	4.41	31.63	51.00	7.10	4.22
L6 × T4	60.76	3.93	35.97	54.00	6.49	3.81
L7 × T1	65.75	4.40	31.82	51.00	7.50	2.97
L7 × T2	67.73	4.18	34.85	54.00	7.12	3.93
L7 × T3	70.70	3.84	34.05	53.00	6.68	3.68
L7 × T4	63.73	4.04	36.80	55.00	5.10	3.31
Mean	56.07	3.88	31.01	50.57	7.10	3.65
CD at $P \leq 0.05$	2.69	0.84	1.29	2.13	0.39	0.33

The hybrid L6 × T1 (189.33) produced maximum number of fruits plant^{-1} followed by L3 × T2 (168) and L7 × T3 (163.67).

4.3.1.9 Yield Plant^{-1} (g)

As indicated by result data in the Table 13, the mean yield plant^{-1} among the parents varied from 260.67 g (T4) to 584.15 g (L4), with an overall mean of 449.70 g. Yield plant^{-1} for lines varied from 449.00 g (L5) to 584.15 g (L4) and among testers it varied from 260.67 g (T4) to 349.67 g (T3). The check hybrids CH-27 and Arka Harita had a fruit yield of 342.43 g and 341.07 g, respectively. The hybrids recorded a range of 276.10 g (L4 × T3) to 849.47 g (L3 × T2), with an overall mean of 542.07 g. The maximum yield was noticed in the hybrid L3 × T2 (849.47 g), which was on par with hybrid L1 × T1 (822.67 g) (Table 14b). The hybrid L6 × T1 (746.13 g) also showed high *per se* performance.

4.3.1.10 Yield Plot^{-1} (kg/6.48 m^2)

The yield plot^{-1} of parents ranged from 7.10 kg (T4) to 16.16 kg (L4), with the overall mean of 12.39 kg. The lines exhibited a range of 12.37 kg (L5) to 16.16 kg (L4) for yield plot^{-1} and among the testers it ranged from 7.10 kg (T4) to 9.50 kg (T3). Mean yield plot^{-1} in check CH-27 and Arka Harita were 9.39 and 9.35 kg, respectively. Yield plot^{-1} in hybrids ranged from 7.53 kg (L4 × T3) to 23.50 kg (L3 × T2), with the overall mean of 14.97 kg.

4.3.1.11 Vitamin C (mg 100 g^{-1})

The vitamin C content of different parents ranged from 71 mg 100 g^{-1} (T1) to 114.67 mg 100 g^{-1} (L3), with an average of 95.58 mg 100 g^{-1}. The vitamin C content among the lines ranged from 94.33 mg 100 g^{-1} (L5) to 114.67 mg 100 g^{-1} (L3) and among the testers it ranged from 87.33 mg 100 g^{-1} (T3) to 93.67 mg 100 g^{-1} (T4). Among 28 hybrids, vitamin C ranged from 72.67 mg 100 g^{-1} (L6 × T4) to 134.00 mg 100 g^{-1} (L3 × T2), with the overall mean of 104.74 mg 100 g^{-1}. The standard checks CH-27 and Arka Harita recorded 98.80 mg 100 g^{-1} and 106.00 mg 100 g^{-1}, respectively.

Table 14b. Mean performance of F_1 hybrids for fruit weight, fruit plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C and carotenoids

Hybrids	Fruit weight (g)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48m^2)	Vitamin C (mg 100 g^{-1})	Carotenoids (mg 100 g^{-1})
L1 × T1	5.20	161.00	822.67	22.83	116.00	275.00
L1 × T2	6.90	79.67	531.23	14.67	99.00	228.33
L1 × T3	4.52	128.33	562.30	15.54	92.33	259.00
L1 × T4	5.30	118.00	617.00	17.04	89.00	272.67
L2 × T1	4.17	152.67	621.75	17.21	115.00	281.67
L2 × T2	4.37	93.67	401.63	11.05	107.67	291.00
L2 × T3	3.70	112.67	400.13	11.00	87.67	305.67
L2 × T4	4.00	121.00	482.67	13.27	82.33	327.33
L3 × T1	4.80	142.00	670.33	18.50	133.00	270.67
L3 × T2	5.20	168.00	849.47	23.50	134.00	259.67
L3 × T3	4.90	134.33	650.10	18.00	120.67	211.67
L3 × T4	4.37	121.33	512.00	14.14	102.33	199.67
L4 × T1	4.50	133.00	589.33	16.30	119.67	363.67
L4 × T2	4.88	93.67	448.25	12.35	122.33	348.33
L4 × T3	3.97	72.33	276.10	7.53	116.67	332.00
L4 × T4	4.20	71.33	287.20	7.84	93.00	324.00
L5 × T1	5.10	68.33	326.70	8.95	100.67	204.33
L5 × T2	5.78	85.33	487.16	13.44	98.67	214.67
L5 × T3	5.10	99.00	502.67	13.79	114.67	195.33
L5 × T4	5.24	89.33	444.48	12.25	103.33	210.67
L6 × T1	4.02	189.33	746.13	20.69	84.33	224.67
L6 × T2	4.20	110.33	454.63	12.53	77.67	241.33
L6 × T3	5.32	117.33	608.50	16.84	89.33	289.00
L6 × T4	4.37	122.67	512.40	14.15	72.67	229.33
L7 × T1	6.00	132.33	774.73	21.49	129.67	287.33
L7 × T2	5.23	112.67	579.15	16.02	109.00	241.00
L7 × T3	3.80	163.67	615.23	17.03	119.33	281.33
L7 × T4	4.02	104.33	403.93	11.11	102.67	297.00
Mean	4.75	117.77	542.07	14.97	104.74	266.65
CD at $P \leq 0.05$	0.32	5.37	36.89	0.60	2.50	5.93

4.3.1.12 Carotenoids (mg 100 g^{-1})

The content of carotenoids among all the parents ranged from 131.00 mg 100 g^{-1} (T2) to 272.00 mg 100 g^{-1} (L2), with an average of 215.00 mg 100 g^{-1}. Among seven lines, L6 recorded the lowest carotenoids (205 mg 100 g^{-1}) and L2 recorded the highest carotenoids (272 mg 100 g^{-1}). In testers, carotenoids varied from 131.00 mg 100 g^{-1} (T2) to 222.67 mg 100 g^{-1} (T4). The hybrids recorded a range of 195.33 mg 100 g^{-1} (L5 × T3) to 363.67 mg 100 g^{-1} (L4 × T1) as compared to standard checks CH-27 (236.67 mg 100 g^{-1}) and Arka Harita (217.33 mg 100 g^{-1}) (Table 14b).

4.3.2 Estimation of Combining Ability Effects

4.3.2.1 Analysis of Variance (ANOVA) for Experimental Design

The results pertaining to the ANOVA for the experimental design are reported in Table 15. The analysis indicated that the mean squares (MS) due to genotypes were highly significant at $P \leq 0.01$ for all the traits studied. The results further indicated that the MS due to replications were significant for fruit length, fruits $plant^{-1}$ and fruit weight and non-significant for primary branches $plant^{-1}$, plant height, days to first harvest, days to first flower, fruit girth, yield $plant^{-1}$, yield $plot^{-1}$, vitamin C, carotenoids and coefficient of infection.

4.3.2.2 Analysis of Variance (ANOVA) for Combining Ability

The results of ANOVA for combining ability for different traits are showed in the Table 16. The MS due to replication were non-significant for all the studied traits except for plant height, fruit length, fruits $plant^{-1}$, fruit weight and yield $plant^{-1}$. The MS due to parents were significant for all the traits. Significant differences due to lines were found for all the traits. Testers differed significantly for all the traits except for coefficient of infection. The hybrids/crosses differed significantly for all the characters. Lines vs Testers showed significant differences for all the traits except for plant height. The MS due to parent vs. crosses showed significant differences for all the traits.

Table 15. Analysis of variance for various characters in 39 treatments (11 parents and 28 F_1 hybrids)

Source of variation	Replication	Genotypes	Error
df	2	38	76
Plant height (cm)	5.99	174.98**	2.65
Primary branches plant^{-1}	0.28	1.80**	0.23
Days to first flower	0.19	29.50**	0.60
Days to first harvest	1.19	33.75**	1.54
Fruit length (cm)	0.83**	7.20**	0.05
Fruit girth (cm)	0.03	0.67**	0.04
Fruit weight (g)	0.10**	2.18**	0.03
Fruits plant^{-1}	680.67**	2935.42**	9.67
Yield plant^{-1} (g)	236.09	64451.41**	403.39
Yield plot^{-1} (kg/6.48m^2)	0.12	50.42**	0.13
Vitamin C (mg 100 g^{-1})	4.33	803.89**	2.39
Carotenoids (mg 100 g^{-1})	0.62	7836.27**	10.65
Coefficient of infection (%)	36.78	555.34**	8.04

Data are mean sums of squares; *significant at $P \leq 0.05$; **significant at $P \leq 0.01$

Table 16. Analysis of variance for combining ability including parents in line × tester design

Source of variation	df	Plant height (cm)	Primary branches Plant^{-1}	Days to first flower	Days to first harvest	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48m^2)	Vitamin C (mg 100 g^{-1})	Carotenoids (mg 100g^{-1})	Coefficient of infection
Replication	2	5.99*	0.28	0.19	1.19	0.83**	0.03	0.10**	680.67**	236.09**	0.12	4.33	0.62	36.78
Parents	10	70.71**	1.47**	31.46**	37.69**	5.86**	0.59**	3.69**	2981.09**	44767.77**	35.25**	803.89**	5396.66**	525.34**
Lines (L)	6	75.35**	1.42**	37.08**	37.23**	6.58**	0.72**	4.87**	2806.85**	6499.92**	5.10**	569.74**	1982.30**	133.73**
Testers (T)	3	84.98**	1.76**	5.17**	8.73**	4.22**	0.51**	0.86**	218.97**	3987.29**	2.90**	181.00**	5341.44**	0.00
Crosses	27	157.64**	1.77**	26.91**	25.18**	5.51**	0.51**	1.64**	2897.95**	66652.64**	52.06**	334.30**	6688.72**	521.73**
Lines vs Testers	1	0.08	0.87**	76.62**	127.37**	6.40**	0.08*	5.10**	12312.91**	396716.32**	313.23**	3608.52**	26048.52**	4451.08**
Parent vs Crosses	1	1685.85**	6.07**	80.04**	225.74**	66.42**	5.65**	1.59**	3490.29**	201854.61**	157.88**	1985.64**	63216.15**	1762.06**
GCA lines	6	488.43**	1.05**	63.74**	62.80**	15.08**	0.99**	3.05**	5319.07**	127365.64**	99.53**	2259.90**	24191.51**	793.80**
GCA testers	3	49.96**	3.76**	8.07**	1.33	4.44**	0.76**	2.59**	5173.94**	127623.57**	100.12**	1749.66**	505.09**	415.26**
SCA crosses	18	65.32**	1.68**	17.77**	16.62**	2.50**	0.30**	1.01**	1711.57**	36253.05**	28.23**	225.36**	1885.07**	448.79**
Error	76	2.65	0.26	0.60	1.54	0.05	0.04	0.03	9.67	403.39	0.13	2.39	10.65	8.04

Data's are mean sums of squares; *significant at $P \leq 0.05$; **significant at $P \leq 0.01$

Table 17. Components of genetic variance and Proportional contributions (%) of Line, Tester and their interactions to total variance for various characters

	Plant height (cm)	Primary branches Plant^{-1}	Days to first flower	Days to first harvest	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48 m^2)	Vitamin C (mg 100 g^{-1})	Carotenoids (mg 100g^{-1})	Coefficient of infection
Components of genetic variance													
$\sigma^2 gca$	2.05	0.02	0.20	0.19	0.06	0.04	0.01	26.36	675.54	0.52	13.90	106.74	1.62
$\sigma^2 sca$	20.87	0.47	5.71	4.97	0.81	0.08	0.32	566.92	11915.02	9.36	74.34	623.97	146.85
$\sigma^2 gca / \sigma^2 sca$	0.09	0.04	0.03	0.03	0.07	0.5	0.03	0.04	0.05	0.05	0.18	0.17	0.01
Proportional contributions (%) of Line, Tester and their interactions to total variance													
Lines	68.85	13.27	52.64	55.40	60.80	43.28	41.35	40.79	42.46	42.48	59.30	80.37	33.81
Testers	3.52	23.54	3.33	0.59	8.95	16.66	17.54	19.84	21.28	21.39	22.96	0.84	8.84
Lines × Testers	27.63	63.19	44.03	44.01	30.25	40.06	41.11	39.37	36.26	36.15	17.74	18.79	57.35

The GCA lines and SCA crosses were significant at P≤ 0.01 for all the vegetative, flowering, yield and quality traits studied. The GCA testers were observed to be significant for all the traits except for days to first harvest. The ratio of σ^2GCA/σ^2SCA was less than unity for all the characters (Table 17). The contribution of lines were more as compared to testers for all the characters except for the primary branches plant^{-1}.

4.3.2.3 Estimation of General Combining Ability (GCA) Effects of Parents and Specific Combining Ability (SCA) Effects of Crosses

The estimates of GCA effects of seven lines and four testers (Table 18) and, SCA effects of 28 F_1 hybrids (Table 19a to 19c) in line × tester mating design for 12 traits are presented below.

4.3.2.3.1 Plant Height (cm)

A perusal of GCA effects revealed that three lines L7 (10.91), L2 (4.31), L6 (3.87) and one tester T1 (2.14) exhibited highly significant and positive GCA effects. Four lines and two testers showed significant negative GCA effects for plant height. The tester T2 exhibited non-significant positive GCA effect (Table 18).

Out of 28 F_1 hybrids evaluated, 17 hybrids manifested significant SCA effects for plant height. The range of SCA effects involving 28 F_1 hybrids varied between -8.31 in the cross L1 × T4 to 7.50 in the cross L1 × T2. Among them, nine crosses have significant positive SCA effects and eight have significant negative effects. The hybrids *viz.*, L1 × T2 (7.50), L1 × T1 (6.25), L3 × T1 (5.35), L2 × T3 (5.26) and L7 × T3 (4.81) exhibited high positive significant SCA effects for plant height (Table 19a). None of the hybrids that displayed significant positive SCA effects for plant height had both parents with positive significant GCA effects. Five hybrids, L1 × T1, L2 × T3, L3 × T1, L6 × T4 and L7 × T3 had one parent with positively significant GCA effects and remaining four hybrids L1 × T2, L3 × T4, L4 × T4 and L5 × T4 had neither of parents with significant positive GCA effects.

4.3.2.3.2 Primary Branches Plant^{1}

Among lines and testers, line L3 (0.34) and tester T1 (0.49) showed significant positive GCA effects for primary braches plant^{-1}. The line L1 and L2 and tester T4 exhibited significant negative GCA effects (Table 18). The lines L4, L6, L7 and tester T3 registered non-significant positive GCA effects.

Among the 28 F_1 hybrids evaluated, eight hybrids manifested significant SCA effects ranging from -1.43 in the cross L6 × T2 to 1.29 in the cross L4 × T2. Among these, four crosses had significant positive SCA effects and four had significant negative SCA effects. The hybrids *viz.*, L4 × T2 (1.29), L3 × T2 (1.08), L6 × T1 (0.71) and L2 × T4 (0.46) showed positive significant SCA effects (Table 19a). None of the hybrids involved both the parents with positive significant GCA effects. Two hybrids L3 × T2 and L6 × T1 had at least one parent with positive and significant GCA effects. Hybrid L2 × T4 and L4 × T2 involved neither of the parents with significant and positive GCA effects.

4.3.2.3.3 Days to First Flower

Lines L5 (-2.92), L4 (-1.90), L3 (-0.94), L1 (-0.85) and tester T1 (-0.83) exhibited highly significant and negative GCA effects for days to first flower. Parental lines L2, L6, L7 and testers T3, T4 exhibited highly significant positive GCA effects. The tester T2 exhibited non-significant negative GCA effects for days to first flower.

Among the 28 hybrids evaluated, 17 hybrids manifested significant SCA effects which ranged from -4.95 in the cross L1 × T4 to 1.00 in the cross L1 × T1. The effects were significant and negative in nine hybrids and positive in the remaining eight crosses. The negative significant SCA effects ranged from -4.95 in the cross L1 × T4 to -0.58 in the cross L6 × T3. Top five hybrids with negative and significant SCA effects identified were L1 × T4 (-4.95), L3 × T2 (-2.83), L3 × T4 (-2.48), L6 × T2 (-2.22) and L7 × T1 (-1.73). Among nine hybrids showing significant negative effects, none of the hybrid showed both parents with significant negative GCA effects. Six hybrids L6 × T1, L7 × T1, L1 × T4, L3 × T2,

Table 18. GCA effects of female and male parents for various characters

Source	Plant height (cm)	Primary branches Plant^{-1}	Days to first flower	Days to first harvest	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48 m^2)	Vitamin C (mg 100 g^{-1})	Carotenoids (mg 100 g^{-1})	Coefficient of infection (CI)
Female parents (Lines)													
L1	-4.77**	-0.37*	-0.85**	0.64	0.05	-0.12	0.72**	3.98**	91.23**	2.56**	-5.65**	-7.90**	-11.96**
L2	4.31**	-0.29*	2.50**	2.68**	-0.87**	-0.29**	-0.70**	2.23*	-65.52**	-1.84**	-6.57**	34.46**	3.78**
L3	-4.53**	0.34*	-0.94**	-1.07**	-0.37**	-0.31**	0.06	23.64**	128.41**	3.57**	17.76**	-31.24**	-1.24
L4	-4.50**	0.20	-1.90**	-2.07**	2.30**	0.34**	-0.37**	-25.19**	-141.85**	-3.96**	8.18**	75.35**	-5.47**
L5	-5.30**	-0.26	-2.92**	-3.31**	0.38**	0.24**	0.55**	-32.27**	-101.82**	-2.86**	-0.40	-60.40**	12.68**
L6	3.87**	0.15	0.73**	0.43	-0.99**	0.32**	-0.28**	17.14**	38.35**	1.09**	-23.74**	-20.57**	5.84**
L7	10.91**	0.24	3.37**	2.68**	-0.50**	-0.18**	0.01	10.48**	51.20**	1.45**	10.43**	10.01	-3.63**
CD at $P \leq 0.05$	0.92	0.27	0.43	0.72	0.13	0.09	0.09	1.84	12.74	0.19	0.86	2.03	1.60
CD at $P \leq 0.01$	1.20	0.35	0.56	0.95	0.17	0.12	0.12	2.41	16.70	0.25	1.13	2.67	2.10
Male parents (Testers)													
T1	2.14**	0.49**	-0.83**	-0.14	-0.19**	-0.09*	0.07	22.04**	108.17**	3.03**	9.31**	5.82**	-2.80**
T2	0.11	-0.05	-0.12	-0.28	0.65**	-0.01	0.47**	-11.58**	-6.14	-0.17*	2.17**	-6.04**	5.83**
T3	-1.09**	0.10	0.47**	0.27	-0.05	0.27**	-0.28**	0.46	-25.63**	-0.72**	1.07**	1.06	-4.05**
T4	-1.17**	-0.54**	0.48**	0.15	-0.41	-0.17**	-0.26**	-10.92**	-73.40**	-2.14**	-12.55**	-0.85	1.02
CD at $P \leq 0.05$	0.68	0.21	0.33	0.54	0.09	0.07	0.07	1.39	9.62	0.15	0.64	1.54	1.21
CD at $P \leq 0.01$	0.89	0.28	0.43	0.71	0.12	0.10	0.10	1.82	12.61	0.20	0.84	4.60	1.59

*Significant at $P \leq 0.05$; **significant at $P \leq 0.01$

L3 × T4 and L4 × T3 had at least one parent with significant and negative GCA effects and three hybrids L2 × T3, L6 × T2 and L6 × T3 involved neither of the parents with negative and significant GCA effects.

4.3.2.3.4 Days to First Harvest

The estimates of combining ability effects revealed that five parental lines showed significant GCA effects of which two were in positive direction and three in negative direction.

The parent line L5 exhibited highest negative significant GCA effects of -3.31 followed by L4 (-2.07) and L3 (-1.07). The testers T1 and T2 exhibited non-significant negative GCA effects for days to first harvest. The lines, L2 and L7 had positive and significant GCA effects.

Among the 28 hybrids, 10 hybrids manifested significant SCA effects which ranged from -5.36 in the cross L1 × T4 to 1.60 in the cross L7 × T4. Negative significant SCA effects were observed in five and positive in remaining five hybrids. Five hybrids *viz.* L1 × T4 (-5.36), L3 × T2 (-3.22), L7 × T1 (-2.11), L4 × T3 (-1.77) and L6 × T2 (-1.72) exhibited highly significant negative SCA effects. None of the hybrids involved both of the parents with significant and negative GCA effects. Two hybrids L3 × T2 and L4 × T3 have at least one parent with negative and significant GCA effects. Three hybrids L1 × T4, L6 × T2 and L7 × T1 involved neither of the parents with negative and significant GCA effects.

4.3.2.3.5 Fruit Length (cm)

Two lines, L4 (2.30) and L5 (0.38), and one tester T2 (0.65) showed positive and significant GCA effects for fruit length. Four lines L2, L3, L6 and L7 and, one tester T1 showed significant and negative GCA effects (Table 18). The line L1 exhibited non-significant positive GCA effects for fruit length.

The SCA effects in fruit length ranged between -1.63 in the cross L6 × T2 to 1.36 in L1 × T2. Among the 28 hybrids, 20 hybrids manifested significant SCA effects. Among these, 10 crosses have positive significant and 10 have negative

Table 19a. Estimation of SCA effects of hybrids for plant height, primary branches plant^{-1}, days to first flower and days to first harvest

Hybrids	Plant height (cm)	Primary branches plant^{-1}	Days to first flower	Days to first harvest
L1 × T1	6.25**	0.12	1.00**	3.93**
L1 × T2	7.50**	-0.13	3.78**	2.07**
L1 × T3	-5.44**	-0.37	0.17	-0.64
L1 × T4	-8.31**	0.38	-4.95**	-5.36**
L2 × T1	-1.88	-0.22	1.05*	-0.11
L2 × T2	-2.84**	-0.23	-0.03	1.03
L2 × T3	5.26**	-0.01	-1.28**	-0.52
L2 × T4	-0.54	0.46**	0.27	-0.40
L3 × T1	5.35**	0.04	1.34**	0.64
L3 × T2	-4.15**	1.08**	-2.83**	-3.22**
L3 × T3	-3.54**	-0.00	3.97**	3.23**
L3 × T4	2.33*	-1.13**	-2.48**	-0.65
L4 × T1	-4.79**	-0.38	-0.46	-0.36
L4 × T2	0.22	1.29**	0.63	0.78
L4 × T3	0.32	0.19	-1.41**	-1.77*
L4 × T4	4.25**	-1.09**	1.24**	1.35
L5 × T1	-0.10	-0.07	-0.25	-1.11
L5 × T2	-1.14	-0.69*	0.07	0.03
L5 × T3	-1.11	0.28	-0.06	0.48
L5 × T4	2.35*	0.48	0.24	0.60
L6 × T1	-1.45	0.71*	-0.95*	-0.86
L6 × T2	-0.23	-1.43**	-2.22**	-1.72*
L6 × T3	-0.31	0.28	-0.58**	-0.27
L6 × T4	1.99*	0.44	3.75**	2.85**
L7 × T1	-3.37**	-0.20	-1.73**	-2.11**
L7 × T2	0.64	0.11	0.60	1.03
L7 × T3	4.81**	-0.37	-0.81	-0.52
L7 × T4	-2.08*	0.46	1.94**	1.60*
CD at $P \leq 0.05$	1.86	0.56	0.88	1.47
CD at $P \leq 0.01$	2.44	0.74	1.15	1.92

*, **: significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

significant SCA effects. Estimates of positive significant SCA effects ranged from 0.29 in the cross L3 × T4 to 1.36 in the cross L1 × T2. The hybrid L1 × T2 exhibited the highest SCA effects of 1.36 followed by L7 × T1 (1.09), L6 × T3 (1.03), L3 × T3 (0.84), L6 × T4 (0.79) and L2 × T2 (0.72) (Table 19b). Among ten hybrids showing significant positive SCA effects only one cross, L4 × T2 had both the parents with positive significant GCA effects for fruit length. Three hybrids L5 × T4, L1 × T2 and L2 × T2 involved at least one parent with positively significant GCA effects and the remaining five hybrids L2 × T1, L3 × T3, L3 × T4, L6 × T3, L6 × T4 and L7 × T1 had neither of the parents with positively significant GCA effects.

4.3.2.3.6 Fruit Girth (cm)

Out of seven lines and four testers evaluated, six lines and three testers showed the significant GCA effects of which three lines and one tester were in the positive direction. Lines L4 (0.34), L6 (0.32) and L5 (0.24) showed high GCA effects for fruit girth. Among testers T3 exhibited highest positive significant GCA effects of 0.27. Lines L2, L3, L7 and, testers T1, T4 had negative and significant GCA effects.

The range of SCA effects for fruit girth varied between -0.61 in the cross L5 × T2 to 0.49 in the cross L2 × T3. Among the 28 hybrids, 9 hybrids manifested significant SCA effects. Among these, four crosses have positive significant and five have negative significant SCA effects. The hybrid L2 × T3 exhibited the highest SCA effects of 0.49 followed by L7 × T2 (0.46), L3 × T1 (0.43) and L5 × T4 (0.42). Two hybrids L2 × T3 and L5 × T4 involved at least one parent with positively significant GCA effects and another two hybrids L3 × T1 and L7 × T2 have neither of the parents with positively significant GCA effects.

4.3.2.3.7 Fruit Weight (g)

Five lines and three testers showed significant GCA effects. Among them, two lines L1 (0.72), L5 (0.55) and one tester T2 (0.47) exhibited positive and significant GCA effects. Three lines (L2, L4 and L6) and two testers (T3 and T4)

exhibited significant and negative GCA effects. Lines L3, L7 and tester T1 expressed non-significant positive GCA effects for fruit weight.

The SCA effects varied between -0.74 in the cross L6 × T2 to 1.17 in the cross L7 × T1. Among the 28 hybrids, 11 hybrids manifested significant SCA effects. Four hybrids had positive significant and seven have negative significant SCA effects. Estimates of positive significant SCA effects ranged from 0.37 in the cross L3 × T3 to 1.17 in the cross L7 × T1. Hybrids exhibiting significant positive SCA effects were L7 × T1 (1.17), L6 × T3 (1.13), L1 × T2 (0.95) and L3 × T3 (0.37). Hybrid L1 × T2 had both the parents with positively significant GCA effects and remaining three hybrids L7 × T1, L6 × T3 and L3 × T3 had neither of parents with significant positive GCA effects.

4.3.2.3.8 Fruits Plant^{1}

The combining ability analysis revealed that seven lines and three testers showed significant GCA effects for fruits plant^{-1}, among them, five lines and one tester were in the positive direction. The line L3 exhibited the highest positive GCA effects (23.64) followed by L6 (17.14), L7 (10.48), L1 (3.98) and L2 (2.23). Tester T1 showed the high positive GCA effects of 22.04. Lines L4, L5 and testers T2, T4 had negative and significant GCA effects.

The SCA effects varied between -39.20 in the cross L5 × T1 to 38.17 in the cross L3 × T2. Among the 28 hybrids, 27 hybrids manifested significant SCA effects. Thirteen crosses have positive significant and 14 have negative significant SCA effects. Estimates of positive significant SCA effects ranged from 6.12 in the cross L1 × T3 to 38.17 in the cross L3 × T2. Top five hybrids exhibiting highly significant positive SCA effects were L3 × T2 (38.17), L7 × T3 (34.95), L6 × T1 (32.38), L4 × T1 (18.38) and L1 × T1 (17.21). Three hybrids namely L1 × T1, L2 × T1 and L6 × T1 possess both the parents with positive significant GCA effects. Six hybrids L1 × T3, L1 × T4, L2 × T4, L3 × T2, L7 × T3 and L4 × T1 have only one parent with positively significant GCA effects and remaining four hybrids L4 × T2, L5 × T2, L5 × T3 and L5 × T4 have neither of parents with significant positive

Table 19b. Estimation of SCA effects of hybrids for fruit length, fruit girth, fruits plant^{-1} and fruit weight

Hybrids	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits plant^{-1}
L1 × T1	-0.51**	0.11	-0.35**	17.21**
L1 × T2	1.36**	0.07	0.95**	-30.50**
L1 × T3	-0.92**	-0.29*	-0.68**	6.12**
L1 × T4	0.07	0.11	0.08	7.17**
L2 × T1	0.62**	-0.12	0.04	10.63**
L2 × T2	0.72**	0.09	-0.16	-14.75**
L2 × T3	-0.59**	0.49**	-0.07	-7.80**
L2 × T4	-0.75**	-0.46**	0.20	11.92**
L3 × T1	-0.28**	0.43**	-0.09	-21.45**
L3 × T2	-0.86**	-0.08	-0.09	38.17**
L3 × T3	0.84**	-0.32**	0.37**	-7.55**
L3 × T4	0.29**	-0.03	-0.19	-9.17**
L4 × T1	0.16	-0.04	0.04	18.38**
L4 × T2	0.35*	0.07	0.03	12.67**
L4 × T3	-0.72**	0.03	-0.14	-20.71**
L4 × T4	0.21	-0.06	0.07	-10.33**
L5 × T1	-0.89**	0.01	-0.28*	-39.20**
L5 × T2	0.20	-0.61**	0.01	11.42**
L5 × T3	0.23	0.18	0.08	13.04**
L5 × T4	0.46**	0.42**	0.19	14.75**
L6 × T1	-0.19	0.02	-0.53**	32.38**
L6 × T2	-1.63**	-0.01	-0.74**	-13.00**
L6 × T3	1.03**	-0.02	1.13**	-18.05**
L6 × T4	0.79**	0.01	0.15	-1.33
L7 × T1	1.09**	-0.41**	1.17**	-17.95**
L7 × T2	-0.13	0.46**	0.00	-4.00*
L7 × T3	0.13	-0.06	-0.68**	34.95**
L7 × T4	-1.09**	0.01	-0.49**	-13.00**
CD at $P \leq 0.05$	0.27	0.21	0.22	3.70
CD at $P \leq 0.01$	0.35	0.28	0.29	4.85

*, **: significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

GCA effects (Table 19b).

4.3.2.3.9 Yield Plant^{-1} (g)

Four lines *viz.*, L3 (128.41), L1 (91.23), L7 (51.20), L6 (38.35) and a tester T1 (108.17) exhibited highly significant and positive GCA effects for yield plant^{-1}. On the other hand, lines L2, L4, L5 and testers T3, T4 exhibited significant and negative GCA effects (Table 18) for yield plant^{-1}.

Out of 28 hybrids, 25 manifested significant SCA effects. The range of SCA effects varied between -221.72 in the cross L5 × T1 to 185.13 in the cross L3 × T2. Fourteen hybrids showed positive and significant SCA effects. The crosses L3 × T2 (185.13), L5 × T3 (88.05), L2 × T4 (82.52), L1 × T1 (81.20) and L5 × T4 (80.63) exhibited high SCA effects (Table 19c) for yield plant^{-1}. Eleven crosses exhibited significant and negative SCA effects. Hybrids L1 × T1, L6 × T1 and L7 × T1 were had both the parents with positive significant GCA effects. The hybrids L1 × T4, L3 × T2, L6 × T3, L7 × T3, L2 × T1 and L4 × T1 had one parent with significant and positive GCA effects and remaining five hybrids L2 × T4, L4 × T2, L5 × T2, L5 × T3 and L5 × T4 involved neither of the parents with significant and positive GCA effects.

4.3.2.3.10 Yield Plot^{-1} (kg/6.48 m^2)

A perusal of GCA effects revealed that four lines and one tester were parents for yield plot^{-1}. Lines L3 (3.57), L1 (2.56), L7 (1.45), L6 (1.09) and tester T1 (3.03) exhibited highly significant and positive GCA effects. Lines L2, L4, L5 and testers T2, T3, T4 exhibited significant negative GCA effects.

Among the 28 hybrids evaluated, 25 hybrids manifested significant SCA effects which ranged from -6.19 in the cross L5 × T1 to 5.14 in the cross L3 × T2. The SCA effects were negatively significant in eleven hybrids and positive in the remaining fourteen crosses. The positive significant SCA effects ranged from 1.05 in the cross L2 × T1 to 5.14 in the cross L3 × T2. Top two hybrids with positive and significant SCA effects identified were L3 × T2 (5.14), L5 × T3 (2.40). Three

hybrids L5 × T4, L2 × T4 and L1 × T1 recorded SCA effects of 2.28. The hybrids L1 × T1, L6 × T1 and L7 × T1 have both the parents with positive significant GCA effects. The hybrids L1 × T4, L3 × T2, L6 × T3, L7 × T3, L2 × T1 and L4 × T1 have at least one parent with significant and positive GCA effects and remaining five hybrids L2 × T4, L4 × T2, L5 × T2, L5 × T3 and L5 × T4 involved neither of the parents with significant and positive GCA effects.

4.3.2.3.11 Vitamin C (mg 100 g^{-1})

Six lines and four testers showed significant GCA effects, of which three lines and three testers exhibited positive significant GCA effects. Lines L3 (17.76), L7 (10.43), L4 (8.18) and testers T1 (9.31), T2 (2.17), T3 (1.07) exhibited significant positive GCA effects. Lines L1, L2, L6 and tester T4 registered significant negative GCA effects.

Twenty-six hybrids manifested significant SCA effects ranging from -12.98 in the cross L5 × T1 to 11.55 in the cross L5 × T4. Among these, thirteen crosses have positive significant SCA effects and thirteen have negative significant SCA effects. The hybrids namely L5 × T4 (11.55), L3 × T2 (9.33), L5 × T3 (9.26), L1 × T1 (7.61) and L2 × T1 (7.52) exhibited high positive significant SCA effects. Among thirteen crosses which showed significant positive SCA effects, five hybrids namely L3 × T2, L4 × T2, L4 × T3, L7 × T1 and L7 × T3 involved both the parents with positive significant GCA effects. Five hybrids namely L1 × T1, L2 × T1, L2 × T2, L5 × T3 and L6 × T3 have one parent with significant and positive GCA effects and remaining three hybrids L1 × T4, L5 × T4 and L6 × T4 involved neither of the parents with significant positive GCA effects.

4.3.2.3.12 Carotenoids (mg 100 g^{-1})

A perusal of GCA effects revealed that two lines and one testers were promising, one line and one tester were average general combiner for carotenoids. Lines L4 (75.35), L2 (34.46) and tester T1 (5.82) exhibited highly significant and positive GCA effects. Parental lines L1, L3, L5, L6 and tester T2 exhibited

significant negative GCA effects. The line L7 and tester T3 exhibited non-significant positive GCA effects (Table 18).

Among the 28 hybrids evaluated, 24 hybrids manifested significant SCA effects which ranged from -34.90 in the cross L3 × T4 to 41.86 in the cross L6 × T3. The effects were positively significant in twelve crosses and negative in the remaining twelve crosses. The positive significant SCA effects ranged from 4.85 in the cross L7 × T1 to 41.86 in the cross L6 × T3. Top five hybrids with positive and significant SCA effects identified were L6 × T3 (41.86), L3 × T2 (30.29), L3 × T1 (29.43), L2 × T4 (26.76) and L7 × T4 (21.18) (Table 19c). Among twelve hybrids showing significant positive effects, only one hybrid L4 × T1 showed both parents with significant positive GCA effects. Five hybrids L2 × T4, L4 × T2, L1 × T1, L3 × T1 and L7 × T1 have at least one parent with significant and negative GCA effects and six hybrids L1 × T4, L3 × T2, L5 × T2, L5 × T4, L6 × T3 and L7 × T4 involved neither of the parents with significant and positive GCA effects.

4.3.2.3.13 Coefficient of Infection (CI)

Six lines and three testers showed significant GCA effects. Among them, three lines L1 (-11.96), L4 (-5.47) and L7 (-3.63), and two testers T1 (-2.80) and T3 (-4.05) exhibited negative and significant GCA effects for coefficient of infection. Lines L2 (3.78), L5 (12.68), L6 (5.84) and tester T2 (5.83) exhibited significant and negative GCA effects.

Among the 28 hybrids, 12 hybrids manifested negatively significant SCA effects. Top four hybrids with negative and significant SCA effects identified were L3 × T2 (-16.56), L6 × T1 (-14.90), L5 × T4 (-13.29) and L6 × T3 (-12.86). Hybrid L4 × T1, L7 × T1 and L7 × T3 had both the parents with negatively significant GCA effects. Six hybrids L1 × T2, L4 × T2, L5 × T3, L6 × T1, L6 × T3 and L7 × T4 had one parent with negative and significant GCA effects and three hybrids L2 × T2, L3 × T2 and L5 × T4 involved neither of the parents with negative and significant GCA effects.

Table 19c. Estimation of SCA effects of hybrids for yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection

Hybrids	Yield plant^{-1} (g)	Yield plot^{-1} (kg/6.48m^2)	Vitamin C (mg100 g^{-1})	Carotenoids (mg100 g^{-1})	Coefficient of Infection (CI) (%)
L1 × T1	81.20**	2.28**	7.61**	10.43**	1.76
L1 × T2	-95.94**	-2.68**	-2.25**	-24.38**	-4.98**
L1 × T3	-45.36**	-1.26**	-7.82**	-0.81	4.81**
L1 × T4	60.10**	1.66**	2.46**	14.76**	-1.58
L2 × T1	37.04**	1.05**	7.52**	-25.57**	1.21
L2 × T2	-68.78**	-1.92**	7.33**	-4.38*	-5.46**
L2 × T3	-50.78**	-1.41**	-11.57**	3.19	4.93**
L2 × T4	82.52**	2.28**	-3.29**	26.76**	-0.68
L3 × T1	-108.31**	-3.06**	1.19	29.43**	5.72**
L3 × T2	185.13**	5.14**	9.33**	30.29**	-16.56**
L3 × T3	5.26	0.18	-2.90**	-24.81**	7.30**
L3 × T4	-82.08**	-2.26**	-7.62**	-34.90**	3.53*
L4 × T1	80.94**	2.27**	-2.56**	15.85**	-3.57*
L4 × T2	54.17**	1.52**	7.25**	12.37**	-11.51**
L4 × T3	-98.49**	-2.76**	2.68**	-11.06**	9.77**
L4 × T4	-36.62**	-1.03**	-7.37**	-17.15**	5.31**
L5 × T1	-221.72**	-6.19**	-12.98**	-7.74**	15.58**
L5 × T2	53.04**	1.51**	-7.83**	14.45**	6.66**
L5 × T3	88.05**	2.40**	9.26**	-11.98**	-8.95**
L5 × T4	80.63**	2.28**	11.55**	5.26*	-13.29**
L6 × T1	57.55**	1.61**	-5.98**	-27.24**	-14.90**
L6 × T2	-119.65**	-3.35**	-5.50**	1.29	10.83**
L6 × T3	53.72**	1.51**	7.26**	41.86**	-12.86**
L6 × T4	8.38	0.24	4.21**	-15.90**	16.93**
L7 × T1	73.30**	2.05**	5.19**	4.85*	-5.80**
L7 × T2	-7.98	-0.22	-8.33**	-29.63**	21.02**
L7 × T3	47.60**	1.33**	3.10**	3.61	-5.00**
L7 × T4	-112.93**	-3.16**	0.05	21.18**	-10.21**
CD at $P \leq 0.05$	25.49	0.41	1.72	4.09	3.23
CD at $P \leq 0.01$	33.43	0.53	2.26	5.37	4.24

*, **: significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

4.3.3 Estimation of Heterosis over Better Parent, Mid Parent and the Standard Checks

The results pertaining to the per cent heterosis expressed over the better parent (BP), mid parent and standard check F_1 hybrids (CH-27 and Arka Harita) has been reported in 13 Tables from 20a to 20m and are presented character wise under the following heads;

4.3.3.1 Plant Height (cm)

The range of heterosis over better parent varied from -12.92% in the cross L1 × T4 to 47.30% in the cross L7 × T3. Out of 28 hybrids evaluated, 21 hybrids showed positive significant heterosis over their respective better parents. Extent of positive heterosis over better parent varied from 6.00% in the cross L3 × T2 to 47.30% in the cross L7 × T3. Five cross combinations namely, L7 × T3 (47.30%), L7 × T2 (41.10%), L7 × T4 (32.70%), L1 × T2 (31.45) and L2 × T3 (24.74) exhibited high positive significant heterosis over the better parent. Mid-parent heterosis for plant height varied from -7.09% (L1 × T4) to 55.51% (L7 × T3). Twenty five hybrids exhibited positive significant heterosis over their respective mid-parents. The range of significant standard heterosis ranged from -27.53% (L1 × T4) to 22.53% (L7 × T3) and from -23.34% (L1 × T4) to 29.60% (L7 × T3) over check hybrids CH-27 (resistant check) and Arka Harita (commercial check), respectively. Twenty-one and 26 cross combinations exhibited significant positive standard heterosis over CH-27 and Arka Harita hybrids, respectively. Top three hybrids namely L7 × T3, L7 × T2 and L7 × T1 exhibited high positive significant standard heterosis over two commercial checks (Table 20a). The hybrids L1 × T4, L4 × T1, L5 × T1 showed high significant negative heterosis for plant height.

4.3.3.2 Primary Branches Plant[1]

The heterosis over better parent varied from -41.05% in the cross L6 × T2 to 99.17% in the cross L4 × T2. Out of 28 hybrids evaluated, four hybrids exhibited positive significant heterosis over the better parent. Extent of positive heterosis

Table 20a. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for plant height (cm)

Hybrids	Plant height (cm)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	8.45**	3.43	9.40**	23.02**
L1 × T2	31.45**	2.09	7.98**	35.71**
L1 × T3	4.31	-22.40**	-17.91**	5.45*
L1 × T4	-12.92**	-27.53**	-23.34**	-7.09**
L2 × T1	10.19**	5.09*	11.16**	13.57**
L2 × T2	11.40**	-0.08	5.68*	19.41**
L2 × T3	24.74**	11.88**	18.33**	36.36**
L2 × T4	13.38**	1.69	7.56**	17.62**
L3 × T1	7.27**	2.30	8.21**	20.73**
L3 × T2	6.00*	-17.68**	-12.92**	8.48**
L3 × T3	9.29**	-18.69**	-14.00**	9.50**
L3 × T4	9.75**	-8.66**	-3.39**	16.11**
L4 × T1	-11.11**	-15.23**	-10.33**	-1.99
L4 × T2	15.80**	-10.06**	-4.87*	15.83**
L4 × T3	13.42**	-11.95**	-6.87**	15.83**
L4 × T4	13.81**	-5.29*	0.18	17.77**
L5 × T1	-4.05	-8.49**	-3.21	-2.66
L5 × T2	3.99	-13.80**	-8.82**	7.38**
L5 × T3	1.53	-15.83**	-10.98**	7.01**
L5 × T4	8.17**	-9.97**	-4.78*	8.39**
L6 × T1	8.27**	5.07*	11.14**	9.21**
L6 × T2	6.82**	3.66	9.65**	18.67**
L6 × T3	4.54	1.45	7.31**	18.35**
L6 × T4	8.51**	5.30*	11.38**	16.83**
L7 × T1	19.47**	13.94**	20.51**	27.62**
L7 × T2	41.10**	17.37**	24.15**	45.94**
L7 × T3	47.30**	22.53**	29.60**	55.51**
L7 × T4	32.70**	10.44**	16.82**	32.74**
SE	1.32			1.15
CD at $P \leq 0.05$	2.58			2.25
CD at $P \leq 0.01$	3.39			2.95

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20b. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for primary branches plant^{-1}

Hybrids	Primary branches plant^{-1}			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	-2.62	31.22*	27.60*	21.32*
L1 × T2	30.00	6.03	3.10	30.00*
L1 × T3	-21.35*	3.19	0.34	-3.00
L1 × T4	-3.12	6.74	3.79	11.34
L2 × T1	-8.68	23.05	19.66	13.77
L2 × T2	29.13	5.32	2.41	29.13*
L2 × T3	-10.81	17.02	13.79	10.00
L2 × T4	1.71	12.06	8.97	16.89
L3 × T1	12.42	51.49**	47.31**	22.62*
L3 × T2	49.18**	67.59**	62.97**	72.86**
L3 × T3	4.86	37.59**	33.79**	12.99
L3 × T4	-27.40*	-18.44	-20.69	-26.69**
L4 × T1	-0.97	33.44*	29.76*	21.39*
L4 × T2	99.17**	69.50**	64.83**	103.40**
L4 × T3	5.97	39.04**	35.21**	28.56**
L4 × T4	-29.19*	-21.99	-24.14	-20.10
L5 × T1	-4.53	28.65*	25.10	0.50
L5 × T2	-24.30*	-8.19	-10.72	-9.48
L5 × T3	-2.73	27.62*	24.10	1.10
L5 × T4	-6.43	13.48	10.34	-1.94
L6 × T1	20.51*	66.67**	62.07**	22.08**
L6 × T2	-41.05**	-18.48	-20.72	-25.84*
L6 × T3	1.79	40.78**	36.90**	4.47
L6 × T4	-9.31	25.43	21.97	0.96
L7 × T1	4.21	40.43**	36.55**	16.99
L7 × T2	26.73*	33.48*	29.79*	42.85**
L7 × T3	-6.49	22.70	19.31	3.75
L7 × T4	17.13	29.04*	25.48*	19.77
SE	0.39			0.34
CD at $P \leq 0.05$	0.76			0.66
CD at $P \leq 0.01$	1.00			0.87

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

over better parent ranged from 20.51% in the cross L6 × T1 to 99.17% in the cross L4 × T2. Four cross combinations namely, L4 × T2 (99.17%), L3 × T2 (49.18%), L7 × T2 (26.73%) and L6 × T1 (20.51%) exhibited significant positive heterosis over the better parent. Out of 28 hybrids, 10 and two hybrids showed significantly positive and negative heterosis over mid parent, respectively. The hybrids which showed high significant positive heterosis over mid parent were L4 × T2 (103.40%), L3 × T2 (72.86%) and L7 × T2 (42.85%) (Table 20b). The range of significant positive heterosis varied from 27.62% (L5 × T3) to 69.50% (L4 × T2) and 25.48% (L7 × T4) to 64.83% (L4 × T2) over commercial hybrids CH-27 and Arka Harita, respectively. Top five hybrids *viz.* L4 × T2, L3 × T2, L6 × T1, L3 × T1 and L6 × T3 exhibited highly significant positive standard heterosis over both check hybrids.

4.3.3.3 Days to First Flower

The negative heterosis is desirable in respect of days to first flower and days to first harvest. For days to first flower, the range of heterobeltiosis varied from -5.61% (L2 × T1) to -28.89% (L1 × T4). Of 28 hybrids, 22 showed significant negative heterosis over better parents. Five cross combinations namely, L1 × T4 (-28.89%), L3 × T2 (-26.18%), L5 × T1 (-24.40%), L3 × T4 (-23.59%) and L4 × T1 (-22.13%) exhibited high negative significant heterosis over the better parent (Table 20c). The range of significant mid parent heterosis ranged from -4.25% (L2 × T4) to -23.66% (L3 × T2). Twenty cross combinations exhibited negative significant mid parent heterosis. The range of significant heterosis over the check hybrids varied from -5.00% (L7 × T3) to -28.32% (L1 × T4) and -3.99% (L7 × T1) to -22.51 (L1 × T4) over check F_1 hybrids CH-27 and Arka Harita, respectively. Top three hybrids namely L1 × T4, L5 × T1 and L3 × T2 showed highly significant negative heterosis over both the check hybrids.

Table 20c. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for days to first flower

Hybrids	Days to first flower			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	-15.12**	-15.36**	-8.49**	-8.18**
L1 × T2	-1.46	-5.65**	2.01	4.61**
L1 × T3	-7.44**	-14.07**	-7.09**	-3.17
L1 × T4	-28.89**	-28.32**	-22.51**	-22.70**
L2 × T1	-5.61**	-5.88**	1.76	-5.22**
L2 × T2	-5.88**	-6.92**	0.64	-4.36**
L2 × T3	-7.72**	-8.74**	-1.33	-4.80**
L2 × T4	-5.15**	-4.39*	3.37	-4.25**
L3 × T1	-16.77**	-14.67**	-7.75**	-15.62**
L3 × T2	-26.18**	-24.32**	-18.18**	-23.66**
L3 × T3	-6.05**	-3.68*	4.14*	-1.39
L3 × T4	-23.59**	-21.66**	-15.30**	-22.94**
L4 × T1	-22.13**	-22.35**	-16.05**	-13.69**
L4 × T2	-13.68**	-17.35**	-10.64**	-6.06**
L4 × T3	-15.33**	-21.39**	-15.01**	-9.15**
L4 × T4	-14.64**	-13.96**	-6.98**	-4.93**
L5 × T1	-24.40**	-24.61**	-18.50**	-13.59**
L5 × T2	-18.27**	-21.74**	-15.39**	-8.21**
L5 × T3	-14.35**	-20.48**	-14.03**	-5.11**
L5 × T4	-20.24**	-19.60**	-13.08**	-8.41**
L6 × T1	-16.17**	-16.41**	-9.62**	-11.31**
L6 × T2	-14.35*	-17.99**	-11.33**	-11.11**
L6 × T3	-4.93	-11.74**	-4.58*	-2.81
L6 × T4	-0.42	0.37	8.52**	5.89**
L7 × T1	-10.94**	-11.20**	-3.99*	-6.03**
L7 × T2	1.57	-2.74	5.15*	5.11**
L7 × T3	2.33	-5.00**	2.71	4.32*
L7 × T4	1.87	2.68	11.02**	8.04**
SE	0.63			0.55
CD at $P \leq 0.05$	1.23			1.07
CD at $P \leq 0.01$	1.61			1.41

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

4.3.3.4 Days to First Harvest

The observed range of significant heterobeltiosis among the hybrids was -5.36% (L3 × T3) to -20.69% (L3 × T2). Out of 28 hybrids, twenty-four showed significant negative heterobeltosis. Hybrids which showed high negative significant heterobeltosis were L3 × T2 (-20.69%), L5 × T1 (-19.30%), L5 × T2 (-18.97%), L1 × T4 (-17.86%) and L4 × T1 (-15.79%). Significant mid-parent heterosis ranged from -3.64% (L3 × T3) to -19.30% (L3 × T2). Hybrids L3 × T2 (-19.30%), L1 × T4 (-14.09%), L3 × T4 (-12.50%) and L5 × T1 (-12.38%) exhibited high negative significant heterosis over respective mid-parents (Table 20d). The range of significant negative heterosis over the check hybrids varied from -5.56% (L6 × T3 and L7 × T1) to -14.81% (L1 × T4, L3 × T2 and L5 × T1) and -4.09% (L1 × T3) to -13.21 (L1 × T4, L3 × T2 and L5 × T1) over check F_1 hybrids CH-27 and Arka Harita, respectively. Three hybrids namely L1 × T4, L3 × T2 and L5 × T1 recorded the high negative heterosis over check hybrids CH-27 and Arka Harita.

4.3.3.5 Fruit Length (cm)

The range of heterosis over better parent varied from -24.11% in the cross L5 × T1 to 74.71% in the cross L6 × T4. Out of 28 crosses evaluated, 19 and six crosses showed positive significant and negative heterobeltiosis, respectively. Extent of positive significant heterosis over better parent ranged from 7.49% in the cross L3 × T1 to 74.71% in the cross L6 × T4. Five cross combinations namely, L6 × T4 (74.71%), L1 × T2 (66.16%), L4 × T2 (63.78%), L1 × T4 (48.12%) and L4 × T4 (44.88%) exhibited significant high positive heterosis over the better parent. Twenty-six hybrids showed significant positive heterosis over mid parent. The hybrid L4 × T4 exhibited highest significant positive mid parent heterosis of 87.44% followed by L1 × T2 (81.22%), L4 × T1 (75.90%), L4 × T2 (75.28%) and L1 × T4 (68.93%) (Table 20e). The range of heterosis over the check hybrid CH-27 and Arka Harita varied from 16.92% (L2 × T4) to 140.00% (L4 × T2) and -10.59% (L2 × T4) to 83.53% (L4 × T2), respectively. All 28 and 24 crosses exhibited positive significant heterosis over CH-27 and Arka Harita, respectively. Hybrids

Table 20d. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for days to first harvest

Hybrids	Days to first harvest			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	-3.51	1.85	3.77	1.85
L1 × T2	-8.62**	-1.85	0.00	-2.75
L1 × T3	-5.86**	-5.86**	-4.09*	-3.17
L1 × T4	-17.86**	-14.81**	-13.21**	-14.02**
L2 × T1	-7.02**	-1.85	0.00	-7.02**
L2 × T2	-6.90**	0.00	1.89	-6.09**
L2 × T3	-7.02**	-1.85	0.00	-4.50**
L2 × T4	-7.02**	-1.85	0.00	-6.19**
L3 × T1	-12.28**	-7.41**	-5.66**	-11.50**
L3 × T2	-20.69**	-14.81**	-13.21**	-19.30**
L3 × T3	-5.36**	-1.85	0.00	-3.64*
L3 × T4	-12.50**	-9.26**	-7.55**	-12.50**
L4 × T1	-15.79**	-11.11**	-9.43**	-8.57**
L4 × T2	-15.52**	-9.26**	-7.55**	-7.55**
L4 × T3	-12.96**	-12.96**	-11.32**	-7.84**
L4 × T4	-10.71**	-7.41**	-5.66**	-3.85*
L5 × T1	-19.30**	-14.81**	-13.21**	-12.38**
L5 × T2	-18.97**	-12.96**	-11.32**	-11.32**
L5 × T3	-11.11**	-11.11**	-9.43**	-5.88**
L5 × T4	-14.29**	-11.11**	-9.43**	-7.69**
L6 × T1	-12.28**	-7.41**	-5.66**	-8.68**
L6 × T2	-15.52**	-9.26**	-7.55**	-11.31**
L6 × T3	-5.56**	-5.56**	-3.77	-4.23*
L6 × T4	-3.57	0.00	1.89	-0.46
L7 × T1	-10.53**	-5.56**	-3.77	-6.99**
L7 × T2	-6.90**	0.00	1.89	-2.41
L7 × T3	-1.85	-1.85	0.00	-0.62
L7 × T4	-1.79	1.85	3.77	1.23
SE	1.01			0.87
CD at $P \leq 0.05$	1.97			1.70
CD at $P \leq 0.01$	2.59			2.23

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20e. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for fruit length (cm)

Hybrids	Fruit length (cm)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	40.22**	48.85**	13.82**	44.94**
L1 × T2	66.16**	111.54**	61.76**	81.22**
L1 × T3	1.37	42.69**	9.12*	15.58**
L1 × T4	48.12**	57.23**	20.24**	68.93**
L2 × T1	11.61**	53.85**	17.65**	29.79**
L2 × T2	27.23**	75.38**	34.12**	32.29**
L2 × T3	-8.20**	29.23**	-1.18	-7.23**
L2 × T4	-15.18**	16.92**	-10.59**	7.34*
L3 × T1	7.49*	44.62**	10.59**	23.72**
L3 × T2	12.06**	50.77**	15.29**	15.16**
L3 × T3	23.50**	73.85**	32.94**	26.29**
L3 × T4	13.49**	52.69**	16.76**	42.34**
L4 × T1	47.51**	116.15**	65.29**	75.90**
L4 × T2	63.78**	140.00**	83.53**	75.28**
L4 × T3	35.96**	99.23**	52.35**	38.69**
L4 × T4	44.88**	112.31**	62.35**	87.44**
L5 × T1	-24.11**	47.69**	12.94**	0.52
L5 × T2	-1.19	92.31**	47.06**	19.47**
L5 × T3	-9.09**	76.92**	35.29**	5.50*
L5 × T4	-10.67**	73.85**	32.94**	26.61**
L6 × T1	33.33**	32.31**	1.18	43.04**
L6 × T2	-6.95*	18.46**	-9.41**	11.19**
L6 × T3	16.39**	63.85**	25.29**	44.65**
L6 × T4	74.71**	49.85**	14.59**	80.79**
L7 × T1	38.12**	73.08**	32.35**	54.16**
L7 × T2	29.00**	64.23**	25.59**	30.02**
L7 × T3	9.56**	54.23**	17.94**	15.93**
L7 × T4	-6.08	17.69**	-10.00**	14.65**
SE	0.18			0.16
CD at $P \leq 0.05$	0.35			0.31
CD at $P \leq 0.01$	0.46			0.41

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

L4 × T2 and L4 × T1 showed positively high significant standard heterosis over both checks.

4.3.3.6 Fruit Girth (cm)

The heterosis range over better parent varied from -13.15% (L7 × T1) to 37.58% (L4 × T3). Out of 28 hybrids evaluated, thirteen hybrids showed positive significant heterosis over the better parent. Extent of positive significant heterosis over better parent ranged from 11.49% in the cross L4 × T2 to 37.58% in the cross L4 × T3. Hybrids L4 × T3 (37.58%), L2 × T3 (32.66%), L6 × T3 (27.94%), L3 × T1 (24.47%) and L4 × T1 (23.83%) exhibited significant high positive heterosis over the better parent. The range of significant heterosis over mid-parent ranges from -15.63% (L5 × T2) to 45.39% (L2 × T3). The hybrids L2 × T3 (45.39%), L4 × T3 (37.82%) and L4 × T1 (34.18%) exhibited significantly high positive heterosis over mid-parent. The range of standard heterosis varied from -18.18% (L2 × T4) to 29.78% (L5 × T3) and 10.88% (L7 × T4) to 45.26% (L5 × T3) over CH-27 and Arka Harita, respectively. Four hybrids namely L5 × T3, L4 × T3, L6 × T3 and L5 × T4 showed positive high significant heterosis over both the checks (Table 20f).

4.3.3.7 Fruit Weight (g)

The range of significant heterosis over better parent varied from -31.54% (L5 × T1, L5 × T3) to 51.65% (L1 × T2). Out of 28 hybrids evaluated, ten hybrids showed positive significant heterosis over the better parent. Extent of significant positive heterobeltiosis ranged from 6.55% in the cross L4 × T2 to 51.65% in the cross L1 × T2. Four cross combinations namely, L1 × T2 (51.64%), L1 × T4 (39.47%), L1 × T1 (36.84%) and L6 × T3 (23.17) displayed significant high positive heterosis over the better parent. Sixteen hybrids showed significant positive heterosis over mid-parent. The hybrid L1 × T2 exhibited highest significant positive mid parent heterosis of 65.27% followed by L1 × T4 (44.22%), L1 × T1 (42.79%), L7 × T1 (37.14%) and L6 × T3 (26.84%). Out of 28 crosses, 27

Table 20f. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for fruit girth (cm)

Hybrids	Fruit girth (cm)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	20.57**	6.58	19.30**	27.34**
L1 × T2	-1.15	7.84	20.70**	9.21*
L1 × T3	13.13*	5.33	17.89**	16.06**
L1 × T4	15.68**	4.08	16.49**	16.70**
L2 × T1	19.84**	-5.33	5.96	21.53**
L2 × T2	-5.17	3.45	15.79**	11.30*
L2 × T3	32.66**	23.51**	38.25**	45.39**
L2 × T4	-9.06	-18.18**	-8.42	-1.88
L3 × T1	24.47**	10.03*	23.16**	31.46**
L3 × T2	-10.63*	-2.51	9.12	-1.27
L3 × T3	5.72	-1.57	10.18	8.46
L3 × T4	4.53	-5.96	5.26	5.45
L4 × T1	23.83**	15.67**	29.47**	34.18**
L4 × T2	11.49*	21.63**	36.14**	20.12**
L4 × T3	37.58**	28.53**	43.86**	37.82**
L4 × T4	20.47**	12.54*	25.96**	22.74**
L5 × T1	-7.61	14.11**	27.72**	12.69**
L5 × T2	-20.56**	-1.88	9.82	-15.63**
L5 × T3	5.08	29.78**	45.26**	19.83**
L5 × T4	0.25	23.82**	38.60**	16.01**
L6 × T1	18.41**	16.93**	30.88**	31.57**
L6 × T2	8.62	18.50**	32.63**	14.03**
L6 × T3	27.94**	26.33**	41.40**	31.70**
L6 × T4	15.56**	14.11**	27.72**	20.93**
L7 × T1	-13.15**	-10.97*	-0.35	-1.90
L7 × T2	7.76	17.55**	31.58**	11.11**
L7 × T3	7.65	10.34*	23.51**	12.82**
L7 × T4	-3.36	-0.94	10.88*	2.93
SE	0.16			0.14
CD at $P \leq 0.05$	0.31			0.27
CD at $P \leq 0.01$	0.41			0.35

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20g. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for fruit weight (g)

Hybrids	Fruit weight (g)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	36.84**	53.09**	47.17**	42.79**
L1 × T2	51.65**	103.14**	95.28**	65.27**
L1 × T3	4.63	32.97**	27.83**	11.29**
L1 × T4	39.47**	56.04**	50.00**	44.22**
L2 × T1	7.30	22.67**	17.92**	13.12**
L2 × T2	-4.03	28.56**	23.58**	3.56
L2 × T3	-14.29**	8.93	4.72	-9.76**
L2 × T4	3.00	17.76**	13.21**	7.62*
L3 × T1	6.67*	41.32**	35.85**	20.25**
L3 × T2	14.29**	53.09**	47.17**	14.92**
L3 × T3	8.89**	44.26**	38.68**	11.15**
L3 × T4	-2.96	28.56**	23.58**	8.49**
L4 × T1	-1.82	32.48**	27.36**	11.57**
L4 × T2	6.55*	43.77**	38.21**	6.93*
L4 × T3	-13.45**	16.78**	12.26**	-10.86**
L4 × T4	-8.36*	23.65**	18.87**	3.28
L5 × T1	-31.54**	50.15**	44.34**	-6.71**
L5 × T2	-22.42**	70.17**	63.58**	-3.67
L5 × T3	-31.54**	50.15**	44.34**	-13.31**
L5 × T4	-29.71**	54.17**	48.21**	-4.79*
L6 × T1	-1.23	18.25**	13.68**	6.40
L6 × T2	-7.69*	23.65**	18.87**	-2.51
L6 × T3	23.17**	56.53**	50.47**	26.84**
L6 × T4	7.38*	28.56**	23.58**	14.66**
L7 × T1	13.92**	76.64**	69.81**	37.14**
L7 × T2	-0.63	54.07**	48.11**	6.62*
L7 × T3	-27.85**	11.87**	7.55	-20.70**
L7 × T4	-23.67**	18.35**	13.77**	-8.81**
SE	0.14			0.12
CD at $P \leq 0.05$	0.28			0.25
CD at $P \leq 0.01$	0.37			0.32

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

and 26 crosses showed positive significant heterosis over check CH-27 and Arka Harita, respectively. The range of significant heterosis over the check hybrids ranged from 11.87% (L7 × T3) to 103.14% (L1 × T2) and 12.26% (L4 × T3) to 95.28% (L1 × T2) over check F_1 CH-27 and Arka Harita, respectively. The hybrids L1 × T2, L7 × T1, L5 × T2, L6 × T3 and L1 × T4 exhibited significant high positive heterosis over both check hybrids (Table 20g).

4.3.3.8 Fruits Plant^{-1}

The observed range of significant heterobeltiosis among hybrids was -48.49% (L1 × T2) to 64.77% (L7 × T3). Significant positive heterosis was observed in 12 hybrids over better parent. Hybrid L7 × T3 exhibited highest positive significant heterosis (64.77%) over its better parent. Three hybrids L6 × T1, L3 × T2 and L7 × T1 showed non-significant difference of 37.86%, 37.33% and 33.22% heterosis, respectively over their respective better parent. The range of heterosis over mid-parent varied from -31.87% (L4 × T3) to 79.52% (L7 × T3). The hybrids L7 × T3 (79.52%), L3 × T2 (75.30%), L6 × T1 (66.81%), L7 × T1 (40.04%) and L5 × T3 (36.24%) recorded significantly high positive heterosis over mid-parent. The range of significant heterosis over the check hybrids ranged from -35.13% (L5 × T1) to 79.75% (L6 × T1) and -31.21% (L5 × T1) to 90.60% (L6 × T1) over CH-27 and Arka Harita, respectively (Table 20h). Hybrids L6 × T1, L3 × T2, L7 × T3 and L1 × T1 recorded significantly high positive heterosis over both check hybrids CH-27 and Arka Harita.

4.3.3.9 Yield Plant^{-1}(g)

The range of significant heterobeltiosis varied from -52.73% in the cross L4 × T3 to 55.87% in the cross L3 × T2. Out of 28 evaluated hybrids, 13 hybrids showed positive significant heterosis over their respective better parents. Extent of positive significant heterosis over better parent ranged from 6.34% in the cross L1 × T4 to 55.87% in the cross L3 × T2. Five cross combinations namely, L3 × T2 (55.87%), L7 × T1 (50.46%), L1 × T1 (41.78%), L6 × T1 (37.03%) and L3 × T1

Table 20h. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for fruits plant^{-1}

Hybrids	Fruits plant^{-1}			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	4.09*	52.85**	62.08**	31.79**
L1 × T2	-48.49**	-24.37**	-19.80**	-28.87**
L1 × T3	-17.03**	21.84**	29.19**	7.99**
L1 × T4	-23.71**	12.03**	18.79**	1.29
L2 × T1	11.98**	44.94**	53.69**	35.10**
L2 × T2	-31.30**	-11.08**	-5.70*	-8.91**
L2 × T3	-17.36**	6.96**	13.42**	2.74
L2 × T4	-11.25**	14.87**	21.81**	12.73**
L3 × T1	16.08**	34.81**	42.95**	33.96**
L3 × T2	37.33**	59.49**	69.13**	75.30**
L3 × T3	9.81**	27.53**	35.23**	30.84**
L3 × T4	-0.82	15.19**	22.15**	20.93**
L4 × T1	2.84	26.27**	33.89**	21.46**
L4 × T2	-27.58**	-11.08**	-5.70*	-5.70*
L4 × T3	-44.07**	-31.33**	-27.18**	-31.87**
L4 × T4	-44.85**	-32.28**	-28.19**	-31.30**
L5 × T1	-23.79**	-35.13**	-31.21**	-10.09**
L5 × T2	23.08**	-18.99**	-14.09**	29.62**
L5 × T3	19.28**	-6.01*	-0.34	36.24**
L5 × T4	14.04**	-15.19**	-10.07**	27.01**
L6 × T1	37.86**	79.75**	90.60**	66.81**
L6 × T2	-19.66**	4.75	11.07**	6.77**
L6 × T3	-14.56**	11.39**	18.12**	6.51**
L6 × T4	-10.68**	16.46**	23.49**	13.76**
L7 × T1	33.22**	25.63**	33.22**	40.04**
L7 × T2	13.42**	6.96**	13.42**	33.60**
L7 × T3	64.77**	55.38**	64.77**	79.52**
L7 × T4	5.03	-0.95	5.03	17.45**
SE	2.53			2.19
CD at $P \leq 0.05$	4.95			4.29
CD at $P \leq 0.01$	6.50			5.62

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20i. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for yield plant^{-1} (g)

Hybrids	Yield plant^{-1} (g)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	41.78**	140.24**	141.20**	86.78**
L1 × T2	-8.44**	55.13**	55.75**	19.63**
L1 × T3	-3.09	64.21**	64.87**	20.94**
L1 × T4	6.34*	80.18**	80.90**	46.75**
L2 × T1	21.73**	81.57**	82.30**	53.25**
L2 × T2	-21.36**	17.29**	17.76**	-1.88
L2 × T3	-21.66**	16.85**	17.32**	-6.99*
L2 × T4	-5.50	40.95**	41.52**	25.14**
L3 × T1	23.00**	95.76**	96.54**	58.53**
L3 × T2	55.87**	148.07**	149.06**	99.20**
L3 × T3	19.28**	89.85**	90.61**	45.33**
L3 × T4	-6.06*	49.52**	50.12**	27.10**
L4 × T1	0.89	72.10**	72.79**	33.21**
L4 × T2	-23.26**	30.90**	31.43**	0.50
L4 × T3	-52.73**	-19.37**	-19.05**	-40.87**
L4 × T4	-50.83**	-16.13**	-15.79**	-32.01**
L5 × T1	-27.24**	-4.59	-4.21	-12.84**
L5 × T2	8.50*	42.26**	42.83**	28.73**
L5 × T3	11.95**	46.79**	47.38**	25.88**
L5 × T4	-1.01	29.80**	30.32**	25.26**
L6 × T1	37.03**	117.89**	118.76**	76.56**
L6 × T2	-16.50**	32.77**	33.30**	6.67*
L6 × T3	11.75**	77.70**	78.41**	36.10**
L6 × T4	-5.90	49.63**	50.23**	27.28**
L7 × T1	50.46**	126.24**	127.15**	89.99**
L7 × T2	12.48**	69.13**	69.81**	40.78**
L7 × T3	19.49**	79.67**	80.39**	42.32**
L7 × T4	-21.55**	17.96**	18.43**	4.16
SE	16.39			14.20
CD at $P \leq 0.05$	32.12			27.83
CD at $P \leq 0.01$	42.12			36.49

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

(23.00%) exhibited high positive significant heterosis over the better parent. Significant mid-parent heterosis ranged from -40.87% (L4 × T3) to 99.20% (L3 × T2). Twenty-one hybrids showed positive significant heterosis over their respective mid parents. The range of significant standard heterosis ranged from -19.37% (L4 × T3) to 148.07% (L3 × T2) and from -19.05% (L4 × T3) to 149.06% (L3 × T2) over check hybrids CH-27 and Arka Harita, respectively. Twenty five crosses showed positive significant standard heterosis over both hybrids. Hybrids namely L3 × T2, L1 × T1, L7 × T1, L6 × T1 and L3 × T1 exhibited high positive significant standard heterosis over both check hybrids (Table 20i).

4.3.3.10 Yield Plot^{-1} (kg/6.48 m^2)

The range of heterobeltiosis varied from -53.39% in the cross L4 × T3 to 56.04% in the cross L3 × T2. Out of 28 hybrids evaluated, thirteen hybrids showed positive significant heterosis over the better parent. Extent of significant positive heterosis over better parent ranged from 6.19% in the cross L1 × T4 to 56.04% in the cross L3 × T2. Four cross combinations namely, L3 × T2 (56.04%), L7 × T1 (51.17%), L1 × T1 (42.31%) and L6 × T1 (37.52%) exhibited significant positive heterosis over the better parent. Out of 28 hybrids, 21 and four showed significantly positive and negative heterosis over mid parent, respectively. The crosses which showed high significant positive heterosis over mid parent were L3 × T2 (100.17%), L7 × T1 (91.59%) and L1 × T1 (88.21%). The range of heterosis varied from -19.78% (L4 × T3) to 150.32% (L3 × T2) and -19.46% (L4 × T3) to 151.34% (L3 × T2) over commercial hybrids CH-27 and Arka Harita, respectively. Top five hybrids *viz.* L3 × T2, L1 × T1, L7 × T1, L6 × T1 and L3 × T1 exhibited highly significant positive heterosis over both the check hybrids (Table 20j).

4.3.3.11 Vitamin C (mg 100 g^{-1})

The observed range of significant heterobeltiosis among hybrids was -24.11% (L6 × T4) to 23.15% (L4 × T2). The hybrids L4 × T2 (23.15%), L5 × T3 (21.55%) and L4 × T1 (20.47%) exhibited high magnitude of heterosis over better

Table 20j. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for yield plot^{-1} (kg/6.48m^2)

Hybrids	Yield plot^{-1} (kg/6.48m^2)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	42.31**	143.23**	144.22**	88.21**
L1 × T2	-8.55**	56.31**	56.95**	19.95**
L1 × T3	-3.13	65.57**	66.25**	21.70**
L1 × T4	6.19**	81.51**	82.25**	47.25**
L2 × T1	22.04**	83.31**	84.06**	54.20**
L2 × T2	-21.67**	17.66**	18.14**	-1.91
L2 × T3	-21.96**	17.21**	17.69**	-6.75**
L2 × T4	-5.92**	41.31**	41.89**	25.16**
L3 × T1	22.84**	97.06**	97.86**	58.94**
L3 × T2	56.04**	150.32**	151.34**	100.17**
L3 × T3	19.54**	91.76**	92.55**	46.60**
L3 × T4	-6.14**	50.57**	51.19**	27.59**
L4 × T1	0.89	73.62**	74.33**	33.74**
L4 × T2	-23.55**	31.56**	32.10**	0.51
L4 × T3	-53.39**	-19.78**	-19.46**	-41.29**
L4 × T4	-51.46**	-16.47**	-16.13**	-32.56**
L5 × T1	-27.68**	-4.69	-4.30	-13.09**
L5 × T2	8.64**	43.16**	43.75**	29.28**
L5 × T3	11.49**	46.92**	47.52**	26.13**
L5 × T4	-1.02	30.44**	30.97**	25.78**
L6 × T1	37.52**	120.40**	121.31**	77.88**
L6 × T2	-16.72**	33.46**	34.01**	6.79**
L6 × T3	11.91**	79.35**	80.09**	37.20**
L6 × T4	-5.97**	50.69**	51.31**	27.77**
L7 × T1	51.17**	128.93**	129.87**	91.59**
L7 × T2	12.65**	70.60**	71.30**	41.50**
L7 × T3	19.76**	81.36**	82.10**	43.58**
L7 × T4	-21.85**	18.34**	18.83**	4.24
SE	0.30			0.26
CD at $P \leq 0.05$	0.58			0.50
CD at $P \leq 0.01$	0.77			0.66

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20k. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for Vitamin C (mg 100 g^{-1})

Hybrids	Vitamin C (mg100 g^{-1})			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	12.62**	17.41**	9.43**	33.33**
L1 × T2	-3.88**	0.20	-6.60**	11.24**
L1 × T3	-10.36**	-6.54**	-12.89**	-2.98*
L1 × T4	-13.59**	-9.92**	-16.04**	-9.49**
L2 × T1	9.18**	16.40**	8.49**	30.43**
L2 × T2	2.22	8.98**	1.57	19.41**
L2 × T3	-16.77**	-11.27**	-17.30**	-9.00**
L2 × T4	-21.84**	-16.67**	-22.33**	-17.25**
L3 × T1	15.99**	34.62**	25.47**	43.27**
L3 × T2	16.86**	35.63**	26.42**	41.30**
L3 × T3	5.23**	22.13**	13.84**	19.47**
L3 × T4	-10.76**	3.58*	-3.46*	-1.76
L4 × T1	20.47**	21.12**	12.89**	40.51**
L4 × T2	23.15**	23.82**	15.41**	40.34**
L4 × T3	17.45**	18.08**	10.06**	25.00**
L4 × T4	-6.38**	-5.87**	-12.26**	-3.63**
L5 × T1	6.71**	1.89	-5.03**	21.77**
L5 × T2	4.59**	-0.13	-6.92**	16.54**
L5 × T3	21.55**	16.06**	8.18**	26.24**
L5 × T4	9.54**	4.59**	-2.52	9.93**
L6 × T1	-11.92**	-14.64**	-20.44**	1.15
L6 × T2	-18.88**	-21.39**	-26.73**	-9.03**
L6 × T3	-6.70**	-9.58**	-15.72**	-2.41*
L6 × T4	-24.11**	-26.45**	-31.45**	-23.27**
L7 × T1	15.77**	31.24**	22.33**	41.71**
L7 × T2	-2.68*	10.32**	2.83*	16.58**
L7 × T3	6.55**	20.78**	12.58**	19.73**
L7 × T4	-8.33**	3.91**	-3.14*	-0.16
SE	1.26			1.09
CD at $P \leq 0.05$	2.46			2.13
CD at $P \leq 0.01$	3.23			2.80

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

parent. Over mid parent, 17 hybrids showed positive significant heterosis. The hybrids L3 × T1 (43.27%), L7 × T1 (41.71%), L3 × T2 (41.30%), L4 × T1 (40.51%) and L4 × T2 (40.34%) exhibited significant high magnitude of heterosis over mid-parent (Table 20k). Sixteen and 12 hybrids showed significant positive standard heterosis over CH-27 and Arka Harita. The hybrids L3 × T2, L3 × T1, L7 × T1, L4 × T2 and L3 × T3 showed high significant positive heterosis over both check hybrids.

4.3.3.12 Carotenoids (mg 100 g^{-1})

The heterobeltiosis ranged from -12.30% in the cross L3 × T4 to 40.98% in the cross L6 × T3. Out of 28 crosses evaluated, 21 and seven crosses showed positive significant and negative heterosis over the better parent, respectively. Extent of positive significant heterosis over better parent ranged from 2.99% in the cross L6 × T4 to 40.98% in the cross L6 × T3. Five cross combinations namely, L6 × T3 (40.98%), L4 × T1 (38.28%), L4 × T2 (32.45%), L1 × T1 (28.30%) and L4 × T3 (26.24%) exhibited significant high positive heterosis over the better parent. Twenty-four crosses showed significant positive heterosis over mid-parent. The hybrid L4 × T2 exhibited highest significant positive mid parent heterosis of 76.82% followed by L4 × T1 (74.00%), L1 × T1 (48.92%), L3 × T2 (44.80%) and L2 × T2 (44.42%). The range of significant heterosis over the check hybrid CH-27 and Arka Harita varied from -17.46% (L5 × T3) to 53.66% (L4 × T1) and -10.12 (L5 × T3) to 67.33% (L4 × T1), respectively. Seventeen and 22 crosses displayed significant positive heterosis over CH-27 and Arka Harita, respectively. Hybrids L4 × T1, L4 × T2, L4 × T3 and L2 × T4 showed positively high significant heterosis over both checks (Table 20l).

4.3.3.13 Coefficient of Infection (CI)

The range of significant negative heterobeltiosis varied from -24.89% in the cross L5 × T4 to -61.36% in the cross L7 × T4. Out of 28 evaluated crosses, nine showed significant negative heterosis over better parents. Top hybrids L7 × T4

Table 20l. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for carotenoids (mg 100 g^{-1})

Hybrids	Carotenoids (mg 100 g^{-1})			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	28.30**	16.20**	26.53**	48.92**
L1 × T2	6.53**	-3.52**	5.06**	32.24**
L1 × T3	20.84**	9.44**	19.17**	24.22**
L1 × T4	22.46**	15.21**	25.46**	24.79**
L2 × T1	3.55**	19.01**	29.60**	31.93**
L2 × T2	6.99**	22.96**	33.90**	44.42**
L2 × T3	12.38**	29.15**	40.64**	28.79**
L2 × T4	20.34**	38.31**	50.61**	32.35**
L3 × T1	18.89**	14.37**	24.54**	41.46**
L3 × T2	14.06**	9.72**	19.48**	44.80**
L3 × T3	-7.03**	-10.56**	-2.61	-1.63
L3 × T4	-12.30**	-15.63**	-8.13**	-11.32**
L4 × T1	38.28**	53.66**	67.33**	74.00**
L4 × T2	32.45**	47.18**	60.28**	76.82**
L4 × T3	26.24**	40.28**	52.76**	42.59**
L4 × T4	23.19**	36.90**	49.08**	33.42**
L5 × T1	-7.54**	-13.66**	-5.98**	8.69**
L5 × T2	-2.87*	-9.30**	-1.23	21.97**
L5 × T3	-11.61**	-17.46**	-10.12**	-7.79**
L5 × T4	-5.39**	-10.99**	-3.07*	-5.03**
L6 × T1	9.59**	-5.07**	3.37**	24.81**
L6 × T2	17.72**	1.97	11.04**	43.65**
L6 × T3	40.98**	22.11**	32.98**	41.78**
L6 × T4	2.99*	-3.10*	5.52**	7.25**
L7 × T1	14.63**	21.41**	32.21**	41.66**
L7 × T2	-3.86**	1.83	10.89**	26.29**
L7 × T3	12.23**	18.87**	29.45**	24.12**
L7 × T4	18.48**	25.49**	36.66**	25.49**
SE	2.66			2.30
CD at $P \leq 0.05$	5.21			4.50
CD at $P \leq 0.01$	6.83			5.91

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 20m. Per cent heterosis of F_1 hybrids over better parent (BP), mid-parent (MP) and standard checks for coefficient of infection (CI)

Hybrids	Coefficient of infection (CI) (%)			
	Per cent heterosis over			
	BP	Checks		MP
		CH-27 F_1	Arka Harita F_1	
L1 × T1	-30.25*	-46.59**	-80.23**	39.51
L1 × T2	-18.25	-37.41**	-76.83**	63.49*
L1 × T3	-18.78	-37.81**	-76.98**	62.43*
L1 × T4	-27.25	-44.29**	-79.38**	45.50
L2 × T1	11.80	27.28**	-52.88**	123.61**
L2 × T2	20.17*	36.80**	-49.35**	140.33**
L2 × T3	22.36*	39.30**	-48.43**	144.72**
L2 × T4	20.05*	36.66**	-49.40**	140.09**
L3 × T1	-0.48	24.78**	-53.80**	99.03**
L3 × T2	-53.42**	-41.59**	-78.38**	-6.84
L3 × T3	0.81	26.40**	-53.20**	101.62**
L3 × T4	5.82	32.68**	-50.88**	111.63**
L4 × T1	-17.86	-40.99**	-78.15**	64.29*
L4 × T2	-13.16	-37.61**	-76.90**	73.68**
L4 × T3	64.00**	17.83**	-56.38**	228.01**
L4 × T4	68.14**	20.80**	-55.28**	236.28**
L5 × T1	52.27**	140.38**	-11.00**	204.53**
L5 × T2	51.41**	139.03**	-11.50**	202.82**
L5 × T3	-27.12**	15.06**	-57.40**	45.77**
L5 × T4	-24.89**	18.57**	-56.10**	50.21**
L6 × T1	-56.52**	-41.05**	-78.18**	-13.05
L6 × T2	66.73**	126.06**	-16.30**	233.47**
L6 × T3	-53.69**	-37.20**	-76.75**	-7.37
L6 × T4	71.31**	132.28**	-14.00**	242.63**
L7 × T1	-59.35**	-42.88**	-78.85**	-18.69
L7 × T2	63.38**	129.57**	-15.00**	226.77**
L7 × T3	-60.88**	-45.04**	-79.65**	-21.77
L7 × T4	-61.36**	-45.71**	-79.90**	-22.73
SE	2.31			2.00
CD at $P \leq 0.05$	4.52			3.92
CD at $P \leq 0.01$	5.93			5.14

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

(-61.36%), L7 × T3 (-60.88%), L7 × T1 (-59.35%) and L6 × T1 (-56.52%) exhibited high negative significant heterosis over the better parent. None of the hybrids displayed significant negative mid-parent heterosis. The range of significant and negative standard heterosis ranged from -37.20% (L6 × T3) to -46.59% (L1 × T1) and from -11.00% (L5 × T1) to -80.23% (L1 × T1) over check hybrids CH-27 and Arka Harita, respectively. Twenty-eight and 12 crosses exhibited significant and negative standard heterosis over Arka Harita and CH-27, respectively. Hybrids namely L1 × T1, L7 × T4, L7 × T3 and L1 × T4 exhibited high negative significant standard heterosis over two both check hybrids (Table 20m).

4.3.4 Incidence of Pest and Disease

4.3.4.1 Incidence of Leaf Curl Disease

All the four testers were symptom-less and among seven lines, two were moderately resistant and remaining five were moderately susceptible. The lines which showed moderate resistant reaction were L1 and L4. Lines *viz.* L2, L3, L5, L6 and L7 showed moderate susceptible reaction (Table 21).

Among 28 F_1 hybrids, none was completely free from ChiLCV incidence. Twelve hybrids showed moderately resistant reaction and the CI of disease ranged from 13.90 in the cross L3 × T2 to 18.13 in the cross L1 × T3. The crosses which showed moderate resistant reaction to ChiLCV included L1 × T1, L1 × T2, L1 × T3, L1 × T4, L3 × T2, L4 × T1, L4 × T2, L6 × T1, L6 × T3, L7 × T1, L7 × T3, L7 × T4. Eleven hybrids were moderately susceptible, among them CI ranged from 28.14 in the cross L4 × T3 to 33.88 in the cross L3 × T4. The cross combinations which showed moderate susceptible reaction were L2 × T1, L2 × T2, L2 × T3, L2 × T4, L3 × T1, L3 × T3, L3 × T4, L4 × T3, L4 × T4, L5 × T3 and L5 × T4. The hybrids which showed susceptible reaction were L5 × T1, L5 × T2, L6 × T2, L6 × T4 and L7 × T2 (Table 21). The resistant check hybrid CH-27 was moderately

Table 21. Reaction of parents and F_1 hybrids to local isolate of ChiLCV under field conditions

Sl. No.	Genotypes	No of plants screened per replication	Mean number of plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]
			0	1	2	3	4	5	6				
1	L1	20	3.67	9.33	2.67	4.33	0.00	0.00	0.00	23.06	81.67	18.85	MR
2	L2	20	4.00	1.67	5.33	4.67	4.33	0.00	0.00	36.39	80.00	29.53	MS
3	L3	20	5.00	2.00	2.33	4.67	6.00	0.00	0.00	37.22	75.00	28.39	MS
4	L4	20	5.00	7.33	3.33	4.33	0.00	0.00	0.00	22.50	75.00	16.92	MR
5	L5	20	2.67	2.00	5.33	5.33	4.67	0.00	0.00	39.44	86.67	34.42	MS
6	L6	20	4.00	1.67	3.00	6.33	5.00	0.00	0.00	38.89	80.00	31.32	MS
7	L7	20	3.33	2.67	4.00	4.00	6.00	0.00	0.00	38.89	83.33	32.60	MS
8	T1	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
9	T2	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
10	T3	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
11	T4	20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
12	L1 × T1	20	6.67	5.00	4.33	4.00	0.00	0.00	0.00	21.39	66.67	14.32	MR
13	L1 × T2	20	5.67	5.67	2.67	6.00	0.00	0.00	0.00	24.17	71.67	17.31	MR
14	L1 × T3	20	5.33	4.67	5.00	5.00	0.00	0.00	0.00	24.72	73.33	18.13	MR
15	L1 × T4	20	7.00	2.00	4.33	6.67	0.00	0.00	0.00	25.56	65.00	16.67	MR
16	L2 × T1	20	3.67	2.00	5.67	5.00	3.67	0.00	0.00	35.83	81.67	29.43	MS
17	L2 × T2	20	3.00	1.67	6.00	5.00	4.33	0.00	0.00	38.33	85.00	32.72	MS
18	L2 × T3	20	3.33	3.33	3.67	4.00	5.67	0.00	0.00	37.78	83.33	31.79	MS
19	L2 × T4	20	3.67	1.67	3.67	5.33	5.67	0.00	0.00	39.72	81.67	32.61	MS
20	L3 × T1	20	3.33	3.00	3.33	5.67	4.67	0.00	0.00	37.78	83.33	31.75	MS
21	L3 × T2	20	7.00	5.00	3.33	4.67	0.00	0.00	0.00	21.39	65.00	13.90	MR
22	L3 × T3	20	3.67	1.67	5.67	4.67	4.33	0.00	0.00	36.94	81.67	30.29	MS

Table 21. continued

Sl. No.	Genotypes	No of plants screened per replication	Mean number of plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]
			0	1	2	3	4	5	6				
23	L3 × T4	20	3.00	1.00	6.33	4.67	5.00	0.00	0.00	39.72	85.00	33.88	MS
24	L4 × T1	20	6.67	4.67	5.00	3.67	0.00	0.00	0.00	21.39	66.67	14.39	MR
25	L4 × T2	20	7.00	2.33	4.33	6.33	0.00	0.00	0.00	25.00	65.00	16.33	MR
26	L4 × T3	20	4.00	3.33	3.67	5.00	4.00	0.00	0.00	34.72	80.00	28.14	MS
27	L4 × T4	20	4.00	4.33	1.67	5.00	5.00	0.00	0.00	35.56	80.00	28.78	MS
28	L5 × T1	20	0.00	0.67	3.00	5.67	4.67	6.00	0.00	60.28	100.00	60.28	S
29	L5 × T2	20	0.00	1.67	2.67	4.67	5.00	6.00	0.00	59.17	100.00	59.17	S
30	L5 × T3	20	4.67	0.67	3.67	6.33	4.67	0.00	0.00	38.06	76.67	29.58	MS
31	L5 × T4	20	4.33	2.67	2.67	5.33	5.00	0.00	0.00	36.67	78.33	29.25	MS
32	L6 × T1	20	6.67	3.00	5.67	4.67	0.00	0.00	0.00	23.61	66.67	15.93	MR
33	L6 × T2	20	1.00	1.33	3.33	4.67	4.33	5.33	0.00	55.00	95.00	52.61	S
34	L6 × T3	20	4.67	8.00	4.00	3.33	0.00	0.00	0.00	21.67	76.67	16.61	MR
35	L6 × T4	20	0.33	1.33	3.00	4.33	3.33	7.67	0.00	60.00	98.33	59.04	S
36	L7 × T1	20	5.00	8.33	3.33	3.33	0.00	0.00	0.00	20.83	75.00	15.79	MR
37	L7 × T2	20	0.00	2.67	3.00	5.33	3.33	5.67	0.00	55.28	100.00	55.28	S
38	L7 × T3	20	5.67	5.67	3.67	5.00	0.00	0.00	0.00	23.33	71.67	16.75	MR
39	L7 × T4	20	7.33	3.00	3.33	4.33	2.00	0.00	0.00	25.56	63.33	16.21	MR
40	Arka Harita	20	0.00	2.00	3.33	5.33	4.67	4.67	0.00	55.56	100.00	55.56	S
41	CH-27	20	4.00	8.00	4.33	3.67	0.00	0.00	0.00	23.06	80.00	18.49	MR
42	Kashi Anmol	20	0.00	0.00	0.00	0.00	1.00	2.67	16.33	55.56	100.00	55.56	HS
	Mean	20	3.53	3.02	3.42	4.29	2.53	0.90	0.39	33.11	72.82	28.07	

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible.

Table 22. Mean population of whitefly, thrips and mites in parents and F_1 hybrids under field conditions

Sl. No.	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
1	L-1	0.85	1.1	0.98	0.00	0.32	0.00	0.00	0.00	0.21
2	L-2	1.1	1.54	0.85	0.00	0.00	0.45	0.00	0.00	0.00
3	L-3	0.75	1.1	0.98	0.00	0.00	0.32	0.00	0.00	0.00
4	L-4	0.98	1.2	1.1	0.00	0.19	0.00	0.00	0.00	0.00
5	L-5	1.54	2.21	1.81	0.52	0.64	0.42	0.00	0.23	0.46
6	L-6	1.1	1.85	1.23	0.00	0.52	0.64	0.00	0.32	0.23
7	L-7	1.11	1.87	1.67	0.00	0.32	0.21	0.00	0.54	0.41
8	T-1	0.78	1.14	0.96	0.00	0.00	0.00	0.00	0.00	0.00
9	T-2	0.99	1.12	1.1	0.00	0.23	0.00	0.00	0.23	0.13
10	T-3	0.99	1.1	0.75	0.12	0.15	0.00	0.00	0.00	0.00
11	T-4	1.13	1.24	0.984	0.00	0.23	0.00	0.00	0.00	0.00
12	1 × 1	1.1	1.21	0.98	0.25	0.00	0.00	0.00	0.23	0.00
13	1 × 2	0.97	1.12	1.24	0.25	0.12	0.00	0.00	0.00	0.00
14	1 × 3	1.1	1.42	1.23	0.00	0.27	0.00	0.00	0.23	0.23
15	1 × 4	0.89	1.51	0.94	0.23	0.25	0.13	0.00	0.23	0.12
16	2 × 1	1.23	1.48	1.2	0.35	0.30	0.31	0.00	0.23	0.00
17	2 × 2	1.98	2.24	2.23	0.56	0.68	0.71	0.00	0.14	0.29
18	2 × 3	1.45	1.98	2.1	0.00	0.13	0.00	0.00	0.00	0.00
19	2 × 4	0.99	1.56	1.43	0.00	0.21	0.12	0.00	0.00	0.00
20	3 × 1	0.85	0.99	1.13	0.00	0.00	0.00	0.00	0.00	0.00
21	3 × 2	0.78	1.13	0.84	0.00	0.00	0.00	0.00	0.00	0.00
22	3 × 3	0.83	0.98	1.18	0.21	0.11	0.32	0.00	0.23	0.00
23	3 × 4	0.78	1.24	1.13	0.12	0.24	0.33	0.00	0.19	0.00
24	4 × 1	0.89	1.25	1.54	0.00	0.12	0.46	0.00	0.00	0.00
25	4 × 2	0.92	1.35	1.13	0.23	0.19	0.19	0.00	0.00	0.00
26	4 × 3	2.84	3.24	2.98	0.21	0.31	0.34	0.00	0.23	0.34
27	4 × 4	2.56	2.98	2.43	0.56	0.63	0.72	0.00	0.34	0.21
28	5 × 1	2.46	2.87	2.93	0.49	0.38	0.29	0.00	0.23	0.28

Table 22. continued

Sl. No.	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
29	5 × 2	2.46	2.23	2.19	0.00	0.49	0.85	0.00	0.19	0.14
30	5 × 3	1.49	2.4	1.13	0.14	0.21	0.32	0.00	0.00	0.00
31	5 × 4	2.56	2.79	2.69	0.16	0.24	0.38	0.00	0.21	0.15
32	6 × 1	1.21	1.59	1.46	0.00	0.00	0.21	0.00	0.00	0.00
33	6 × 2	1.98	2.37	2.21	0.00	0.21	0.49	0.00	0.21	0.14
34	6 × 3	0.98	1.45	1.28	0.00	0.00	0.00	0.00	0.17	0.00
35	6 × 4	1.89	2.89	2.34	0.56	0.71	0.63	0.00	0.23	0.24
36	7 × 1	0.89	1.12	0.76	0.00	0.00	0.00	0.00	0.00	0.00
37	7 × 2	0.74	0.89	1.23	0.00	0.21	0.00	0.00	0.00	0.00
38	7 × 3	0.95	1.45	1.68	0.00	0.42	0.21	0.00	0.00	0.00
39	7 × 4	2.79	2.68	2.94	0.52	0.43	0.47	0.00	0.31	0.32
Checks										
40	CH-27	1.29	1.47	1.13	0.35	0.39	0.49	0.00	0.24	0.34
41	Arka Harita	1.89	1.79	2.12	0.46	0.48	0.59	0.00	0.23	0.43
C.D. 5%		0.069	0.073	0.054	0.013	0.015	0.016	0.00	0.007	0.005
SE (m)		0.025	0.026	0.019	0.005	0.005	0.008	0.00	0.002	0.002

DAT- Days after transplanting

Table 23. Mean per cent incidence of bacterial wilt and fruit rot in parents and F_1 hybrids under field conditions

Sl. No.	Genotypes	Mean per cent incidence	
		Bacterial wilt	Fruit rot
1	L-1	1.19	2.00
2	L-2	1.19	6.00
3	L-3	1.19	1.00
4	L-4	0.00	2.00
5	L-5	1.19	2.00
6	L-6	1.19	3.00
7	L-7	0.00	2.00
8	T-1	1.19	4.00
9	T-2	0.00	2.00
10	T-3	2.38	2.00
11	T-4	0.00	6.00
Hybrids			
12	L1 × T1	0.00	3.00
13	L1 × T2	2.38	2.00
14	L1 × T3	2.38	4.00
15	L1 × T4	2.38	2.30
16	L2 × T1	0.00	3.00
17	L2 × T2	0.00	3.00
18	L2 × T3	0.00	5.00
19	L2 × T4	0.00	1.00
20	L3 × T1	1.19	3.00
21	L3 × T2	0.00	4.30
22	L3 × T3	1.19	2.00
23	L3 × T4	2.38	4.00
24	L4 × T1	0.00	2.00
25	L4 × T2	1.19	2.20
26	L4 × T3	1.19	3.00
27	L4 × T4	2.38	2.40
28	L5 × T1	2.38	4.20
29	L5 × T2	2.38	1.00
30	L5 × T3	0.00	0.00
31	L5 × T4	1.19	4.00
32	L6 × T1	1.19	3.00
33	L6 × T2	2.38	2.00
34	L6 × T3	1.19	3.00
35	L6 × T4	2.38	5.00
36	L7 × T1	1.19	3.00
37	L7 × T2	0.00	2.00
38	L7 × T3	0.00	2.00
39	L7 × T4	1.19	3.00
F_1 hybrid checks			
40	CH-27	1.19	5.00
41	Arka Harita	1.19	3.00
C.D. 5%		0.069	0.115
SE (m)		0.024	0.041
SE (d)		0.034	0.058

resistant with 18.49 CI and the variety Kashi Anmol was highly susceptible. The hybrid Arka Harita showed susceptible reaction.

4.3.4.2 Incidence of Whiteflies, Thrips and Mites

Incidence of whiteflies, thrips and mites were found to be negligible. The mean number of whitefly, thrips and mites population per leaf at 30, 60 and 90 days after transplanting is given in the Table 22.

4.3.4.3 Incidence of Bacterial Wilt and Fruit rot

Two lines (L4 and L7), two testers (T2 and T4) and ten hybrids were free from bacterial wilt incidence. The fruit rot incidence in parents ranged from 1.00% (L3) to 6.00% (L2 and T4). Among hybrids it ranged from 1.00% (L2 × L4 and L5 × L2) to 5.00% (L2 × L3 and L6 × L4) (Table 23).

4.4 GENERATION MEAN ANALYSIS

Three superior crosses identified from line (L) × tester (T) analysis *viz.*, L1 × T1 (cross 1), L3 × T2 (cross 2) and L7 × T1 (cross 3) were utilized for generation mean analysis. The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three crosses were developed [experiment VI (a)] and evaluated [experiment VI (b)] to identify magnitude and nature of gene action for primary branches plant^{-1}, plant height, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection.

4.4.1 Estimation of Scaling Test, Gene Effects

Different workers have estimated the nature of gene actions governing quantitative and qualitative traits, by using various mating designs. To detect the epistasis, simple scaling test (Mather, 1949) and joint scaling test (Cavalli, 1952) were used. In the absence of epistasis, genetic components of variance were estimated as suggested by Mather (1949). The significance of any one of the scales and significant joint scaling value (χ^2) suggested the involvement of epistasis.

Further, gene effects of three (m, d and h) and six parameter model (m, d, h, i, j, and l) suggested by Jinks and Jones (1958) and Hayman (1958) was used to partition gene effects into epistatic components.

4.4.1.1 Plant Height (cm)

The estimates of scaling test and their standard errors are presented in Table 24a. The estimates of simple scaling tests for plant height revealed that all four scales A, B, C and D were significant in cross 1 and 2, whereas scales A, B and C were significant in cross 3 suggesting inadequacy of additive dominance model and existence of inter allelic interactions. In addition, all three cross combinations had significant joint scaling test value (χ^2) in three parameter model again indicating the inadequacy of additive dominance model and need for fitting six parameter model to estimate the probable epistatic components present.

Fitting of six parameter model revealed that additive [d] gene effect was significant and negative in all three cross combinations. Dominance [h] gene effect and additive × additive [i] gene interaction were found positive and significant in cross 1 and 3, but negative in cross 2. The magnitude of dominant gene effect was relatively more than additive gene effect in the cross 1 and 3.

Additive × dominance [j] gene interaction was positive and significant in cross 1, while this interaction was negatively significant in cross 2 and 3. Positive significant non-allelic gene interaction dominance × dominance [l] was observed in cross 2 and 3, whereas in cross 1, this interaction was negatively significant.

4.4.1.2 Primary Branches Plant^{1}

Scales B, C and D were significant in cross 1 and 3, whereas in cross 2, A, B and D were significant, indicating the inadequacy of additive-dominance model and presence of inter allelic interactions. Significant χ^2 values in joint scaling test were also suggested the presence of epistasis.

Six parameter model indicated negative and significant additive [d] gene effect in cross 1. However, additive [d] gene effect was negative and non-

Table 24a. Estimation of scaling tests and gene effects with respect to different crosses for plant height (cm) and primary branches plant^{-1}

1. Plant height (cm)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	13.61**±0.88	6.62**±0.80	-16.46**±0.97
B	8.15**±1.32	9.93**±1.08	-11.48**±0.97
C	7.97**±1.79	38.59**±1.54	-31.06**±1.56
D	-6.89**±0.85	11.01**±0.49	-1.55±0.86
Joint scaling test (three-parameter model)			
m ± SE	35.81**±1.73	64.35**±1.04	48.68**±1.73
[d] ± SE	-6.40**±0.32	-0.93**±0.33	-2.33**±0.21
[h] ± SE	57.28**±4.49	-24.27**±2.88	-8.11±4.40
χ^2 (3 df)	26.33**	95.76**	55.94**
Six-parameter model			
m ± SE	55.56** ± 0.30	53.57**±0.15	50.83**±0.31
[d] ± SE	-3.66** ± 0.60	-2.59**±0.38	-4.82**±0.58
[h] ± SE	21.72** ± 1.83	-18.81**±1.21	16.71**±1.78
[i] ± SE	13.78** ± 1.70	-22.02**±0.99	3.11**±1.72
[j] ± SE	2.73** ± 0.68	-1.65**±0.51	-2.49**±0.62
[l] ± SE	-35.55** ± 3.01	5.45*±2.18	24.83**±2.82
Type of epistasis	D	D	C

2. Primary branches plant^{-1}

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	0.04±0.07	-1.61**±0.07	0.18±0.10
B	-1.42**±0.07	-0.61**±0.07	-0.57**±0.10
C	-0.63**±0.14	0.08±0.15	-1.42**±0.20
D	0.37**±0.05	1.15**±0.07	-0.52**±0.09
Joint scaling test (three-parameter model)			
m ± SE	4.04** ± 0.11	5.25**±0.14	2.70**±0.19
[d] ± SE	-0.89** ± 0.02	0.48**±0.02	-0.46**±0.03
[h] ± SE	-2.11** ± 0.27	-4.78**±0.33	2.27**±0.45
χ^2 (3 df)	45.98**	61.46**	84.64**
Six-parameter model			
m ± SE	3.51** ± 0.02	3.99**±0.03	3.67**±0.03
[d] ± SE	-0.16** ± 0.03	-0.01±0.03	-0.08±0.05
[h] ± SE	0.00 ± 0.12	-0.24±0.15	1.61**±0.19
[i] ± SE	-0.74** ± 0.11	-2.31**±0.14	1.04**±0.18
[j] ± SE	0.73** ± 0.04	-0.50**±0.04	0.38**±0.06
[l] ± SE	2.12** ± 0.18	4.54**±0.21	-0.66**±0.29
Type of epistasis	-	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

significant in cross 2 and 3. Significant and positive dominance [h] gene effect was observed in cross 3 while, cross 1 and 2 exhibited positive non-significant and negative non-significant dominance [h] gene effect, respectively.

In cross 3, 'i' gene interaction was positively significant, while in cross 1 and 2, it was negative and significant. Additive × dominant [j] gene interaction was significant and positive in the cross 1 and 3, it was significant and negative in cross 2. Dominance × dominance [l] gene interaction was significant and positive in cross 1 and cross 2, and it was negatively significant in the cross 3 (Table 24a).

4.4.1.3 Days to First Flower

All four scales were significant in cross 1, while scales A, C and D were significant in cross 2. In cross 3, scales A, B and D were significant. This suggested the involvement of all three types of epistasis. In addition, all three cross combinations had significant joint scaling test value (χ^2) in three parameter model, which indicated the inadequacy of additive dominance model and need for fitting six parameter model to estimate the probable epistatic components present.

In six parameter model, additive gene effect was significant and negative in cross 1 and cross 2. In cross 3, it was positive and non-significant. Cross 1 and 3 exhibited significant negative dominance [h] gene effect, while cross 2 exhibited non-significant positive dominance [h] gene effect (Table 24b).

In cross 1 and 3, 'i' interaction was significant and negative, while cross 2 exhibited positive and significant 'i' gene interaction. 'j' and 'l' interactions were found positive and significant in cross 1 and 3, while these interactions were negative and significant in cross 2.

4.4.1.4 Days to First Harvest

In all the three crosses, the model of simple additive dominance was inadequate. The involvement of epistasis was further confirmed by joint scaling test. In six parameter model, 'd' gene effects are significant and negative in the

Table 24b. Estimation of scaling tests and gene effects with respect to different crosses for days to first flower and days to first harvest

3. Days to first flower

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-5.64**±0.45	-5.84**±0.33	-3.00**±0.81
B	-7.46**±0.47	-0.36±0.47	-7.91**±1.04
C	-5.06**±1.03	-13.83**±0.62	-0.00±1.75
D	4.02**±0.42	-3.81**±0.24	5.45**±0.86
Joint scaling test (three-parameter model)			
m ± SE	40.65**±0.86	28**±0.51	44.41**±1.76
[d] ± SE	-2.67**±0.16	0.88**±0.14	-1.63**±0.30
[h] ± SE	-31.21**±1.97	2.27**±1.40	-35.11**±4.26
χ^2 (3 df)	32.75**	70.62**	73.98**
Six-parameter model			
m ± SE	30.33**±0.19	28.99**±0.07	32.31**±0.35
[d] ± SE	-1.76**±0.18	-1.85**±0.19	0.82±0.50
[h] ± SE	-10.05**±0.91	0.85±0.56	-13.28**±1.81
[i] ± SE	-8.04**±0.84	7.62**±0.49	-10.91**±1.73
[j] ± SE	0.90**±0.24	-2.73**±0.24	2.45**±0.59
[l] ± SE	21.15**±1.27	-1.42**±0.99	21.83**±2.67
Type of epistasis	D	-	D

4. Days to first harvest

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-8.57**±0.77	-4.85**±0.71	1.73**±0.97
B	-10.34**±0.56	-3.14**±0.38	-5.56**±1.17
C	-11.41**±1.17	-9.10**±0.78	2.06**±1.72
D	3.74**±0.39	-0.55**±0.34	2.95**±0.85
Joint scaling test (three-parameter model)			
m ± SE	61.48**±0.86	55.40**±0.70	59.90**±1.73
[d] ± SE	-2.88**±0.33	-0.72**±0.15	-2.60**±0.36
[h] ± SE	-33.95**±2.18	-12.33**±2.00	-18.56**±4.44
χ^2 (3 df)	39.80**	41.10**	39.17**
Six-parameter model			
m ± SE	-51.10**±0.16	50.96**±0.08	53.05**±0.31
[d] ± SE	-1.99**±0.23	-1.57**±0.29	1.05±0.58
[h] ± SE	-7.54**±0.93	-5.45**±0.77	-8.83**±1.80
[i] ± SE	-7.49**±0.79	1.11±0.69	-5.90**±1.70
[j] ± SE	0.88*±0.40	-0.85*±0.33	3.65**±0.68
[l] ± SE	26.41**±1.50	6.88**±1.43	9.73**±2.89
Type of epistasis	D	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

cross 1 and cross 2. Whereas, it was non-significant and positive in cross 3. The 'h' gene effect was negative and significant in all the three cross combinations.

Additive × additive [i] gene interaction was negatively significant in cross 1 and cross 3, but positive and non-significant in cross 2. Gene interaction 'j' were significant and positive in cross 3 and cross1, while negatively significant in cross 2. In all the three crosses, 'l' gene interaction was significant and positive (Table 24b).

4.4.1.5 Fruit Length (cm)

The simple scaling test and joint scaling test revealed the involvement of non-allelic interactions. In all the crosses, 'd' and 'h' gene effects were observed as positive and significant. Gene effect 'h' was more than 'd' in the crosses 1 and 3 whereas, 'd' gene effect was superior to 'h' gene effect in cross 2 (Table 24c).

Gene interaction 'i' was significant and positive in the crosses 1 and 3. Gene interactions 'j' and 'l' were recorded as positively significant in the cross 2 whereas, gene interaction 'l' was negatively significant in cross 1.

4.4.1.6 Fruit Girth (cm)

The significant values of A, B, C and D scales in the crosses 1 and 3; B and D in cross 2 showed the inadequacy of simple additive-dominance model. The significant values of χ^2 in joint scaling test further revealed the presence of digenic interactions.

Additive [d] gene effect was positive and significant in all three crosses in six-parameter model. The 'h' and 'i' gene interaction were positive and significant in crosses 1 and 3 and these effects were significant and negative in the cross 2. Gene interaction 'j' was positively significant in the crosses 1 and 2 while, 'l' gene interaction was positively significant in cross 2 and negatively significant in the crosses 1 and 3 (Table 24c).

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Table 24c. Estimation of scaling tests and gene effects with respect to different crosses for fruit length (cm) and fruit girth (cm)

5. Fruit length (cm)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	1.32**±0.06	-1.89**±0.10	-0.45**±0.09
B	1.32**±0.05	-2.56**±0.06	-0.29**±0.08
C	2.35**±0.14	-3.94**±0.16	-1.75**±0.12
D	-0.14**±0.06	0.25**±0.07	-0.50**±0.06
Joint scaling test (three-parameter model)			
m ± SE	4.11**±0.13	6.09**±0.16	3.91**±0.13
[d] ± SE	0.09**±0.02	0.19**±0.01	0.52**±0.03
[h] ± SE	5.20**±0.30	-4.72**±0.39	3.60**±0.36
χ^2 (3 df)	79.76**	15.21**	18.59**
Six-parameter model			
m ± SE	5.98**±0.03	4.98**±0.03	5.64**±0.02
[d] ± SE	0.09**±0.02	0.52**±0.05	0.45**±0.04
[h] ± SE	2.25**±0.14	0.24**±0.16	3.34**±0.14
[i] ± SE	0.29**±0.13	-0.51**±0.15	1.00**±0.13
[j] ± SE	0.00±0.03	0.33**±0.05	-0.07±0.05
[l] ± SE	-2.95**±0.18	4.97**±0.25	-0.26±0.23
Type of epistasis	D	C	-

6. Fruit girth (cm)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	0.88**±0.09	0.03±0.10	-0.11**±0.07
B	0.66**±0.06	-0.97**±0.09	0.33**±0.09
C	0.76**±0.19	0.07±0.16	-0.80**±0.14
D	-0.39**±0.09	0.50**±0.08	-0.51**±0.05
Joint scaling test (three-parameter model)			
m ± SE	2.03**±0.19	4.25**±0.17	1.98**±0.11
[d] ± SE	0.18**±0.01	-0.33**±0.01	0.40**±0.03
[h] ± SE	3.67**±0.43	-3.00**±0.43	2.23**±0.30
χ^2 (3 df)	14.32**	14.11**	92.22**
Six-parameter model			
m ± SE	3.29**±0.04	3.24**±0.03	2.78**±0.02
[d] ± SE	0.29**±0.04	0.17**±0.05	0.17**±0.03
[h] ± SE	1.34**±0.19	-1.04**±0.18	0.98**±0.12
[i] ± SE	0.78**±0.18	-1.01**±0.17	1.02**±0.11
[j] ± SE	0.10**±0.04	0.50**±0.06	-0.22**±0.05
[l] ± SE	-2.33**±0.26	1.95**±0.28	-1.25**±0.20
Type of epistasis	D	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

4.4.1.7 Fruit Weight (g)

All four scales exhibited significance in crosses 1 and 2, and scale A in cross 3. In three parameter model, significant χ^2 values was observed for all the three crosses.

Significant and positive 'd' gene effect was recorded in all three cross combinations. Gene component 'h' was negatively negatively significant in the cross 2 (Table 24d). In all three crosses, gene interaction 'i' was significant and negative. The 'j' gene interactions showed significant positive value in the cross 2 whereas, in the cross 3 negatively significant. The 'l' gene interaction were recorded positive and significant in all three crosses.

4.4.1.8 Fruits Plant^{1}

The significant estimates of all four scales in all three cross combinations suggested the involvement of all the types of non-allelic gene interactions. The gene effect 'd' was observed positive and significant in all three crosses. However, gene effect 'h' was observed positively significant in cross 1 and 2.

In the crosses 2 and 3, gene interaction 'i' was significant and negative. Gene interaction 'j' was found significant and negative in cross 1 and 2 whereas, significant and positive in cross 3. Gene interaction 'l' was significantly positive in crosses 1 and 3, and negatively significant in cross 2 (Table 24d).

4.4.1.9 Yield Plant^{1} (g)

The simple additive-dominance model was inadequate in all the cross. Further, joint scaling test followed in three-parameter model indicated the presence of digenic interactions due to significant values of χ^2. Positive and significant 'd' gene effects were observed in all crosses whereas, gene effects 'h' were significant and positive in cross 1 and 2.

Gene interactions 'i' and 'j' were recorded as negatively significant in all the three crosses. Gene interaction 'l' was found positive and significant in all three

Table 24d. Estimation of scaling tests and gene effects with respect to different crosses for fruit weight (g) and fruits plant^{-1}

7. Fruit weight (g)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	0.31**±0.07	-0.10**±0.03	-0.34**±0.12
B	0.19*±0.08	-0.58**±0.06	0.31±0.11
C	2.07**±0.12	0.66**±0.08	2.04±0.20
D	0.78**±0.07	0.67**±0.03	1.03±0.10
Joint scaling test (three-parameter model)			
m ± SE	5.20**±0.15	5.85**±0.07	6.36**±0.21
[d] ± SE	0.16**±0.01	-0.00±0.02	0.89**±0.03
[h] ± SE	-1.03**±0.39	-2.72**±0.18	-2.44**±0.54
χ^2 (3 df)	27.43**	45.10**	13.73**
Six-parameter model			
m ± SE	4.95**±0.02	5.00**±0.01	5.66**±0.04
[d] ± SE	0.21**±0.05	0.23**±0.02	0.56**±0.06
[h] ± SE	0.01±0.15	-0.67**±0.07	-0.35±0.22
[i] ± SE	-1.56**±0.15	-1.35**±0.06	-2.06**±0.21
[j] ± SE	0.05±0.05	0.24**±0.03	-0.32**±0.07
[l] ± SE	1.05**±0.24	2.04**±0.12	2.00**±0.34
Type of epistasis	-	D	D

8. Fruits plant^{-1}

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-24.76**±1.11	4.49**±0.93	-23.23**±1.00
B	8.68**±0.95	46.93**±1.30	-28.65**±1.18
C	-18.68**±1.76	82.84**±2.22	4.86**±2.21
D	-1.30**±1.00	15.70**±0.84	28.37**±0.97
Joint scaling test (three-parameter model)			
m ± SE	118.00**±2.02	126.86**±1.77	150.31**±1.98
[d] ± SE	32.72**±0.23	27.04**±0.55	4.96**±0.37
[h] ± SE	29.64**±5.02	63.28**±4.20	-126.55**±4.69
χ^2 (3 df)	71.52**	19.22**	13.11**
Six-parameter model			
m ± SE	136.20**±0.38	153.50**±0.37	114.20**±0.41
[d] ± SE	16.00**±0.64	5.82**±0.39	7.67**±0.51
[h] ± SE	43.12**±2.05	43.27**±1.88	-17.91**±2.07
[i] ± SE	2.60±2.01	-31.41**±1.69	-56.75**±1.94
[j] ± SE	-16.72**±0.68	-21.22**±0.67	2.70**±0.63
[l] ± SE	13.48**±3.10	-20.01**±2.72	108.63**±3.01
Type of epistasis	C	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

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crosses. The values of 'h' and 'l' were of the same sign, which indicated the presence of complementary type (gene effect) of epistasis in cross 1 and 2 (Table 24e).

4.4.1.10 Yield Plot^{-1} (kg/6.48m^2)

The simple scaling test revealed significant estimates of all scales in crosses 1 and 2, A, B, and D scales in cross 3 indicated the involvement of all the three type of epistatic interactions.

In all the crosses, 'd' gene effects were positive and significant. The magnitude of additive [d] gene effect was lower than dominance [h] gene effect in the cross 1 and 3. Gene interactions 'i' and 'j' were significant and negative in all three crosses. However, 'l' gene interaction was significantly positive in all crosses (Table 24e).

4.4.1.11 Vitamin C (mg 100 g^{-1})

The scaling tests A, B, C and D in cross 1 and 3; A and D in cross 2 were found significant. Significant χ^2 values also confirmed the results of simple scaling test. Six-parameter model indicated positive and significant 'd' gene effect in the cross 1 and 3. Gene effect 'h' was negatively significant in all the three crosses. Gene interaction 'i' and 'j' were observed significant and negative in all the crosses. Gene interaction 'l' was significant and positive in all the three crosses (Table 24f).

4.4.1.12 Carotenoids (mg 100 g^{-1})

The presence of all types of non-allelic gene interactions were confirmed based on simple scaling test and joint scaling tests. Six-parameter model indicated positive and significant additive [d] gene effect in cross 2 and 3, whereas, it was significant and negative in cross 1. Dominance [h] gene effect was positively significant in cross 1 and 2, and negatively significant in cross 3. Additive × additive [i] gene interaction was also found positively significant in cross 1 and 2 while, negative significant in cross 3. Additive × dominance [j] and dominance × dominance [l] gene interactions were negatively significant in cross 1 and 2. In the

Table 24e. Estimation of scaling tests and gene effects with respect to different crosses for yield plant^{-1} (g) and yield plot^{-1} (kg/6.48m^2)

9. Yield plant^{-1} (g)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-79.20**±4.02	6.11**±1.84	-161.20**±1.27
B	-12.16**±3.49	132.73**±2.03	-139.55**±1.36
C	103.34**±6.71	518.67**±2.26	96.66**±1.80
D	97.35**±1.04	189.91**±1.40	198.70**±0.91
Joint scaling test (three-parameter model)			
m ± SE	632.28**±2.69	801.79**±2.87	803.65**±1.89
[d] ± SE	142.04**±1.69	122.36**±0.63	107.10**±0.51
[h] ± SE	-104.49**±7.66	-193.90**±7.90	-726.55**±5.09
χ^2 (3 df)	90.93**	58.68**	48.64**
Six-parameter model			
m ± SE	651.56**±0.42	765.08**±0.39	614.91**±0.28
[d] ± SE	108.52**±0.61	59.05**±1.16	96.27**±0.70
[h] ± SE	181.59**±3.86	47.06**±2.92	-28.38**±1.95
[i] ± SE	-194.71**±2.08	-379.82**±2.80	-397.41**±1.82
[j] ± SE	-33.51**±1.80	-63.31**±1.32	-10.82**±0.87
[l] ± SE	286.08**±7.15	240.97**±5.16	698.16**±3.34
Type of epistasis	C	C	D

10. Yield plot^{-1} (kg/6.48m^2)

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-2.34**±0.15	-0.37*±0.17	-4.39**±0.18
B	1.07**±0.11	2.88**±0.15	-2.74**±0.12
C	2.61**±0.22	12.04**±1.79	0.09±0.24
D	1.94**±0.08	4.76**±0.89	3.61**±0.08
Joint scaling test (three-parameter model)			
m ± SE	15.84**±0.17	21.14**±1.79	18.42**±0.19
[d] ± SE	3.81**±0.05	3.35**±0.05	2.95**±0.08
[h] ± SE	1.53**±0.46	4.94±3.60	-11.36**±0.51
χ^2 (3 df)	10.18**	44.02**	19.93**
Six-parameter model			
m ± SE	17.90**±0.03	20.43**±0.44	16.33**±0.03
[d] ± SE	2.10**±0.05	1.73**±0.07	2.13**±0.05
[h] ± SE	6.68**±0.19	2.08±1.79	3.01**±0.20
[i] ± SE	-3.88**±0.17	-9.53**±1.78	-7.23**±0.17
[j] ± SE	-1.70**±0.07	-1.62**±0.09	-0.82**±0.10
[l] ± SE	5.15**±0.31	7.02**±1.82	14.37**±0.34
Type of epistasis	C	C	C

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

Table 24f. Estimation of scaling tests and gene effects with respect to different crosses for vitamin C (mg100 g^{-1}) and carotenoids (mg100 g^{-1})

11. Vitamin C (mg100 g^{-1})

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	-26.49**±1.46	-39.41**±0.96	-12.50**±0.99
B	-8.55**±1.48	-0.75±1.10	4.30**±1.12
C	5.30**±2.54	2.98±1.91	83.80**±1.96
D	20.30**±1.23	21.57**±1.01	46.00**±0.92
Joint scaling test (three-parameter model)			
m ± SE	126.71**±2.50	139.22**±2.05	182.86**±1.91
[d] ± SE	14.09**±0.42	18.25**±0.31	17.60**±0.50
[h] ± SE	-88.62**±6.26	-89.61**±4.98	-157.13**±4.60
χ^2 (3 df)	45.79**	19.18**	29.47**
Six-parameter model			
m ± SE	101.25**±0.47	115.25**±0.40	129.35**±0.38
[d] ± SE	5.12**±0.79	-1.07±0.60	9.20**±0.50
[h] ± SE	-13.23**±2.61	-6.29**±2.09	-56.60**±1.94
[i] ± SE	-40.35**±2.47	-43.15**±2.03	-92.00**±1.85
[j] ± SE	-8.97**±0.89	-19.33**±0.68	-8.40**±0.71
[l] ± SE	75.39**±4.07	83.31**±3.07	100.20**±2.81
Type of epistasis	D	D	D

12. Carotenoids (mg100 g^{-1})

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	26.56**±1.77	-9.26**±3.65	-60.80**±1.06
B	86.00**±1.55	81.25**±1.58	-14.41**±1.50
C	39.06**±3.55	25.32**±5.03	64.46**±2.27
D	-36.74**±1.64	-23.33**±1.60	69.84**±0.94
Joint scaling test (three-parameter model)			
m ± SE	113.11**±3.32	132.60**±3.68	343.85**±1.96
[d] ± SE	26.34**±0.42	48.20**±1.78	46.96**±0.55
[h] ± SE	345.19**±7.77	236.32**±8.82	-271.48**±4.90
χ^2 (3 df)	32.75**	27.47**	84.97**
Six-parameter model			
m ± SE	239.19**±0.70	221.10**±0.75	216.83**±0.37
[d] ± SE	-3.38**±0.84	2.94**±0.58	23.77**±0.57
[h] ± SE	159.13**±3.46	117.66**±3.79	-56.58**±2.07
[i] ± SE	73.49**±3.29	46.66**±3.21	-139.68**±1.88
[j] ± SE	-29.72**±0.94	-45.26**±1.88	-23.19**±0.79
[l] ± SE	-186.06**±4.91	-118.65**±5.54	214.90**±3.23
Type of epistasis	D	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

Table 24g. Estimation of scaling tests and gene effects with respect to different crosses for coefficient of infection

13. Coefficient of infection

Cross	Cross 1	Cross 2	Cross 3
Parameters	Scaling test		
A	0.28±0.29	2.13**±0.34	1.95**±0.28
B	3.69**±0.20	3.50**±0.29	3.27**±0.28
C	17.06**±0.85	15.13**±0.60	14.31**±0.58
D	6.54**±0.43	4.75**±0.33	4.54**±0.29
Joint scaling test (three-parameter model)			
m ± SE	15.87**±0.86	12.89**±0.68	12.73**±0.59
[d] ± SE	1.76**±0.07	2.39**±0.06	2.64**±0.05
[h] ± SE	-20.57**±1.85	-12.20**±1.64	-12.07**±1.39
χ^2 (3 df)	15.23**	11.12**	9.52**
Six-parameter model			
m ± SE	7.86**±0.20	7.76**±0.13	7.66**±0.12
[d] ± SE	0.06±0.14	1.71**±0.20	1.98**±0.15
[h] ± SE	-11.46**±0.87	-8.33**±0.69	-8.20**±0.61
[i] ± SE	-13.08**±0.86	-9.50**±0.67	-9.09**±0.59
[j] ± SE	-1.70**±0.16	-0.68**±0.21	-0.66**±0.16
[l] ± SE	9.10**±1.03	3.86**±1.00	3.87**±0.86
Type of epistasis	D	D	D

*,**: Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively. m: Mean, d: Additive effects, h: Dominance effect, i: additive × additive, j: additive × dominance, l: dominance × dominance

cross 3, the additive × dominant [j] gene interaction was negative, whereas in the same cross dominance × dominance [l] gene interactions was positive (Table 24f).

4.4.1.13 Coefficient of Infection (CI)

In simple scaling test, all four scales were significant in crosses 2 and 3, whereas in cross 1 scales B, C and D were significant suggesting the presence of inter allelic interactions. In addition, all three cross combinations had significant joint scaling test value (χ^2) in three parameter model also indicated the presence of epistasis.

In six parameter model, 'd' gene effect was significant and positive in crosses 2 and 3. Dominance [h] gene effect, 'i' and 'j' gene interactions were negative and significant in all three crosses. Gene interaction 'l' was significant and positive in all the crosses (Table 24g).

4.4.2 Incidence of Pest and Disease

4.4.2.1 Incidence of Leaf Curl Disease

In cross 1, among six generations P2 showed symptom-less reaction with 0.00% disease incidence (DI). Parent P1, F_1, BC_1 and BC_2 were moderately resistant with DI of 77.78%, 84.44%, 74.17% and 74.17%, respectively. F_2 population was found to be susceptible with 100.00% DI (Table 25).

In cross 2, P2 was symptom-less and F_2 showed susceptible reaction. The parent P1 and BC_1 showed moderate susceptible reaction with DI of 100.00% and 92.50%, respectively, whereas, F_1 and BC_2 showed moderate resistant reaction with DI of 80.00% and 72.50%, respectively.

In cross 3, P1 and F_2 were moderately susceptible with 100.00% DI. P2 showed symptom-less reaction with 0.00% DI. BC1 was moderately susceptible with 95.00% DI. Moderate resistant reaction was observed in F_1 and BC2.

4.4.2.2 Incidence of Whiteflies, Thrips and Mites

Incidence of whiteflies, thrips and mites were found to be negligible. The mean number of whitefly, thrips and mites population per leaf at 30, 60 and 90 days after transplanting is given in the Table 26.

4.4.2.3 Incidence of Bacterial Wilt and Fruit Rot

Incidence of bacterial wilt and fruit rot was found to be negligible (Table 27).

Table 25: Reaction of six generations of three crosses to local isolate of ChiLCV under field conditions

Sl. No.	Six generations	No of plants screened per replication	Mean number of plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]
			0	1	2	3	4	5	6				
Cross 1													
1	P1	15	3.33	3.67	4.67	3.33	0.00	0.00	0.00	25.56	77.78	19.88	MR
2	P2	15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
3	F_1	15	2.33	7.67	3.00	2.00	0.00	0.00	0.00	21.85	84.44	18.47	MR
4	F_2	60	0.00	10.00	2.67	1.67	29.33	16.33	0.00	60.93	100.00	60.93	S
5	BC1	40	10.33	9.33	4.67	15.67	0.00	0.00	0.00	27.36	74.17	20.30	MR
6	BC2	40	10.33	10.33	4.00	15.33	0.00	0.00	0.00	26.81	74.17	19.89	MR
Cross 2													
7	P1	15	0.00	7.00	3.67	2.33	2.00	0.00	0.00	32.59	100.00	32.59	MS
8	P2	15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
9	F_1	15	3.00	4.33	5.00	2.67	0.00	0.00	0.00	24.81	80.00	19.85	MR
10	F_2	60	0.00	7.00	10.33	3.33	21.00	18.33	0.00	59.26	100.00	59.26	S
11	BC1	40	3.00	7.00	8.00	12.33	9.67	0.00	0.00	41.11	92.50	38.03	MS
12	BC2	40	11.00	5.00	12.33	11.67	0.00	0.00	0.00	26.94	72.50	19.53	MR

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

Table 25. continued

Sl. No.	Six generations	No of plants screened per replication	Mean number of plants in six classes (symptom severity grade 0-6)							Mean PDI[1] (%)	Mean DI[2] (%)	Mean CI[3] (%)	Disease reaction[4]
			0	1	2	3	4	5	6				
Cross 3													
13	P1	15	0.00	5.00	3.00	4.33	2.67	0.00	0.00	38.52	100.00	38.52	MS
14	P2	15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	SL
15	F_1	15	3.00	5.33	3.33	3.33	0.00	0.00	0.00	24.44	80.00	19.56	MR
16	F_2	60	0.00	8.67	8.00	5.00	22.33	16.00	0.00	58.06	100.00	58.06	S
17	BC1	40	2.00	8.00	10.00	8.00	12.00	0.00	0.00	41.67	95.00	39.58	MS
18	BC2	40	11.00	7.00	12.00	10.00	0.00	0.00	0.00	25.42	72.50	18.43	MR
	Mean	28.33	3.30	5.85	5.26	5.61	5.50	2.81	0.00	29.74	72.39	26.83	
CD 5%										2.29	2.12	2.39	
SE (m)										0.79	0.73	0.82	
SE (d)										1.12	1.04	1.17	

PDI[1] - Per cent Disease Index, DI[2] - Disease Incidence, CI[3] - Coefficient of Infection

[4]SL-Symptom less, HR-Highly resistant, R-Resistant, MR-Moderately resistant, MS-Moderately susceptible, S-Susceptible, HS-Highly susceptible

Table 26. Mean population of whitefly, thrips and mites in six generations of three crosses under field conditions

Crosses	Genotypes	Mean number of population per leaf								
		Whitefly			Thrips			Mites		
		30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT	30 DAT	60 DAT	90 DAT
Cross 1	P1	1.2	1.12	0.95	0.23	0.22	0.23	0.00	0.23	0.34
	P2	0.85	0.9	1.11	0.35	0.36	0.34	0.00	0.34	0.21
	F1	1.23	1.54	1.14	0.57	0.56	0.55	0.00	0.23	0.28
	F2	1.34	1.12	0.85	0.21	0.20	0.22	0.00	0.19	0.14
	BC1	1.1	1.42	1.23	0.12	0.12	0.12	0.00	0.00	0.00
	BC2	1.23	1.48	1.2	0.00	0.00	0.00	0.00	0.23	0.13
Cross 2	P1	1.98	2.24	2.23	0.22	0.24	0.23	0.00	0.00	0.00
	P2	1.1	1.54	0.85	0.12	0.12	0.12	0.00	0.23	0.23
	F1	1.1	1.85	1.23	0.21	0.21	0.21	0.00	0.23	0.12
	F2	0.98	1.2	1.1	0.22	0.20	0.21	0.00	0.23	0.00
	BC1	1.54	2.21	1.81	0.22	0.24	0.23	0.00	0.34	0.21
	BC2	0.85	1.1	0.98	0.21	0.21	0.21	0.00	0.23	0.28
Cross 3	P1	1.13	1.24	0.984	0.11	0.12	0.12	0.00	0.19	0.14
	P2	0.97	1.12	1.24	0.12	0.12	0.12	0.00	0.00	0.00
	F1	0.89	1.51	0.94	0.00	0.00	0.00	0.00	0.21	0.14
	F2	1.1	1.42	1.23	0.22	0.24	0.23	0.00	0.17	0.00
	BC1	0.75	1.1	0.98	0.24	0.25	0.24	0.00	0.23	0.24
	BC2	0.99	1.12	1.1	0.25	0.26	0.25	0.00	0.14	0.29
Mean		1.12	1.40	1.17	0.20	0.16	0.17	0.00	0.19	0.15
C.D. 5%		0.054	0.075	0.051	0.01	0.02	0.01	0.00	0.008	0.009
SE (m)		0.019	0.026	0.018	0.04	0.03	0.05	0.00	0.003	0.003

DAT- Days after transplanting

Table 27. Mean per cent incidence of bacterial wilt and fruit rot in six generations of three crosses under field conditions

Crosses	Genotypes	Mean per cent incidence	
		Bacterial wilt	Fruit rot
cross 1	P1	0.00	2.00
	P2	0.17	2.50
	F1	0.22	3.00
	F2	0.33	4.33
	BC1	0.22	4.00
	BC2	0.33	3.43
cross 2	P1	0.22	2.43
	P2	0.22	2.10
	F1	0.11	2.00
	F2	0.11	3.00
	BC1	0.22	3.00
	BC2	0.33	3.00
cross 3	P1	0.33	1.74
	P2	0.44	1.74
	F1	0.22	1.08
	F2	0.33	1.00
	BC1	0.22	1.34
	BC2	0.44	2.00
	Mean	0.24	2.42
	C.D. 5%	0.02	0.5

Discussion

5. DISCUSSION

Chilli is an important vegetable, spice, medicinal and cash crop grown throughout India and it is valued for its sensory attributes of colour, pungency and flavour. Chilli suffers from many diseases and insect problems. *Chilli leaf curl virus* (ChiLCV) disease is one of the serious production constraints in tropical and subtropical regions of the world. Various cultural and chemical approaches that tried to manage the disease proved ineffective. Development of disease resistant or tolerant varieties/hybrids is the most environment friendly and only practical approach for successful cultivation of chilli where disease infestation is severe. Screening of chilli germplasm against leaf curl disease would help in identification of available resistant sources against the disease, which can be further utilized for chilli improvement program.

In recent years, cultivation of chilli F_1 hybrids have become very popular and profitable than open-pollinated cultivars because the chilli grown from hybrid seeds are high yielding with uniform fruits. Superior performance of hybrids is manifested due to better plant vigour, faster growth and development, earliness, increased productivity, better fruit quality and higher levels of resistance to biotic and abiotic stresses.

The information regarding resistance sources, heterosis and combining ability and nature of gene action are the basic requirements to develop high yielding chilli hybrid with ChiLCV resistance. Hence, the most ideal breeding objective for chilli development would be to develop a hybrid with high fruit yield and quality coupled with resistance to ChiLCV. Keeping above points in view, the chilli germplasm was screened under natural field conditions against ChiLCV. The symptomless and highly resistant genotypes from field screening were further subjected to artificial screening (whitefly mediated and graft inoculation) and the molecular detection of virus was carried out from inoculated plants. The seven genotypes (lines) with high yield and quality were crossed with four highly resistant genotypes (testers) to produce 28 F_1 hybrids and were

evaluated for vegetative, flowering, fruit, yield, quality characters and ChiLCV resistance. The nature and magnitude of gene action for vegetative, flowering, fruit, yield, quality characters and leaf curl virus resistance was studied from three superior F_1 crosses through generation mean analysis.

The results obtained from the present investigation entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" are discussed here under different headings and sub headings.

5.1 EVALUATION OF CHILLI GENOTYPES FOR YIELD, QUALITY AND LEAF CURL VIRUS RESISTANCE

5.1.1 Analysis of Variance for the Experimental Design

The results pertaining to the analysis of variance (ANOVA) for the experimental design indicated that MS due to genotypes were significant at $P \leq 0.01$ for all the characters *viz.,* plant height, primary branches, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection suggesting potential genetic differences among 70 genotypes. The MS due to replications were non-significant for all characters studied, indicating that the experimental plot was homogeneous with respect to soil fertility. Significant differences among chilli genotypes were earlier reported by Singh *et al.* (2014) for plant height, days to flowering, early yield, number of fruits, fruit length and width, fruit weight and total yield; by Butcher *et al.* (2013) for fruit length and diameter, fruit weight and vitamin C; by Naresh *et al.* (2016) for fruit length, fruit width and total carotenoids.

5.1.2 Mean Performance of Chilli Genotypes for Vegetative, Flowering, Fruit Yield and Quality Characters

The present study revealed significant differences among the 70 genotypes of chilli for vegetative, flowering, fruit, yield and quality characters.

5.1.2.1 Vegetative Characters

The important vegetative characters which influence the growth and development of chilli include plant height and primary branches plant^{-1}. In the present study, high variability was observed for vegetative characters as obvious from the wide range of values. The mean performance for plant height in genotypes ranged from 31.33 cm (T_{22}) to 73.33 cm (T_{58}), with the overall mean of 46.59 cm. The genotypes T_{58} and T_{31} were superior for plant height. Earlier, the plant height range from 33.10 cm to 55.72 cm was observed by Lohithaswa *et al.* (2000); 26.67 cm to71.67 cm by Bhutia *et al.* (2015); and 31.63 cm to 62.07 cm by Marame *et al.* (2009). Considerable variation in plant height was also reported by Legesse *et al.* (2000), Rodrigues *et al.* (2012), do Rego *et al.* (2009), Payakhapaab *et al.* (2012) and Singh *et al.* (2014).

The genotype T_{51} had maximum number of primary branches (4.77). Among genotypes it ranged from 2.07 (T_{16}) to 4.77 (T_{51}), with the overall mean of 3.27. The results are in conformity with the findings of Marame *et al.* (2009) and Bhutia *et al.* (2015) for primary branches plant^{-1}.

5.1.2.2 Flowering Characters

Commencement of flowering within minimum number of days is a desirable character since it denotes earliness. The genotypes T_{10} and T_{32} were early to flower whereas, the genotype T_{61} was late to flower (38.70). Among genotypes, the overall mean for days to first flowering was 34.52. Similar variation for days to first flower was reported by Prasath and Ponnuswami (2008), Bhutia *et al.* (2015) and Geleta and Labuschagne (2006). The parental line DL 161 took 32.40 days to flower after transplanting followed by PS 403 (34.23), SD 463 (36.67) and SL 461 (36.37) (Singh *et al.*, 2014).

The genotype T_{19} required less number of days for first harvest (42.00) and the genotype T_{11} required maximum number of days for first harvest (61.76). Two genotypes T_{10} and T_{32} required less number of days for first flower and first

harvest. Earlier, Hasanuzzaman *et al.* (2012) observed the range from 33.17 (CCA 5) to 41.37 (CCA 11) among parents for days to green fruit maturity.

5.1.2.3 Fruit and Yield Characters

In chilli, fruit length and fruit girth determines the fruit size. The genotypes T_{10}, T_{31} and T_{28} produced maximum fruit length while the genotype T_{38} and T_{70} produced minimum fruit length.

The average for fruit length in genotypes varied from 3.20 cm to 8.50 cm. Similar variation in fruit length (3.49 cm to 8.80 cm) was reported by Bhutia *et al.* (2015). The fruit length range from 6.05 cm to 11.92 cm was reported by Naresh *et al.* (2016); from 6.35 cm to 12.32 cm by Marame *et al.* (2009); from 4.41 cm to 7.60 cm by Singh *et al.* (2014); from 3.08 cm to 6.87 cm by Prasath and Ponnuswami (2008); and from 2.3 cm to 13.2 cm by Geleta and Labuschagne (2006).

Among the genotypes, the maximum fruit girth was recorded by T_{10} (4.78 cm) while the minimum was observed in T_{38} (1.98 cm). The genotype T_{10} recorded maximum fruit length and fruit girth. Earlier, Singh *et al.* (2014) and Bhutia *et al.* (2015) reported the fruit width range in parents from 0.91 cm (PA 401) to 1.44 cm (US 501) and from 0.49 cm (BCC-1) to 8.9 cm (Chaitali), respectively.

The fruit weight directly contributes towards total fruit yield. Among the genotypes, the minimum fruit weight was observed in the genotype T_{65} (2.20 g) while the maximum was observed in T_{10} (7.57 g). The genotype T_{58} and T_{31} were also superior for fruit weight. Earlier, Singh *et al.* (2014) reported the range of fruit weight of parental lines from 2.35 g to 5.61 g with an average of 3.54 g. The highest mean value of 19.18 g was obtained in the parent SP 128 for fruit weight (Butcher *et al.*, 2013).

Fruits plant^{-1} was highly influenced by the genotypes. Among genotypes, fruits plant^{-1} ranged from 137.33 (T_{53}) to 49.33 (T_{35}), with average of 90.46. Genotypes T_{53}, T_{34}, T_6 and T_{22} were superior for fruits plant^{-1}. In chilli, Hasanuzzaman *et al.* (2012) observed fruits plant^{-1} from 75 (CCA 11) to 179.96

(CCA 15). Number of fruit plant^{-1} in parents ranging from 37.64 to 75.52 has been reported by Rodrigues *et al.* (2012); from 80.08 to 104.75 by Rohini *et al.* (2017), and from 31.22 to 234.69 by Singh *et al.* (2014).

Yield is a polygenic trait which is highly influenced by various parameters like fruit length, fruit girth, number of fruits and fruit weight. The genotype T_{32} produced the maximum yield plant^{-1} of 587.33 g followed by T_{34} (547.67 g), T_{52} (546.67 g), T_{56} (521.00 g), T_{53} (513.33 g), T_{48} (490.33 g) and T_{10} (455.00 g). The genotypes registered an overall mean of 322.80 g. These data were in close agreement with the report of Singh *et al.* (2014) who observed the highest fruit yield of 570.33 g plant^{-1} in the parent PS 403. Bhutia *et al.* (2015) observed the maximum fruit yield plant^{-1} in the parent BCCH Sel-4 (277.97 g) whereas minimum was in Kashi Anmol (140.80). Hasanuzzaman *et al.* (2012) reported the range of fruit yield from 189.60 g (CCA 5) to 373.30 g (CCA 19) in parental lines.

The genotype T_{32} and T_{48} produced high fruit yield plot^{-1} while genotype T_{35} recorded the lowest yield plot^{-1}. The overall mean of genotypes for yield plot^{-1} was 8.85 kg/6.48 m^2. Payakhapaab *et al.* (2012) observed the parent CA 1450 and the hybrid CA 1450 × CA 1448 with maximum fruit yield.

5.1.2.4 Quality Characters

Green chillies are rich source of Vitamin C. Among genotypes the vitamin C content varied from 120.33 mg 100 g^{-1} to 43.00 mg 100 g^{-1}. The genotype T_8 and T_6 were the superior for vitamin C. The overall mean of genotypes was 81.52 mg 100 g^{-1}. Butcher *et al.* (2013) observed the highest ascorbic acid content (µg g^{-1} fruit weight) in the genotype Pap5 (2078.36) followed by PapP26 (1781.36), SP2 (1599.78), PapP30 (1420.81) and S48 (1492.87). Bhutia *et al.* (2015) observed the parent BCC-1 with highest vitamin C content of 211.47 mg/100 g followed by BCCH Sel-4 (129.97 mg/100 g) and Chaitali (112.33 mg/100 g).

The carotenoid content (mg 100 g^{-1}) among the genotypes ranged from 331.33 (T_{18}) to 134.33 (T_3). The genotype T_{18} and T_{17} exhibited superior *per se*

performance for carotenoids. In chilli, Naresh *et al.* (2016) reported the total carotenoids content (mg 100 g^{-1}) from 80.42 (IHR 3453) to 287.61 (IHR 4506) in parental lines.

5.1.3 Selection Index

Superior genotypes from a germplasm stock can be selected by employing a suitable index with the help of discriminant function based on selecting reliable characters. Discriminant function analysis gives information on the proportionate weightage to be given to yield components (Fisher, 1936) and helps in isolating superior genotypes based on the phenotypic and genotypic correlations. Hence, selection index was formulated to increase the efficiency of selection by taking into account all the characters. A selection based on suitable index was more efficient than individual selection based on individual characters (Hazel, 1943). Based on selection index including both quantitative and qualitative characters top ranking seven genotypes *viz.*, T_{32} (CA-32), T_{53} (CHIVAR-7), T_{52} (CHIVAR-6), T_{56} (CHIVAR-10), T_{34} (Keerthi), T_{48} (CHIVAR-3) and T_{10} (Vellayani Athulya) were selected and used as female parents (lines) in line × tester hybridization programme. Earlier, Rani and Rani (1996), Jose (2001) and Mini (2003) also used selection indices for ranking of chilli genotypes.

5.1.4 Field Screening of Chilli Genotypes for ChiLCV Resistance

Identification of resistance sources is of utmost important in any resistant breeding program. Identification of true resistance from large population through artificial challenge inoculation becomes difficult and cumbersome. Keeping this in mind, natural field screening seemed best to eliminate the genotypes which showed obvious susceptible reaction under natural epiphytotic conditions.

Natural whitefly-mediated inoculation is most commonly used technique which does not alter the natural virus-vector-host relationships but it's very difficult to control inoculum pressure (Pico *et al.* 1998). In the present experiment, seventy genotypes were screened under natural disease conditions.

The phenotypic observations suggested that the chilli plants infected at an early stage remained severely stunted. Their terminal and axillary shoots tend to stay erect and their leaflets were reduced in size and abnormally shaped. A wide range of leaf curl virus symptoms variability was noticed under natural field conditions. Enations on leaves and vein thickening were pronounced in some plants. Upward curling of leaves, leaf bending and cupping was also observed. Severely affected plants showed bushy appearance (stunted growth) due to shortened internodes with numerous small and curly leaves in the upper portion of the plants. These plants were also devoid of flowers and fruits. Senanayake *et al.* (2012) observed most notable field symptoms like curling, mottling, puckering and stunting of plants under field conditions.

Out of 70 genotypes screened [experiment I (b)], ten genotypes *viz.*, T_2, T_3, T_5, T_{46}, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67} were found to be completely free from ChiLCV infection, and were, therefore regarded as symptom-less (SL) genotypes (Plate 13).

Five genotypes *viz.*, T_{51}, T_{60}, T_{61}, T_{68} and T_{69} showed highly resistant (HR) reaction and the days to first disease appearance was ranged from 45 days to 60 days after transplanting. Genotypes T_4, T_6, T_{23}, T_{28}, T_{58} and T_{64} showed resistant (R) reaction. These genotypes expressed early (T_6) and late (T_4, T_{23}, T_{28}, T_{58} and T_{64}) symptom development after transplanting. Twelve genotypes were moderately resistant (MR) and the first disease symptoms in T_{59} was delayed up to 60 days after transplanting. Twenty three genotypes were found to be moderately susceptible (MS). Twelve genotypes showed susceptible (S) reaction and two genotypes T_{35} and T_{38} showed highly susceptible (HS) reaction (Figure 9).

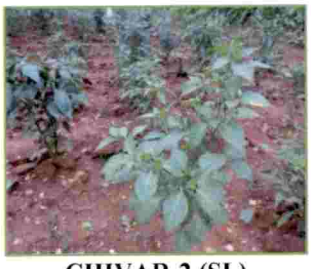
The susceptible genotypes T_{35} (Pusa Jwala) and T_{38} (Kashi Anmol) showed very severe disease infection (highly susceptible) with 100% disease incidence and the first symptoms of the disease were observed within 15 days after transplanting of the crop. Development of early and severe symptoms on

CHIVAR-1 (SL)

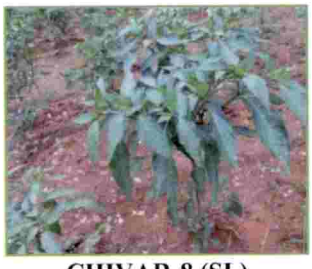
Sel-3 (SL)

Sel-4 (SL)

Sel-6 (SL)



CHIVAR-2 (SL)



CHIVAR-8 (SL)

VS-9 (SL)

Sel-40 (SL)

Sel-7-1 (SL)

Sel-36-1 (SL)

CHIVAR-4 (HR)

Japani Longi (HR)

Sel-20-1 (HR)

Perennial (HR)

Plate 13. Symptomless (SL) and Highly resistant (HR) genotype under field conditions

these genotypes suggested that the disease was in epidemic form and screening under natural field conditions was effective.

The differential response of genotypes to ChiLCV incidence and symptom expression could be attributed to the fact that the disease incidence and its spread are influenced by the occurrence and population dynamics of the vector whitefly and the weather conditions in the agro-ecosystem (Moriones and Navas-Castillo, 2000). Whiteflies had affinity for some particular genotypes than others and this resulted in some hybrids being more susceptible to the virus than others under field conditions (Vidavski *et al.*, 2008).

Pico *et al.* (1998) illustrated that natural infection was too low for most of the wild accessions, which remained uninfected or with low infection percentages. The symptom-less reaction of genotypes can either be attributed due to non-preference mechanism or simply due to escape of whiteflies (Banerjee and Kalloo, 1987).

Several resistant or tolerant genotypes identified so far are mainly based on field screening. Jose *et al.* (2003) screened 37 chilli lines under natural field conditions in Kerala. They identified eight tolerant genotypes namely Kotti Kulam, Mangalapuram local, Chandera local, Pant C-1, Kottiyan local, Haripuram local, Nayattinkara local and Alampady local-1. Kumar *et al.* (2006) screened 307 genotypes of chilli and sweet pepper against ChiLCV under natural field condition. Based on Coefficient of Infection (CI) 49 genotypes were highly resistant, 40 were resistant and 19 were symptom-less. Four highly resistant genotypes *viz.,* Kalyanpur Chanchal, VR-339, CM-334 and CV-1, and two symptomless genotypes Punjab Lal and CV-2 were identified by Kumar *et al.* (2009) under natural field conditions in Indian Institute of Vegetable Research (IIVR). On the basis of mean CI value from three consecutive seasons, Kumar *et al.* (2011) identified seven symptomless genotypes namely BS-35, EC-497636, GKC-29, IC-3640632, IC-383072, Punjab Lal and CV-2 under open field conditions. Srivastava *et al.* (2017) screened 60 germplasm lines against chilli

leaf curl disease under natural conditions and they identified three resistant lines namely WBC-Sel-5, DLS-Sel-10 and PBC-142. Among them, two lines DLS-Sel-10 and WBC-Sel-5 were found resistant to *Chilli leaf curl virus* (ChiLCV) and *Tomato leaf curl New Delhi virus* (ToLCNDV) under field conditions. On the basis of CI, Ahmad *et al.* (2016) identified one highly resistant (VS-9) and three resistant lines (Japani Loungi, Perennial and S-217621) under natural field conditions. All these lines showed disease symptoms under whitefly mediated inoculation

5.2 ARTIFICIAL SCREENING FOR ChiLCV RESISTANCE

Under natural conditions, resistance exhibited by some lines cannot be inferred as a true resistance because those lines may manage to escape from white fly (vector) and hence weren't infected. Sometimes it may also due to feeding of other sucking pests that lead to slight resemblance of leaf curl symptoms. The incidence and severity of virus are strongly influenced by annual, seasonal and local variations under natural field conditions (Pico *et al.,* 1998). So in order to identify their nature of resistance, the lines that were screened as highly resistance (5) and symptomless (10) under field conditions were subjected to artificial whitefly and graft inoculation in experiment II (a).

5.2.1 Whitefly Mediated Inoculation under Insect Proof Cage

In whitefly mediated screening, the test plants were inoculated by using viruliferous whiteflies under single plant micro cages. The ten genotypes which showed symptomless reaction under field conditions expressed varied level of resistance under artificial whitefly mediated inoculation. Genotypes T_2, T_3, T_5, T_{46}, T_{50} and T_{57} were remained symptomless under artificial whitefly inoculation (Plate 14). The genotype T_{65} and T_{66} showed slight curling and clearing of upper leaves under whitefly mediated inoculation and rated as highly resistant. Genotypes T_{63} and T_{67} showed mild curling and swelling of veins, hence rated as resistant. The five genotypes which were highly resistant (T_{51}, T_{60}, T_{61}, T_{68} and

Sel-3

CHIVAR-1

Sel-4

Sel-6

CHIVAR-8

Plate 14. Symptomless reaction of chilli genotypes under whitefly mediated inoculation

T_{69}) under field screening were turned out to be resistant(T_{51} and T_{68}) and moderate resistant (T_{60}, T_{61} and T_{69}) under whitefly inoculation conditions.

The differential response of genotypes under natural and artificial conditions could be attributed to several reasons. Under artificial conditions, high and uniform inoculum pressure is ensured (Pico *et al.,* 1998). Despite efforts to ensure inoculum under the field conditions, some plants still escape infection (Vidavski *et al.,* 1998) and are erroneously regarded as symptomless or resistant. One of the reasons for escape under high disease pressure could be due to host non-preference by the vector, whitefly. Symptoms on moderately resistant or tolerant genotypes grown in the field could be inconspicuous especially if the plant escapes early infection (Kasrawi *et al.,* 1988; Pico *et al.,* 1998). Pico *et al.* (1998) suggested that artificial cage inoculation is the most efficient, adequate and reliable technique to screen against ToLCV (*Tomato leaf curl virus*) and screening of tomato for ToLCV resistance under natural infestation conditions could be misleading. For resistance breeding, screening of the test material by inoculating the individual test plants by force feeding by the viruliferous whitefly is essential.

Earlier, Kumar *et al.* (2006) identified genotypes, EC-497636, BS-35 and GKC-29 with no symptoms under whitefly challenged conditions. Kumar *et al.* (2009) screened six field resistant genotypes by using viruliferous whiteflies through micro cage inoculation. They found that all resistant genotypes turned out to be highly susceptible. Rai *et al.* (2014) identified eight symptomless genotypes namely, C00309, C00304, NMCA-40008, BS-35, GKC-29, IC-383072, Bhut Jolokia and Lankamura Collection under advanced micro cage inoculation technique.

5.2.2 Graft Inoculation Under Greenhouse Conditions

Graft inoculation is a non-whitefly mediated screening. Graft inoculation allows continuous exposure of a test plant to high levels of viral inoculum with high-transmission efficiency (Friedmann *et al.*, 1998; Abou-Jawdah, 1995;

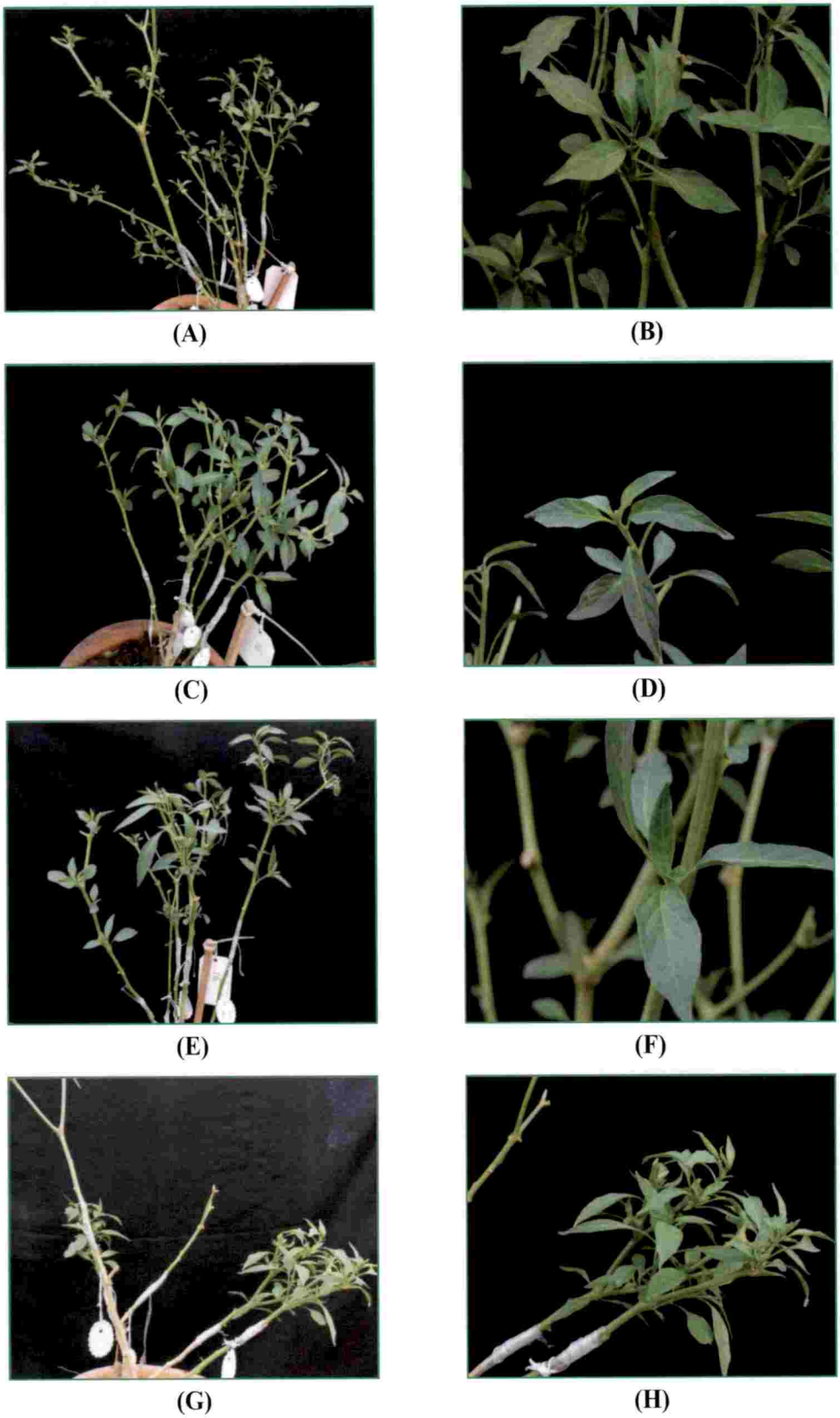
Fargette *et al.*, 1996; Kasrawi *et al.*, 1988) which leads to breakdown of natural resistance in test plants. Out of 10 symptomless genotypes under field conditions in the present investigation, none of the genotypes showed symptomless reaction (disease severity of 0). Earlier, Singh *et al.* (2016) reported that infection by begomoviruses and their interaction inside the host plant leads a permissive cellular environment which leads to breakdown of resistance in otherwise resistant chilli genotypes. This may be one of probable reasons for observing mild symptoms in graft inoculated plants.

Four genotypes *viz.*, T_2, T_3, T_5 and T_{46} showed highly resistant reaction (Plate 15) and the first disease symptoms appeared 32.00, 34.33, 33.33 and 34.33 days after graft inoculation, respectively. Remaining six genotypes showed moderately resistant reaction and the days to first disease appearance ranged from 25.67 to 27.33. The genotypes which showed highly resistant reaction under field conditions were moderately susceptible under artificial graft inoculation and they displayed early symptoms appearance. Artificial screening against ChiLCV revealed that overall disease score was higher with graft inoculation than under the whitefly mediated inoculation conditions (Figure 8).

Mishra *et al.* (1963) confirmed the resistance of the variety Puri Red and Puri Orange by graft inoculation. Kumar *et al.* (2006) performed graft inoculation technique in chilli genotypes (GKC-29, BS-35 and EC-497636) to identify real resistance against PepLCV (*Pepper Leaf Curl Virus*). They did not observe any symptoms on the tested genotypes even 50 days after graft inoculation. In tomato, Friedmann *et al.* (1998) observed symptomless reaction in resistant plants even after grafting with TYLCV (*Tomato yellow leaf curl virus*) infected branch.

5.2.3 Molecular Detection of ChiLCV by Polymerase Chain Reaction (PCR)

After whitefly inoculation, six genotypes were symptomless, two were highly resistant and two were resistant. Out of these six symptomless genotypes, four genotypes namely T_2, T_3, T_5 and T_6 did not show any amplification for presence of virus whereas, two genotypes (T_{50} and T_{57}) showed the presence of



(A) (B)

(C) (D)

(E) (F)

(G) (H)

Plate 15. Highly resistant (HR) reaction of chilli genotypes under graft inoculation

(A) & (B): Sel-3 **(C) & (D): Sel-4**

(E) & (F): Sel-6 **(G) & (H): CHIVAR-1**

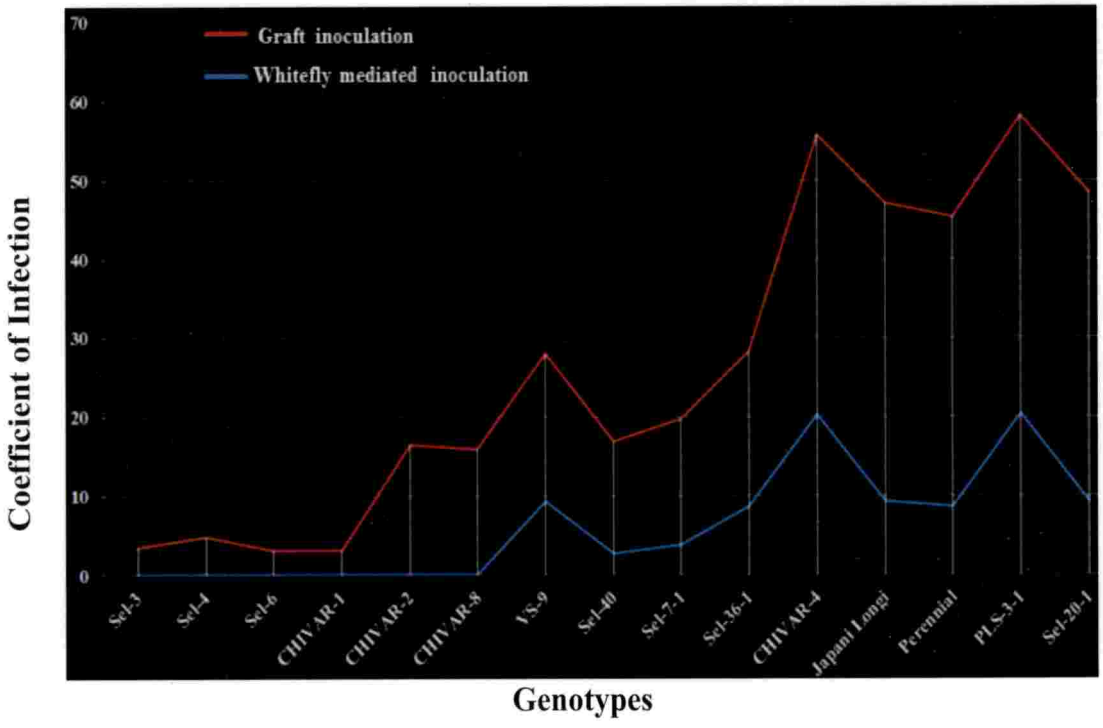


Figure 8. Reaction of chilli genotypes to ChiLCV under artificial inoculation conditions

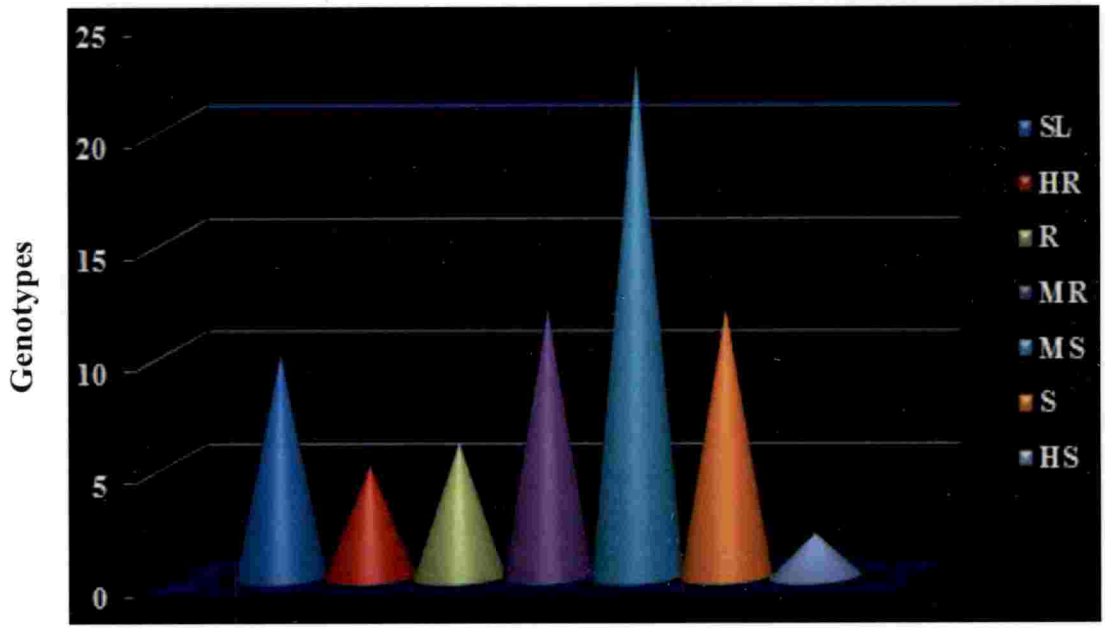


Figure 9. Reaction of chilli genotypes to ChiLCV under field conditions

viral genomes in the plants when subjected to PCR amplification using degenerate primers.

After graft inoculation, all the ten genotypes showed symptom development. These genotypes were confirmed for presence of virus by amplification of 560 bp DNA fragment specific to viral genome. Though virus is present in all the graft inoculated plants, the apparent symptoms vary with genotypes i.e. four genotypes (T_2, T_3, T_5 and T_{46}) were highly resistant and six (T_{50}, T_{57}, T_{63}, T_{65}, T_{66}, T_{67}) were moderately resistant. This suggests that there is a better resistance mechanism working in highly resistant genotypes T_2, T_3, T_5 and T_{46} and they could be used as testers in the hybridization programme of the present investigation.

To confirm the resistance in the symptomless genotypes *viz.*, GKC-29, BS-35 and EC-49 (after graft inoculation), Kumar *et al.* (2006) subjected these plant samples to PCR amplification by using degenerate primers (Wyatt and Brown, 1996) and they confirmed the absence of viral genome from these symptomless plants. Senanayake *et al.* (2007) and Sahu *et al.* (2016) used begomovirus specific primers AVF28/AV29R for detection of ChiLCV whereas Kushwaha *et al.* (2015) used AC1 (nt 521-2606) specific primers FP 5'GGATCCTAATGCCTAGGGCTGGGAGA3' and RP 5' GAGCTCTCAACGCGTCGACGCCTGGTCC-3' for detection of ChiLCV. To identify *Begomovirus* associated with chilli leaf curl, Kumar *et al.* (2012) used degenerate primers (PAL1v1978 / PAR1c496) for detection of Begomovirus DNA-A (Rojas *et al.*, 1993) and Beta01/Beta02 for DNA β (Briddon *et al.*, 2002).

5.2.4 Molecular Characterization of Virus

Homology check of the generated sequence (Begomovirus Vellayani isolate) showed 93 % similarity with *Tomato leaf curl Karnataka virus.* This isolate can be considered as a strain of *Tomato leaf curl Karnataka virus* in accordance with ICTV classification. This suggested the possibility in the predominance of the strain of *Tomato leaf curl Karnataka virus* (India: Kerala:

2016-KX246859.1-ToLCKaV-(IN:Ker:16)) under Vellayani region. However, Kumar *et al.* (2012) had reported the presence of begomovirus in chilli named Chilli leaf curl Vellanad virus. Recently, Kumar *et al.* (2012) identified a new chilli infecting begomovirus, named as *Chilli leaf curl Vellanad virus* (ChiLCVV) in Vellanad region of Kerala.

5.3 EVALUATION OF CHILLI F_1 HYBRIDS

Seven genotypes (lines) with high yield and quality were selected based on selection index ranking and were crossed with four highly resistant genotypes (testers) in a line × tester mating design to produce 28 one-way F_1 hybrids. These hybrids, their parents and two checks (CH-27 and Arka Harita) were evaluated for vegetative, flowering, fruit and yield, quality traits and ChiLCV resistance.

5.3.1 Mean Performance of Parents and Hybrids

5.3.1.1 Plant Height (cm)

The average plant hieght in lines varied from 42 (L1) to 56 cm (L6). For testers, the range varied from 42.93 (T3) to 55.03 cm (T1). The overall mean of the parents were 47.63 cm. The hybrid L7 × T3 was the tallest with 70.70 cm followed by L7 × T3, L7 × T2, L7 × T1, L2 × T3 and L7 × T4. The overall mean for plant height in hybrids was 56.07 cm. Earlier, do Rego *et al.* (2009) reported the range of plant height in hybrids from 54.40 (4 × 24) to 142.00 cm (24 × 58). Payakhapaab *et al.* (2012) observed the maximum plant height in the hybrid CA 1449 × CA 1448 with 78.78 cm followed by CA 1445 × CA 683 (74.89 cm) and CA 1449 × CA 683 (74.45 cm). In a diallel analysis, Singh *et al.* (2014) reported the plant height of crosses from 70.73 cm in the hybrid SL 461 × PP 402 to 101.27 cm in the hybrid CC 141 × VR 521.

5.3.1.2 Primary Branches Plant^{-1}

Among the lines, Primary branches plant^{-1} ranged from 2.56 (L1 and L2) to 4.33 (L6), and it varied from 2.56 (T2) to 4.22 (T1) among testers. Among hybrids, it varied from 2.44 (L4 × T4) to 5.31 (L4 × T2), with overall mean of

3.88. Rohini *et al.* (2017) reported the maximum primary branches in the hybrid Arka Lohit × LCA 334 (13.50) followed by PKM1× Pusa Jwala (10.00), K1 × LCA 625 (9.97) and LCA 625 × PKM1 (9.43). The minimum number of primary branches was observed in the hybrid LCA 334 × Pusa Jwala (7.00). In chilli hybrids, Prasath and Ponnuswami (2008) reported the range from 25.13 to 79.46 with mean of 53.72 for total number of branches.

5.3.1.3 Days to First Flower

The parental lines took 26.79 (L5) to 36.74 days (L3) to first flowering whereas, testers took 33.27 (T3) to 36.12 days (T4). The hybrid L1 × T4 (25.69) was earliest for flowering followed by L5 × T1 (27.02). Singh *et al.* (2014) observed the range of days to fist flowering from 29.87 (SL 461 × PS 403) to 47.73 (PA 401 × PS 403).

5.3.1.4 Days to First Harvest

In lines days to harvest varied from 48.00 (L4 and L5) to 57.00 days (L2). The testers took 54 (T3) to 58 (T2) days to first harvest. Hybrids L1 × T4 (46), L3 × T2 (46), L5 × T1 (46), L5 × T2 (47), L4 × T3 (47), L5 × T4 (48), L5 × T3 (48) and L4 × T1 (48) were early for first harvest. Bhutia *et al.* (2015) identified the parent AC-575 for early fruiting (102.67 days) followed by Chaitali (107.67 days) and BCCH Sel-4 (108.00 days) under severe leaf curl disease conditions. Days to green fruit maturity among parents ranges from 33.17 (CCA 5) to 41.37 (CCA 11) (Hasanuzzaman *et al.*, 2012).

5.3.1.5 Fruit Length (cm)

Fruit length in lines ranged from 3.72 cm (L6) to 8.43 cm (L5) whereas in testers it ranged from 3.47 cm (T4) to 6.10 cm (T3). Among hybrids, it varied from 5.07 cm (L2 × T4) to 10.40 cm (L4 × T2). In chilli hybrids, Geleta and Labuschagne (2006) reported the range of fruit length from 3.7 cm in Kalocsai 'M' Cseresznye × C00916 to 14.1 cm in Szegedi × Bakko Local for fruit length. The hybrids fruit length ranged from 5.44 to 9.87 cm with overall mean of 7.40

cm (Singh *et al.*, 2014). Naresh *et al.* (2016) observed the range of fruit length from 6.32 cm (IHR 450 × IHR 2451) to 14.20 cm (IHR 4507 × IHR 3476) in hybrids.

5.3.1.6 Fruit Girth (cm)

The fruits with maximum girth was produced by the line L5 (4.12 cm) and the tester T2 (3.64 cm). Hybrids L5 × T3 (4.33 cm), L4 × T3 (4.29 cm), L6 × T3 (4.22 cm), L5 × T4 (4.13 cm), L2 × T3 (4.12 cm) and L4 × T2 (4.06 cm) exhibited superior *per se* performance for fruit girth. In hybrids, Geleta and Labuschagne (2006) observed the range of fruit diameter from 1.4 cm (Mareko Shole × PBC 142A) to 6.2 cm (Kalocsai 'M' Cseresznye × Pepper 1976). Rodrigues *et al.* (2012) reported the range of fruit diameter in hybrids from 24.42 mm (UENF 1616 × UENF 1624) to 51.47 mm (UENF 1732 × UENF 1639). The fruit width of hybrids varied from 0.85 to 1.43 cm, with average of 1.18 cm (Singh *et al.*, 2014).

5.3.1.7 Fruit Weight (g)

Among lines, fruit weight varied from 3.70 g (L1) to 7.45 g (L5) while in testers it varied from 3.55 g (T1 and T4) to 4.40 g (T2). In crosses the fruit weight varied from 3.70 g (L2 × T3) to 6.90 g (L1 × T2). Hybrids L1 × T2 (6.90 g), L7 × T1 (6.00 g) and L5 × T2 (5.78 g) showed superior *per se* performance (Figure 3). The current results are in close agreement with the findings of Singh *et al.* (2014), they reported the range of fruit weight from 2.43 g (PA 401 × PS 403) to 6.70 g (US 501 × SD 463) in hybrids. Hybrids SD 463 × PP 402 (6.57 g), SL 461 × SD 463 (6.45 g) and SL 461 × PP 402 (6.33 g) showed high mean performance. The fruit weight of hybrids varied from 71.50 g in the hybrid Kalocsai 'M' Cseresznye × Pepper 1976 to 6.40 g in the hybrid Kalocsai 'M' Cseresznye × PBC 142A (Geleta and Labuschagne, 2006). The fruit weight of hybrids varied from 12.85 g (UENF 1624 × UENF 1639) to 25.76 g (UENF 1624 × UENF 1639) (Rodrigues *et al.*, 2012).

5.3.1.8 Fruits Plant^{-1}

The fruits plant^{-1} in lines varied from 57.00 (L5) to 148.00 (L1) and among testers, it varied from 63.00 (T2) to 84.00 (T3). The hybrid L6 × T1 (189.33) produced maximum number of fruits followed by L3 × T2 (168) and L7 × T3 (163.67) (Figure 4). The fruits plant^{-1} of hybrids varied from 7 (Kalocsai 'M' Cseresznye × Pepper 1976) to 71 (C00916 × PBC 142A) (Geleta and Labuschagne, 2006). Rodrigues *et al.* (2012) reported the range of number of fruit plant^{-1} in hybrids from 44.54 to 108.90. In chilli hybrids, Rohini *et al.* (2017) observed the range from 98.50 to 173.80 for fruits plant^{-1}. Singh *et al.* (2014) reported the highest number of fruits in the hybrid MS 341 × DL 161 (325.09) followed by SL 462 × US 501 (316.54) and SL 461 × SL 462 (311.15).

5.3.1.9 Yield Plant^{-1} (g)

The range of yield plant^{-1} for lines varied from 449.00 g (L5) to 584.15 g (L4) and among testers it ranged from 260.67 g (T4) to 349.67 g (T3). The hybrids recorded a range of 276.10 g (L4 × T3) to 849.47 g (L3 × T2), with an overall mean of 542.07 g (Figure 5). The highest yield was recorded in the hybrid L3 × T2 (849.47 g) followed by L1 × T1 (822.67 g), L7 × T1 (774.73 g) and L6 × T1 (746.13 g). Based on *per se* performance, Singh *et al.* (2014) identified the superior hybrids *viz.*, DL 161 × PP 402 (1095.80 g plant^{-1}), CC 141 × VR 521 (1091.00 g plant^{-1}), SL 462 × VS 501 (1082.20 g plant^{-1}) and SL 461 × DL 161 (1080.17 g plant^{-1}) for total fruit yield. Payakhapaab *et al.* (2012) reported the range of fruit weight plant^{-1} in hybrids from 0.53 to 1.06 kg plant^{-1}. Geleta and Labuschagne (2006) observed the range of fruit yield from 129.60 to 423.70 g in parents and in hybrids from 123.40 to 538.80 g.

5.3.1.10 Yield Plot^{-1} (kg/6.48m^2)

Among lines yield plot^{-1} varied from 12.37 kg (L5) to 16.16 kg (L4) and among the testers it ranged from 7.10 kg (T4) to 9.50 kg (T3). The hybrids were in the range of 7.53 kg (L4 × T3) to 23.50 kg (L3 × T2), with the overall mean of

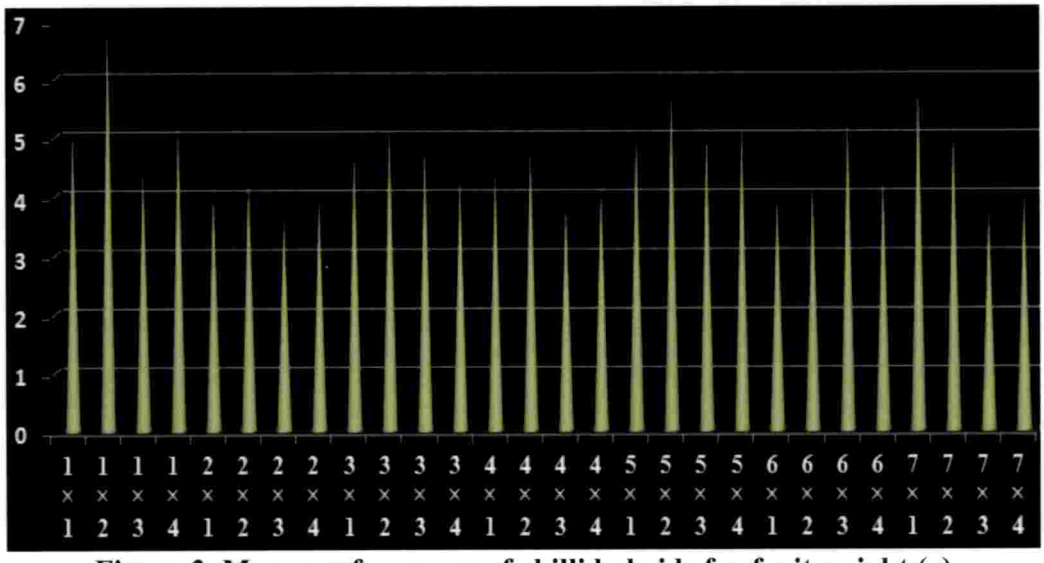


Figure 3. Mean performance of chilli hybrids for fruit weight (g)

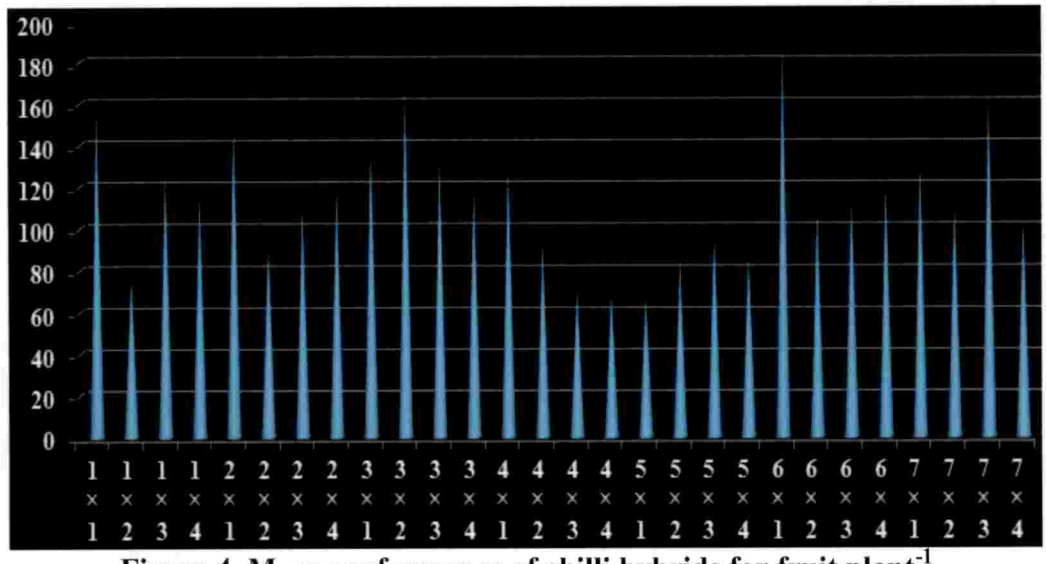


Figure 4. Mean performance of chilli hybrids for fruit plant^{-1}

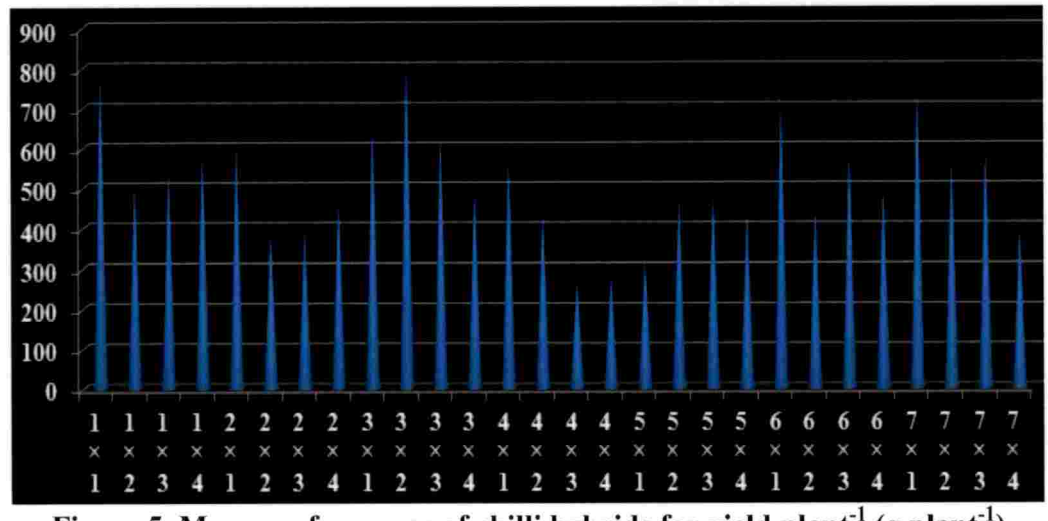


Figure 5. Mean performance of chilli hybrids for yield plant^{-1} (g plant^{-1})

14.97 kg. The parent CA 1450 and the hybrid CA 1450 × CA 1448 produced maximum yield (Payakhapaab *et al.*, 2012).

5.3.1.11 Vitamin C (mg 100 g^{-1})

The vitamin C content among the lines ranged from 94.33 mg 100^{-1} g (L5) to 114.67 mg 100^{-1} g (L3) and among the testers, it ranged from 87.33 mg 100^{-1} g (T3) to 93.67 mg 100^{-1} g (T4). Among 28 hybrids, the vitamin C ranged from 72.67 mg 100^{-1} g (L6 × T4) to 134.00 mg 100^{-1} g (L3 × T2), with the overall mean of 104.74 mg 100^{-1} g (Figure 6). In chilli hybrids, Rohini *et al.* (2017) observed the range from 85.70 to 158.39 mg/100 g for vitamin C content. Bhutia *et al.* (2015) observed the parent BCC-1 with highest vitamin C content of 211.47 mg/100 g followed by BCCH Sel-4 (129.97 mg/100 g) and Chaitali (112.33 mg/100 g).

5.3.1.12 Carotenoids (mg 100 g^{-1})

The line L6 recorded the lowest carotenoids (205 mg 100^{-1} g) and L2 recorded the highest carotenoids (272 mg 100^{-1} g). In testers carotenoids varied from 131.00 mg 100^{-1} g (T2) to 222.67 mg 100^{-1} g (T4). The hybrids recorded a range of 195.33 mg 100^{-1} g (L5 × T3) to 363.67 mg 100^{-1} g (L4 × T1) (Figure 7). Naresh *et al.* (2016) observed the carotenoids content (mg/100g) of hybrids varied from 79.70 (IHR 4506 × IHR 2451) to 276.31 (IHR 3476 × IHR 500). Maradana, (2016) reported the range of total carotenoids content in hybrids from 186.49 (LCA 607 × G4) to 397.32 mg/100 g (LCA 466 × LCA 453).

5.3.2 Estimation of Combining Ability Effects

5.3.2.1 Analysis of Variance for Experimental Design

The mean squares (MS) due genotypes were significant at $P \leq 0.01$ for all the characters studied suggesting the existence of potential genetic differences among genotypes i.e. parents, F_1 hybrids and standard checks. The results further revealed that the MS due to replications were significant for fruit length, fruits $plant^{-1}$ and fruit weight; and non-significant for plant height, primary branches,

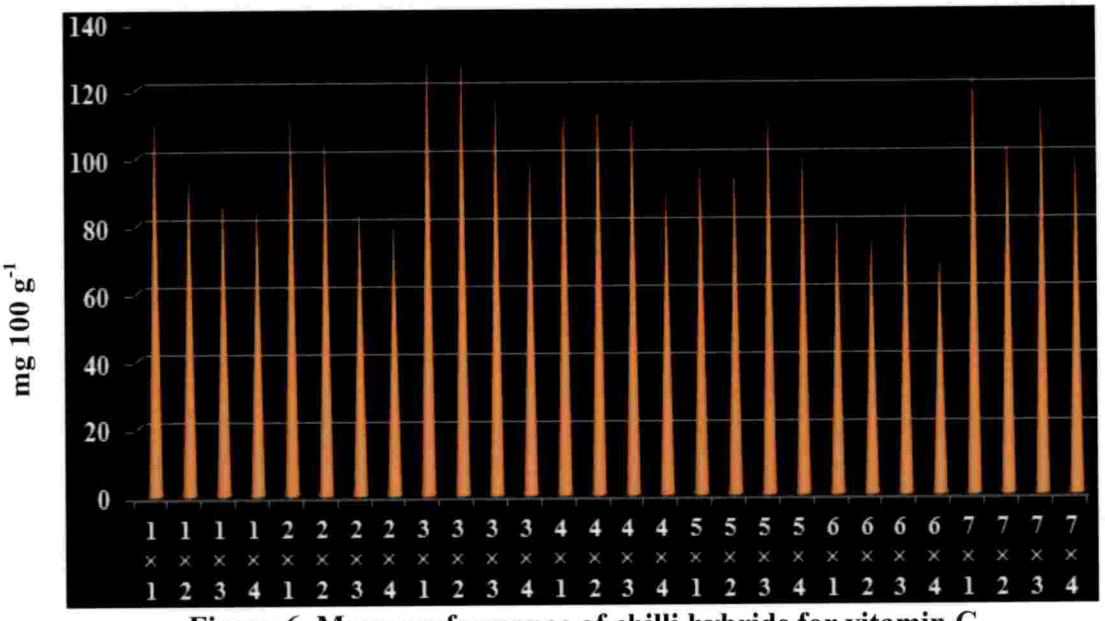


Figure 6. Mean performance of chilli hybrids for vitamin C

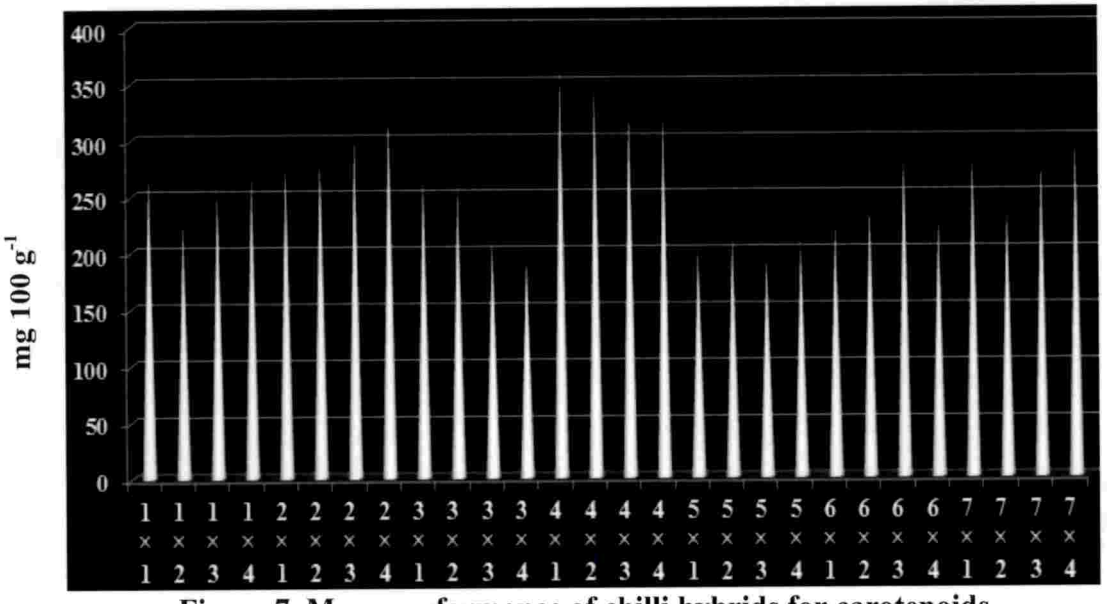


Figure 7. Mean performance of chilli hybrids for carotenoids

days to flower, days to harvest, fruit girth yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection. This indicated that the experimental plot was heterogeneous with respect to soil fertility and blocking of the experiment was effective to account for the variation due to replications thus minimizing the experimental error. Earlier, Hasanuzzaman *et al.* (2012) observed significant MS for replication for days to 50% flowering, days to green fruit maturity and fruits plant^{-1}. Significant differences among genotypes was reported by Rodrigues *et al.* (2012) for plant height, days to fruiting, fruit length, fruit diameter, fruit weight and fruits plant^{-1}; Geleta and Labuschagne (2006) for days to flower, fruit diameter, fruit length, fruit weight, fruits number and fruit yield.

5.3.2.2 Analysis of Variance for Combining Ability

The total genetic variability was partitioned into the general combining ability (GCA) and the specific combining ability (SCA) effects. The MS due to parents were significant for all the characters. Significant differences due to lines were found for all the characters. The MS due to testers were non-significant for coefficient of infection. The hybrids/crosses differed significantly for all the characters. Lines vs testers showed significant differences for all the characters except for plant height. The MS due to parent vs crosses showed significant differences for all the characters. The indicated considerable differences among genotypes i.e. parents (lines and testers) and their 28 F_1 hybrids.

The MS due to GCA of lines and SCA of crosses were significant at $P \leq 0.01$ for all vegetative, flowering, yield and quality traits studied. The GCA of testers were significant for all the traits except for days to first harvest. Highly significant variation due to GCA of lines and GCA of testers, and SCA of crosses indicated the importance of additive as well as non-additive types of gene effects in inheritance of the traits studied. As the experiment was not repeated over the environments, it was not possible to study genotype × environment interaction. Therefore, the estimates of MS reported in this study were expected to be on higher side. Significance of both additive and non-additive genetic variation

suggested that genetic improvement of chilli for the traits under study could be achieved both by hybrid development and pure line breeding. The analysis further revealed that the σ^2GCA/σ^2SCA ratio was less than unity for all the studied traits which indicated the predominance of non-additive gene effects for these traits. The contribution of lines were more as compared to testers for all the characters except for the primary branches plant^{-1}.

Predominating role of the non-additive gene action makes it difficult to gather desirable genes, because these genes are not fixed in the population (Reddy *et al.*, 2008). Through the line × tester analysis, Payakhapaab *et al.* (2012) found significant difference due to crosses and line × testers for plant height, fruits plant^{-1}, fruit weight, yield, fruit length and fruit width. Through diallel analysis, Bhutia *et al.* (2014) found highly significant components of GCA and SCA mean squares for fruit yield traits and Per cent Disease Index (PDI) of leaf curl virus. This suggested that inheritance of these characters were apparently due to both additive and non-additive gene action.

Singh *et al.* (2014) observed the predominance of additive gene effects for fruit weight, fruit width, fruit length and days to flowering. Naresh *et al.* (2016) reported that the mean sum of squares due to genotypes, parents and hybrids, and parent vs hybrids were highly significant for fruit length, fruit width, dry yield plant^{-1} and total carotenoids.

5.3.2.3 Estimation of General Combining Ability (GCA) Effects of Parents and Specific Combining Ability (SCA) Effects of Crosses

The usefulness of parents could be predicted based on their individual performance. However, combining ability is an effective tool, which gives useful genetic information for the choice of parents in terms of performance of their hybrids (Chezhian *et al.*, 2000). It is, therefore, necessary to assess genetic potential of parents in hybrid combinations through systematic studies in relation to general and specific combining ability effects.

The term "general combining ability (GCA)" is used to designate the average performance of a parent in hybrid combinations. It estimates the magnitude of the additive portion of the genetic effects, and it means that the particular parent has good genes in general. The estimates of general combining ability effects provides a measure of GCA of each genotype, thus helping in selection of the superior parents for hybrid breeding programmes. The GCA effects of parents and SCA effects of hybrids are discussed character wise as under:

5.3.2.3.1 Plant Height (cm)

A perusal of GCA effects revealed that three lines L7 (10.91), L2 (4.31), L6 (3.87) and one tester T1 (2.14) exhibited highly significant and positive GCA effects and were good general combiners for tallness. The line L7 and the tester T1 were the best general combiners with GCA effects of 10.91 and 2.14, respectively. Four lines and two testers showed negative significant GCA effects for plant height indicating that they were good general combiners for dwarfness. The tester T2 was regarded as average general combiner for plant height. Earlier, parent PBC 972 was identified as best general combiner with GCA effects of 3.55 for tallness by Legesse (2000); parent 132 (4.01) by Ferreira *et al.* (2015); CCA 2 (5.26) by Hasanuzzaman *et al.* (2012); Chickballapur (1.72) by Lohithaswa *et al.* (2000); CA-UGK1 09-4 by Nsabiyera *et al.* (2012); UENF (3.34) by Rodrigues *et al.*(2012); CB 38 (20.9) by do Rego *et al.* (2009); CC 141 (11.59) by Singh *et al.*(2014); and Arka Lohit (19.29) by Prasath and Ponnuswami (2008). In line × tester, analysis Payakhapaab *et al.* (2012) identified line CA 1449 (5.83) and tester CA 683 (5.20) with high GCA effects for plant height.

In the current study, nine crosses manifested positive significant SCA effects. The hybrids namely L1 × T2 (7.50), L1 × T1 (6.25), L3 × T1 (5.35), L2 × T3 (5.26) and L7 × T3 (4.81) exhibited high positive significant SCA effects for plant height. None of the hybrids showed high (positive) × high (positive) GCA combination indicating the absence of additive × additive gene interaction in the

hybrids. Three cross combination namely L2 × T3, L6 × T4 and L7 × T3 were the outcome of high × low GCA effects suggesting the involvement of additive × dominant interaction. These hybrids could have greater chance for producing transgressive segregants in later generations. The hybrid L1 × T1 (6.25) and L3 × T1 (5.35) had low × high GCA effects of their respective parents indicating the involvement of dominant × additive gene action. From these crosses, selection for tall plants could be postponed to later generation in recombination breeding. Earlier, Legesse (2000) reported high SCA effects for plant height in three hybrids, namely 6 × 7 (12.02), 1 × 5 (11.88) and 2 × 3 (10.50). Hasanuzzaman *et al.* (2012) identified a hybrid (CCA 5 × CCA 11) with highest SCA effects of 7.67; Lohithaswa *et al.* (2000) reported a best hybrid Pant C-1 × Pusa Jwala (5.76) based on high SCA effects. The cross combination CA UGCE 09-3 × PP9852-115 exhibited high SCA effects (Nsabiyera *et al.*, 2012). do Rego *et al.* (2009) observed the SCA effects up to 38.84 in the cross combination CB 24 × CB 58; up to 6.58 (UENF 1629 × UENF 1732) by Rodrigues *et al.* (2012); up to 13.32 (RHRC-50-1 × Punjab Surkh) by Saritha *et al.* (2005) and up to 9.38 (MS 341 × PP 402) by Singh *et al.* (2014). The current study results are also in corroboration with findings of Devi and Arumugam (1999), Muthuswamy (2004), Khereba *et al.* (2008), Syukur *et al.* (2013), Payakhapaab *et al.* (2012) and Prasath and Ponnuswami (2008).

5.3.2.3.2 Primary Branches Plant^{-1}

Among lines and testers, line L3 (0.34) and tester T1 (0.49) were considered as good general combiners for primary braches plant^{-1}. The line L1 and L2 and tester T4 were poor combiners, and the lines L4, L6, L7 and tester T3 were average combiners. Nsabiyera *et al.* (2012) observed three parents namely, CA-UGK1 09-4 (0.94), CA-UGK1 09-6 (0.56) and CA-UGCE 09-3 (0.53) with significant positive GCA effects for primary branches plant^{-1}. The parent K1 and LCA 625 showed significant GCA effects of 0.53 and 0.47, respectively (Rohini *et al.*, 2017). The parent Arka Lohit showed highest GCA effects (8.79) for

primary branches plant^{-1} (Prasath and Ponnuswami, 2008).

Among the 28 F_1 hybrids evaluated, only four hybrids have positive significant SCA effects and they were L4 × T2 (1.29), L3 × T2 (1.08), L6 × T1 (0.71) and L2 × T4 (0.46). None of the hybrids involved both parents with high (good) × high (good) GCA effects. The hybrid L3 × T2 had high (good) × low (poor) GCA effects of their respective parents whereas, hybrid L6 × T1 had low (average) × high (good) GCA effects of their parents. The hybrid L2 × T4 and L4 × T2 involved parents with low (poor) × low (poor) GCA effects. This suggested that non-additive gene effects were predominantly involved in the superior performance of these hybrids which can be exploited through heterosis breeding. Earlier, Saritha *et al.* (2005) reported significant SCA effects up to 1.55 in the hybrid 5 × 4. Prasath and Ponnuswami (2008) identified three hybrids with significant SCA effects namely, S1 × Bydagi Kaddi (good × poor), Arka Lohit × MDU Y (good × poor) and Arka Lohit × Co 4 (good × average). Rohini *et al.* (2017) observed the SCA effects of 3.25 in the hybrid Arka Lohit × LCA 334 and RCA (reciprocal combining ability) effects of 2.14 in the hybrid LCA 625 × K1. The present data were also in close agreement with those reported by Jagadeesh (1995), Patil (1997), Shukla *et al.* (1999), Chadchan (2008) and Pandey *et al.* (2012).

5.3.2.3.3 Days to First Flower

Negative GCA and SCA effects are desirable for days to first flower that denote early floweing. Early flowering is generally an indication of early yield. Lines L5 (-2.92), L4 (-1.90), L3 (-0.94), L1 (-0.85) and tester T1 (-0.83) were considered as good general combiners for days to first flower. Lines L2, L6, L7 and testers T3, T4 were poor general combiners. The tester T2 was considered as average general combiner.

Earlier, parent 'DL 161' was identified as a good general combiner for days to flowering by Singh *et al.* (2014); MDU Y (-1.08), Bydagi Kaddi (-1.33) and Co 4 (-1.62) by Prasath and Ponnuswami (2008); UENF 1639 by Rodrigues

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et al. (2012); PP0537-7504 (-2.62), PP9852-115 (-3.28) and CA-UGCE 09-3 (-3.17) by Nsabiyera *et al.* (2012); IHR 1822-1/3-1/5 (-0.91) and Pusa Jwala (-1.56) by Lohithaswa *et al.* (2000); Mareko Fana, PBC 485, PBC 510 and PBC 731 by Legesse (2000); CCA 5(2) and CCA 11(4) by Hasanuzzaman *et al.* (2012). The parents Kalocsai M, Szegedi 178 and C00916 showed high GCA effects under both greenhouse and open field conditions for days to flowering (Geleta and Labuschagne, 2006).

Among the 28 hybrids evaluated, nine crosses showed significant and negative SCA effects. Top five hybrids with negative and significant SCA effects identified were L1 × T4 (-4.95), L3 × T2 (-2.83), L3 × T4 (-2.48), L6 × T2 (-2.22) and L7 × 1T (-1.73). Among nine hybrids showing significant negative SCA effects, none of the hybrids had both parents with significant negative GCA effects, six hybrids had one parent with significant and negative GCA effects and neither of the parents of three hybrids had negative and significant GCA effects. The contributions to the SCA effects of these hybrids pointed to non-additive gene effects. The desirable effects exhibited by these crosses could be exploited through heterosis breeding.

These results are in accordance with the outcome of Geleta and Labuschagne, (2006); Hasanuzzaman *et al.* (2012); Legesse (2000); Lohithaswa *et al.* (2000) and Rodrigues *et al.* (2012). Earlier, Prasath and Ponnuswami (2008) reported that the crosses Arka Abhir × MDU Y (-3.35), S1 × MDU Y (-3.00) and Arka Lohit × Bydagi Kaddi (-2.83) exhibited highly significant SCA effects for days to first flowering. Singh *et al.* (2014) identified SL 462 × PA 401 (-5.88) to be the best specific combiner for days to flowering. The hybrids namely, CA-UGKI 09-4 × UGKI 09-6 (-15.8), CA-UGKI 09-6 × PP0337-7562 (-6.7), CA-UGKI 09-6 × PP0537-7504 (-8.8) and CA-UGCE 09-3 × PP0337-7562 (-6.5) showed significant negative SCA effects (Nsabiyera *et al.*, 2012).

5.3.2.3.4 Days to First Harvest

The parents L5 (-3.31), L4 (-2.07) and L3 (-1.07) were identified as good

general combiners for days to first harvest. The testers T1 and T2 were found to be average general combiners. The lines, L2 and L7 were found to be poor general combiners for days to first harvest. Earlier, do Nascimento *et al.* (2014) reported that the parent 01 with highest GCA effects of -4.61 for days to harvest. Hasanuzzaman *et al.* (2012) identified a good general combiner CCA 5 (2) with highest GCA effects of -2.26 for days to green fruit maturity. Nsabiyera *et al.* (2012) identified three parents namely, PP0337-7562 (-3.50), PP9852-115 (-5.45) and CA-UGCE 09-3 (-2.85) with significantly negative GCA effects for days to fruit maturity. Three parents, PP402, SL461 and US501 were identified as good general combiner for early yield (Singh *et al.*, 2014).

Among the 28 hybrids, five hybrids *viz.* L1 × T4 (-5.36), L3 × T2 (-3.22), L7 × T1 (-2.11), L4 × T3 (-1.77) and L6 × T2 (-1.72) were regarded as good specific combiners for days to first harvest. None of the hybrids involved both parents with significant and negative GCA effects, two hybrids had one parent with significant and negative GCA effects and neither of the parents of three hybrids had significant and negative GCA effects. The contribution to the SCA effects of all these hybrids have come from the non-additive gene effects. Superior performance of these hybrids can be exploited through heterosis breeding. do Nascimento *et al.* (2014) reported that the cross 77.1 × 01 showed maximum SCA effects (-3.97) and the maximum RCA effects (-2.00) was observed in the hybrid 01 × 137. Hasanuzzaman *et al.* (2012) reported that the hybrid CCA 11 × CCA 19 had high SCA value of -4.83 followed by BARI Morich 1 × CCA 19 (-4.61), CCA 11 × CCA 15 (-2.67), CCA 2 × CCA 15 (-2.65) and BARI Morich 1 × CCA 11 (-1.20). Nsabiyera *et al.* (2012) identified a best specific combiner 29 × 25 (-12.60) for days to fruit maturity. The hybrid, EL 181 × US 501 was identified as best specific combiner for early yield by Singh *et al.* (2014).

5.3.2.3.5 Fruit Length (cm)

Lines L4 (2.30) and L5 (0.38), and tester T2 (0.65) were found to be good general combiners for fruit length. Lines L2, L3, L6 and L7 and, tester T1 were

considered as poor general combiners. The line L1 was considered as average general combiner. Earlier, do Nascimento *et al.* (2014) reported maximum positive and significant GCA effects for fruit length in the parent 132 (1.01). The parent (Pepper 1976) were identified as good general combiner by Geleta and Labuschagne, (2006); CCA 11(4) and CCA 15(5) by Hasanuzzaman *et al.* (2012); L-S 5-6 by Khalil and Hatem (2014); Bako Local and PBC 485 by Legesse (2000); P 36-R by Marchesan *et al.* (2009); parent 28 by Nsabiyera *et al.* (2012); Genotype C by Ganefianti and Fahrurrozi (2018); Genitor 24 by do Rego *et al.* (2009); IHR 3849 (1.27), IHR 3453 (1.07), IHR 4506 (0.93), IHR 4507 (1.40) and IHR 3476 (0.93) by Naresh *et al.* (2016). Present results are in conformity with findings of Rodrigues *et al.* (2012), Prasath and Ponnuswami (2008), Singh *et al.* (2014) and Payakhapaab *et al.* (2012).

Among the 28 hybrids, 10 crosses have positive significant SCA effects. The hybrids *viz.*, L1 × T2 (1.36), L7 × T1 (1.09), L6 × T3 (1.03), L3 × T3 (0.84), L6 × T4 (0.79) and L2 × T2 (0.72) were good specific combiners for fruit length. Among ten hybrids that exhibited significant positive SCA effects, only one cross (L4 × T2) had both parents with positive significant GCA effects for fruit length. This suggested the involvement of additive gene effects in heterotic performance of this hybrid. The hybrid populations derived from this cross could be pursued further to recover transgressive segregants with longer fruits. Three hybrids involved at least one parent with positively significant GCA effects and the remaining five hybrids had neither of the parents with positively significant GCA effects. This suggested that non-additive gene effects were predominantly involved in superior performance of these hybrids which can be exploited through heterosis breeding. Earlier, do Nascimento *et al.* (2014) identified Kalocsai M Cseregzyne × Bakko Local and Mareko shote × PBC 142A crosses with high SCA effects for fruit length. High SCA effects for fruit length were observed by Hasanuzzaman *et al.* (2012) in the cross CCA 2 × CCA 15; by Marchesan *et al.* (2009) in Quantum-R × HV-12, P36-R × HV-12 and Rubia-R × HV-12; by Saritha *et al.* (2005) in L5 ×

T1 (2.81); by Ganefianti and Fahrurrozi (2018) in Genotype C × Genotype G (2.52); by Rego *et al.* (2009) in 4 × 24, 4 × 58, 38 × 50; and by Naresh *et al.* (2016) in IHR 4507 × IHR 3476 (2.05). The present results are also in accordance with the findings of Medeiros *et al.* (2014), Nsabiyera *et al.* (2012), Rodrigues *et al.* (2012), Prasath and Ponnuswami (2008), Singh *et al.* (2014) and Payakhapaab *et al.* (2012).

5.3.2.3.6 Fruit Girth (cm)

Lines L4 (0.34), L6 (0.32) and L5 (0.24) and, tester T3 (0.27) were found to be good general combiners for fruit girth. Lines L2, L3, L7 and testers T1, T4 were regarded as poor general combiners. Earlier, MDU Y and Byadagi Kaddi were identified as good general combiner for fruit girth by Prasath and Ponnuswami (2008); PP 402 and US 501 for fruit width by Singh *et al.* (2014); parent 4 (7.7), parent 24 (0.9) and parent 50 (8.6) for maximum fruit width by do Rego *et al.* (2009); Genotype B (1.44), Genotype D (0.69) and Genotype G (0.59) by Ganefianti and Fahrurrozi (2018); PP0337-7562 (0.79) for fruit width by Nsabiyera *et al.* (2012); CCA 11 (0.69) for fruit width by Hasanuzzaman *et al.* (2012), parent 137 (0.10) for fruit girth by do Nascimento *et al.* (2014) and IHR 3476 (1.95) for fruit width by Naresh *et al.* (2016). The present studies were also in accordance with the outcomes of Geleta and Labuschagne, (2006), Khalil and Hatem (2014), Legesse (2000), Marchesan *et al.* (2009), Medeiros *et al.* (2014), Rodrigues *et al.* (2012) and Payakhapaab *et al.* (2012).

Among the 28 hybrids, four crosses have positive significant SCA effects. The hybrid L2 × T3 exhibited the highest SCA effects of 0.49 followed by L7 × T2 (0.46), L3 × T1 (0.43) and L5 × T4 (0.42). Hybrid L2 × T3 was the outcome of low × high GCA effects of their respective parents. L5 × T4 was the outcome of high × low GCA effects of their corresponding parents. The contribution to the SCA effects of these hybrids denoted the non-additive gene effects. Superior performance of these hybrids could be exploited through heterosis breeding. The hybrid L3 × T1 and L7 × T2 were the outcome of high × high parental GCA

effects. Thus, there exists greater scope for developing true breeding lines with higher fruit girth from the segregating populations generated from these two crosses. Earlier, Prasath and Ponnuswami (2008) reported that the crosses MDU Y × Arka Abhir (good × poor), Arka Lohit × Bydagi Kaddi (poor × good), Arka Lohit × Co 4 (poor × average) were the best specific combiners for fruit girth with significantly high SCA effects. Naresh *et al.* (2016) reported that the crosses IHR 3849 × IHR 2451 (0.37), IHR 4507 × IHR 3476 (0.32), IHR 4503 ×IHR 3476 (0.28) and IHR 4516 × IHR 2451 (0.24) were the best specific combiners for fruit width with significantly high SCA effects. The SCA effects up to 0.27 in hybrid EL 181 × PA 401 was identified by Singh *et al.* (2014) up to 0.32 (CA-UGCE 09-3 × PP9852-115) by Nsabiyera *et al.* (2012); up to 1.37 (CCA 15 × CCA 19) by Hasanuzzaman *et al.* (2012) for fruit width. The hybrid 50 × 44 showed highest SCA effects of 6.2 for fruit diameter (do Rego *et al.,* 2009). Ganefianti and Fahrurrozi (2018) identified Genotype D × Genotype G (0.84) and Genotype E × Genotype B (0.79) crosses with high SCA effects for fruit diameter. The present study results are also in conformity with the findings of do Nascimento *et al.* (2014), Geleta and Labuschagne, (2006), Khalil and Hatem (2014), Legesse (2000), Marchesan *et al.* (2009), Medeiros *et al.* (2014), Rodrigues *et al.* (2012) and Payakhapaab *et al.* (2012).

5.3.2.3.7 Fruits Weight (g)

The estimates of combining ability effects revealed that five lines and three testers showed significant GCA effects. Among them, two lines and one tester were good general combiners. The line L1 (0.72), L5 (0.55) and tester T2 (0.47) were better general combiners for fruit weight. Lines L2, L4, L6 and testers T3, T4 were considered as poor general combiners for fruit weight. Lines L3, L7 and tester T1 were regarded as average general combiners for fruit weight. Earlier, do Rego *et al.* (2009) revealed that parents CB 24 (6.9), CB 50 (5.0) and CB 4 (4.2) showed high GCA for fruit weight. CCA 11 (0.86) was identified as good general combiner for fruit weight by Hasanuzzaman *et al.* (2012); 137

(0.31) and 132 (0.27) by do Nascimento *et al.* (2014); SD 463 (1.10) and PP 402 (1.06) by Singh *et al.* (2014); MDU Y (3.70) and Bydagi Kaddi (0.87) by Prasath and Ponnuswami (2008); and KA-2 (1.11) by Tembhurne and Rao (2012). The present studies were in accordance with the outcomes of Geleta and Labuschagne, (2006), Legesse (2000), Lohithaswa *et al.* (2000), Marchesan *et al.* (2009), Medeiros *et al.* (2014) and Rodrigues *et al.* (2012).

Among the 28 hybrids, four crosses have positive significant SCA effects. Estimates of positive significant SCA effects ranged from 0.37 in the cross L3 × T3 to 1.17 in the cross L7 × T1. Hybrids exhibiting significant positive SCA effects were L7 × T1 (1.17), L6 × T3 (1.13), L1 × T2 (0.95) and L3 × T3 (0.37) were considered as good general combiners for fruit weight. Hybrid L1 × T2 have both of the parents with positively significant GCA effects. This suggested the involvement of additive gene effects for heterotic performance of this cross. The heterotic performance of this cross can be exploited through pure line breeding by fixing the additive gene effects. Neither of parents of the three hybrids had significant positive GCA effects and these hybrids were the outcome of low × low GCA effects of their respective parents. The contribution to the SCA effects of all these hybrids pointed non-additive gene effects. Superior performance of these hybrids could be exploited through heterosis breeding. Earlier, Prasath and Ponnuswami (2008) reported that the cross MDU Y × Arka Abhir (good × poor) with high SCA effects of 7.21 was the best specific combiner for fruit weight. This was followed by S1 × Bydagi Kaddi (2.7) (good × average) and Arka Lohit × Bydagi Kaddi (1.72) (poor × good). do Rego *et al.* (2009) reported high positive and significant SCA effects for fruit weight by CB 4 × CB 24, CB 24 × CB 50, CB 38 × CB 46, CB 50 × CB 44 and CB 44 × CB 56. Tembhurne and Rao (2012) identified the cross ACA2/GOK-2 (0.8) and Singh *et al.* (2014) identified the hybrid PP 402 × PS 403 with high SCA effects for fruit weight. The current study results were in conformity to the findings of Khereba *et al.* (2008), do Nascimento *et al.* (2014), Lohithaswa *et al.* (2000), Marchesan *et al.* (2009),

Medeiros *et al.* (2014), Rodrigues *et al.* (2012), Geleta and Labuschagne, (2006) and Legesse (2000).

5.3.2.3.8 Fruits Plant^{-1}

The line L3 showed the highest positive GCA effects (23.64) followed by L6 (17.14), L7 (10.48), L1 (3.98) and L2 (2.23). Tester T1 showed high positive GCA effects of 22.04. These four lines and one tester were regarded as good combiners for fruits plant^{-1}. Two lines L4, L5 and two testers T2, T4 were regarded as poor general combiners for fruits plant^{-1}. Hasanuzzaman *et al.* (2012) reported that the maximum GCA effects for fruits plant^{-1} were recorded by CCA 19 (6), followed by BARI Morich 1 (3), CCA 5 (2) and CCA 2 (1) whereas Perez-Grajales *et al.* (2009) found Huatusco I with highest GCA effects (2.6), followed by Peru (2.5), Zorgolica (2.3) and Chiapas (1.4). do Rego *et al.* (2009) identified genotypes 44 (162.2), 56 (191.6) and 58 (39.7); Singh *et al.* (2014) identified DL 161 (65.36) and VR 521 (27.14); Ganefianti and Fahrurrozi (2018) identified Genotype C (KG6) (16.43); Rohini *et al.* (2017) identified LCA 625 (8.76); Lohithaswa *et al.* (2000) identified Pant C-1 (9.49); and Nsabiyera *et al.* (2012) identified parent 29 (9.16) and 35 (5.67) having positive and highly significant GCA effects as a good combiners for fruit plant^{-1}. The current study results were also in corroboration with the outcomes of Geleta and Labuschagne, (2006), Khalil and Hatem (2014), Legesse (2000), Medeiros *et al.* (2014), Rodrigues *et al.* (2012) and Payakhapaab *et al.* (2012).

Among the 28 hybrids, thirteen crosses expressed positive significant SCA effects and it ranged from 6.12 in the cross L1 × T3 to 38.17 in the cross L3 × T2. Top five hybrids exhibiting highly significant positive SCA effects were L3 × T2 (38.17), L7 × T3 (34.95), L6 × T1 (32.38), L4 × T1 (18.38) and L1 × T1 (17.21), and these hybrids were considered as good specific combiners for fruits plant^{-1}. Three hybrids namely L1 × T1, L2 × T1 and L6 × T1 involved both the parents with positive significant GCA effects. All these hybrids were good combiners with high × high parental GCA effects suggesting the influence of additive ×

additive gene effects on these hybrids. This suggested the involvement of additive gene effects for The heterotic performance of these crosses can be exploit through pure line breeding by fixing the additive gene effects. heterotic performance of these three crosses. It was indicated that population involving these parental lines in multiple crossing programme might be used for isolating desirable lines. Six hybrids have at least one parent with positively significant GCA effects and remaining four hybrids have neither of parents with significant positive GCA effects. This suggested that non-additive gene effects were predominantly involved in superior performance of these hybrids. The genetic variation exhibited by these crosses can be exploited through heterosis breeding. Earlier, do Rego *et al.* (2009) reported that the cross 44 × 56 showed maximum SCA effects (189.46) followed by 46 × 50, 4 × 24 and 24 × 50 for fruits plant^{-1}. Rohini *et al.* (2017) identified the cross Arka Lohit × LCA 334 with maximum SCA effects of 36.13 and the maximum reciprocal effects (31.54) was observed in the hybrid LCA 625 × K1. Perez-Grajales *et al.* (2009) reported that the cross combination Zong × Pue (8.65), Peru × Chis (8.11), Huall × Pue (3.20) and Zong × Peru (2.78) were the best specific combiners for fruits plant^{-1}. High SCA effects for fruits plant^{-1} was observed by Hasanuzzaman *et al.* (2012) in cross BARI Morich 1 × CCA 19 (195.19) and CCA 2 × CCA 19 (144.28); by Lohithaswa *et al.* (2000) in the cross Pant C-1 × Pusa Jwala; by Nsabiyera *et al.* (2012) in the cross 29 × 28 (26.9); by Ganefianti and Fahrurrozi (2018) in the cross Genotype C × Genotype F (29.62); and by Singh *et al.* (2014) in the cross CC 141 × VR 521 (113.46). The current results were also in close agreement with those reported by Patil (1997), Nandadevi and Hosamani (2003), Ajith (2004) and Sharma and Munish (2013).

5.3.2.3.9 Yield Plant^{-1} (g)

Lines L3 (128.41), L1 (91.23), L7 (51.20), L6 (38.35) and tester T1 (108.17) were regarded as good general combiners for yield plant^{-1}. Three lines, L2, L4, L5 and two testers, T3, T4 were considered as poor general combiners for yield plant^{-1}. Earlier, do Rego *et al.* (2009) reported that the maximum GCA

effects for yield plant^{-1} were recorded by parent 4 (783.8), followed by parent 24 (765.7) and parent 50 (741.9) whereas, Singh *et al.* (2014) found SL 461 (160.44), DL 161 (142.46) and PP 402 (139.16) as good general combiner for yield plant^{-1}. Prasath and Ponnuswami (2008) identified parental lines Bydagi Kaddi (144.37) and Co 4 (77.72) with high GCA effects for fresh fruit yield plant^{-1}. Hasanuzzaman *et al.* (2012) through diallel cross analysis found that parental lines CCA 5 (52.37), BARI Morich 1 (77.40) and CCA 19 (24.48) were good general combiners for yield plant^{-1}. Perez-Grajales *et al.* (2009) identified two landraces 'Pueble' and 'Chiapas' as better general combiners for fruit yield. Line CA1450 (0.11) and tester CA1447 (0.085) were identified as good combiners for fruit yield by Payakhapaab *et al.* (2012). do Nascimento *et al.* (2014) identified parents 137 and 132 with high GCA effects. The present results were also in accordance with the findings of Geleta and Labuschagne (2006); Legesse (2000) and Khalil and Hatem (2014).

Fourteen hybrids exhibited significant and positive SCA effects and therefore, regarded as good specific combiners. The crosses L3 × T2 (185.13), L5 × T3 (88.05), L2 × T4 (82.52), L1 × T1 (81.20) and L5 × T4 (80.63) were found to be good specific combiners with high SCA effects. Hybrids L1 × T1, L6 × T1 and L7 × T1 were from the parents with positive × positive significant GCA effects for both. This suggested the involvement of additive gene effects for heterotic performance of these crosses which can be fixed through selection for obtaining chilli genotypes with higher yield plant^{-1}. Six hybrids have at least one parent with significant and positive GCA effects and five hybrids involved parents without positive and significant GCA effects. This suggested the non-additive gene effects predominantly involved for superior performance of these hybrids which could be exploited through heterosis breeding. Earlier, Singh *et al.* (2014) reported that positive SCA effects for yield plant^{-1} were exhibited by CC 141 × VR 521 (484.41), SL 462 × US 501 (422.30), SD 463 × VR 521 (334.52), PP 402 × VR 521 (257.72), MS 341 × PP402 (256.72), SL 461 × VR 521

(230.65), DL 161 × EL 181 (224.39), DL 161 × PS 403 (219.02), SL 462 × PP 402 (220.29) and US 501 × SD 463 (224.27). do Rego *et al.* (2009) identified 4 × 24, 24 × 50, 44 × 56, 44 × 58 to be better specific combiners for fruit yield. Payakhapaab *et al.* (2012) reported that the crosses CA 1449 × CA 683 (0.131), CA 1449 × CA 1447 (0.108) and CA 1450 × CA 1448 (0.214) were the best specific combiners for fruit yield. Cross 137 × 77.2 (6.75) was identified as good specific combiner for fruit yield by do Nascimento *et al.* (2014); BARI Morich I × CCA 19 (706.32) and CCA 2 × CCA 19 (337.94) by Hasanuzzaman *et al.* (2012) and L2 × T7 (425.40) and L5 × T3 (314.70) by Saritha *et al.* (2005). Prasath and Ponnuswami (2008) reported that the cross Arka Lohit × S1 (284.34) with high SCA effects. This cross had low × low GCA effects of their parents. The hybrids S1 × Kaddi and MDU Y × Co 4 were the products of low × high GCA effects of their individual parent. Perez-Grajales *et al.* (2009) identified three crosses, Zongolica × Puebla, Huatusco II × Puebla, Puebla × Huatusco I with significant values of SCA effects for fruit yield.

5.3.2.3.10 Yield Plot^{-1} (kg/6.48m^2)

Lines L3 (3.57), L1 (2.56), L7 (1.45), L6 (1.09) and tester T1 (3.03) exhibited highly significant and positive GCA effects and were good general combiners for yield plot^{-1}. Three lines L2, L4, L5 and three testers T2, T3 and T4 were considered as poor general combiners for yield plot^{-1}. In line × tester analysis, Payakhapaab *et al.* (2012) identified line CA 1450 (0.702) and tester CA 1447 (0.545) with high significant GCA effects for yield.

The positive significant SCA effects ranged from 1.05 in the cross L2 × T1 to 5.14 in the cross L3 × T2. Top two hybrids with positive and significant SCA effects identified were L3 × T2 (5.14), L5 × T3 (2.40). The hybrids L1 × T1, L6 × T1 and L7 × T1 had both parents with positive significant GCA effects. These hybrids were representation of high (positive) × high (positive) GCA combination suggesting additive × additive gene interaction. These hybrids could produce desirable segregants as the additive gene effects are fixable. Six hybrids

had one parent with significant and positive GCA effects and remaining five hybrids involved parents without positive and significant GCA effects. The contribution to the SCA effects of all these hybrids denoted non-additive gene effects. Superior performance of these crosses could be exploited through heterosis breeding. These hybrids could produce desirable transgressive segregants in advanced generations. Payakhapaab *et al.* (2012) identified three superior specific combiners namely, CA 1449 × CA 683 (0.843), CA 1449 × CA 1447 (0.688) and CA 1450 × CA 1448 (0.136) with significant positive SCA effects. These results were in accordance with the outcomes of Pandian and Shanmugavelu (1992), Jagadeesh (1995), Ahmed *et al.* (1997), Shukla *et al.* (1999), Gandhi *et al.* (2000), Srivastava *et al.* (2005) and Chaudhary *et al.* (2013).

5.3.2.3.11 Vitamin C (mg 100 g^{-1})

Six lines and four testers showed significant GCA effects, among them three lines and three testers exhibited positive significant GCA effects. Lines L3 (17.76), L7 (10.43), L4 (8.18) and testers T1 (9.31), T2 (2.17), T3 (1.07) exhibited significant positive GCA effects and were considered as good general combiners for vitamin C content. Lines L1, L2, L6 and tester T4 registered significant negative GCA effects and were considered as poor combiners. Earlier, do Nascimento *et al.* (2014) found parent 1 (17.02), parent 77.1 (18.49) and parent 77.2 (5.76) as good general combiners for vitamin C content with positive and significant GCA effects. Geleta and Labuschagne (2006) reported maximum GCA effects for vitamin C in parent Mareko Shote (37.6), followed by PBC 142A (13.4) whereas, Rohini *et al.* (2017) found LCA625 (8.66) and Pusa Jwala (6.64) as good general combiner for vitamin C. The parent 'Big Dipper' (46.79) was identified as good general combiner for vitamin C by Khalil and Hatem (2014).

Thirteen crosses manifested positive significant SCA effects. The hybrids namely L5 × T4 (11.55), L3 × T2 (9.33), L5 × T3 (9.26), L1 × T1 (7.61) and L2 × T1 (7.52) showed high positive significant SCA effects and were regarded as best specific combiner for vitamin C. Five hybrids namely L3 × T2, L4 × T2, L4 × T3,

L7 × T1 and L7 × T3 possess both the parents with positive significant GCA effects. Thus, there is greater scope of developing true breeding lines with high content of vitamin C in fruits from the segregating populations generated from these five crosses. Five hybrids have one parent with significant and positive GCA effects and three hybrids involved parents without positive and significant GCA effects. This suggested that non-additive gene effects were predominantly involved in superior performance of these hybrids which could be exploited through heterosis breeding.

Earlier, Khalil and Hatem (2014) identified Big Dipper × LS 2-2, Big Dipper × W 5-15, Big Dipper × LS 5-6, Big Dipper × B 16-10, LS 5-6 × B 23-5, W 5-15 × LS 5-6 and W 5-15 × B 23-5. Geleta and Labuschagne (2006) identified Kalocsai 'M' Csereszny × Bakko Local, Kalocsai 'M' Csereszny × Syegedi 178; and Saritha *et al.* (2005) identified L1 × T9 (25.89) and L2 × T3 (38.95) crosses with high SCA effects for vitamin C content. The hybrid 77.1 × 77.2 (13.29) was found to be superior based on SCA effects while, the reciprocal hybrid 137 × 77.1 (30.38) was best performing based on RCA effects (do Nascimento *et al.*, 2014). The high performing hybrids for ascorbic acid based on SCA effects were K1 × LCA 334 (20.35) and LCA 334 × Pusa Jwala (20.36). The reciprocal hybrids Pusa Jwala × K1 (15.51) and PKM 1 × LCA 625 (19.32) were high performing hybrids based on RCA effects (Rohini *et al.*, 2017). The current results were also in corroboration with findings of Manju (2001), Bini (2004), Choudhary and Samadia (2004), Shirshat *et al.* (2007) and Dandunayak (2008).

5.3.2.3.12 Carotenoids (mg 100 g^{-1})

Two lines and one tester were good general combiners for carotenoids. Lines L4 (75.35), L2 (34.46) and tester T1 (5.82) exhibited highly significant and positive GCA effects and were good general combiners for carotenoids. Parental lines L1, L3, L5, L6 and tester T2 were regarded as poor general combiners for carotenoids. The line L7 and tester T3 were average general combiners for carotenoids. In a diallel analysis, Naresh *et al.* (2016) evaluated 45 F_1 hybrids and

their 10 parents for red, yellow and total carotenoids to determine the combining ability effects. The parental lines IHR 3476 (26.86), IHR 4506 (20.56) and IHR 4507 (6.05) were identified as good general combiners for red carotenoids; IHR 3849 (27.13), IHR 4503 (19.72), IHR 2451 (7.78) and IHR 4506 (3.66) for yellow carotenoids; IHR 3849 (25.82) and IHR 4506 (24.23) for total carotenoids.

Top five hybrids with positive and significant SCA effects identified were L6 × T3 (41.86), L3 × T2 (30.29), L3 × T1 (29.43), L2 × T4 (26.76) and L7 × T4 (21.18). Among twelve hybrids showing significant positive SCA effects, only one hybrid L4 × T1 had both parents with significant positive GCA effects for carotenoids indicating the predominant role of additive gene effects. From hybrid population derived from this cross, there could be possibilities of developing true breeding lines rich in carotenoids content. Five hybrids have one parent with significant and negative GCA effects and six hybrids involved parents without positive and significant GCA effects. The non-additive gene effects played predominant role in their expression and it could be exploited through heterosis breeding. Earlier, Naresh *et al.* (2016) identified best hybrids based on high SCA effects were IHR3476 × IHR500, IHR4503 × IHR2451 and IHR4507 × IHR4503 for yellow carotenoid content; IHR3476 × IHR500 and IHR4516 × IHR2451 for red carotenoid content; and IHR3476 × IHR500, IHR4507 × IHR4503, IHR4506 × IHR4507 and IHR4503 × IHR2451 for total carotenoid content. Present investigation were also in consonance with the findings of Olaiya and Poloamina (2013).

5.3.2.3.13 Coefficient of Infection (CI)

For coefficient of infection negative GCA and SCA effects are desirable. The lines L1 (-11.96), L4 (-5.47), L7 (-3.63) and testers T1 (-2.80), T3 (-4.05) were the best general combiners for low coefficient of infection. Lines L2 (3.78), L5 (12.68), L6 (5.84) and tester T2 (5.83) showed significant and positive GCA effects and were considered as poor general combiners for low coefficient of infection. Earlier, Bhutia *et al.* (2015) observed parents BCCK Sel-4 (-4.72), AC-

575 (-0.89) and Chaitali (-0.83) as good general combiners for low PDI (Per cent disease Index) of leaf curl disease. Muthuswamy *et al.* (2004) identified lines Pollakada local (-18.67) and Kottikulam local (-9.78), and tester Neyyatinkara local (-6.22) with high and negatively significant GCA effects for Vulnerability Index.

Hybrids L3 × T2 (-16.56), L6 × T1 (-14.90), L5 × T4 (-13.29) and L6 × T3 (-12.86) exhibited significant and negative SCA effects, therefore, they were considered as good specific combiners for low coefficient of infection. Hybrid L4 × T1, L7 × T1 and L7 × T3 had both parents with negatively significant GCA effects. This suggested the involvement of additive gene effects for heterotic performance of these crosses which could be fixed through selection for obtaining chilli genotypes with low coefficient of infection for leaf curl disease. Six hybrids had one parent with significant and negative GCA effects and three hybrids involved parents without negative and significant GCA effects. Thus, there is an considerable scope of developing true breeding lines with low coefficient of infection from the segregating populations generated from these crosses. Earlier, Bhutia *et al.* (2015) obtained hybrids with high SCA effects (low × low category) in desirable direction for PDI of leaf curl disease. Muthuswamy (2004) identified Jwalamukhi × Haripuram local, Jwalamukhi × Neyyatinkara local, Kottikulam local × Haripuram local and Pollakada local × Alampady local with high SCA effects in desirable direction for Vulnerability Index of leaf curl virus disease.

Overall, the parents identified on the basis of high GCA effects included L7, L2 and T1 for plant height; L3 and T1 for primary branches plant^{-1}; L5, L4 and T1 for days to first flower; L5 and L4 for days to first harvest; L4, L5 and T2 for fruit length; L4, L6, L5 and T3 for fruit girth; L3, L6 and T1 for fruits plant^{-1}; L1, L5 and T2 for fruit weight; L3, L1 and T1 for yield plant^{-1}; L3, L1 and T1 for yield plot^{-1}; L3, L7 and T1 for vitamin C; L4, L2 and T1 for carotenoids; and L1, L4, T3 and T1 for coefficient of infection. Summary depicting best parents and general combiners are presented in Table 28.

The crosses identified on the basis of high specific combining ability (SCA) effects included L1 × T2 (7.50), L1 × T1 (6.52), L3 × T1 (5.32) and L2× T3 (5.26) for plant height; L4 × T2 (1.29) and L3 × T2 (1.08) for primary branches plant^{-1}; L1 × T4 (-4.95), L3 × T2 (-2.83), L3 × T4 (-2.48) and L6 × T2 (-2.22) for days to first flower; L1 × T4 (-5.36), L3 × T2 (-3.22) and L7 × T1 (-2.11) for days to first harvest; L1 × T2 (1.36), L7 × T1 (1.09) and L 6× T3 (1.03) for fruit length; L2 × T3 (0.49), L7 × T2 (0.46), L3 × T1 (0.43) and L5 × T4 (0.42) .for fruit girth; L3 × T2 (38.17), L7 × T3 (34.95) and L6 × T1 (32.38) for fruits plant^{-1}; L7 × T1 (1.17), L6 × T3 (1.13) and L1 × T2 (0.95) for fruit weight; L3 × T2 (185.13), L5 × T3 (88.05), L2 × T4 (82.52), L1 × T1 (81.20) and L7 × T1 (73.30) for yield plant^{-1}; L3 × T2 (5.14) for yield plot^{-1}; L5 × T4 (11.55), L3 × T2 (30.29) and L5 × T3 (9.26) for vitamin C; L6 × T3 (41.86), L3 × T2 (30.29), L3 × T1 (29.43) and L2 × T4 (26.76) for carotenoids; L3 × T2 (-16.56), L6 × T1 (-14.90), L5 × T4 (-13.29), L6 × T3 (-12.86), L4 × T2 (-11.51) and L7 × T4 (-10.21) for coefficient of infection. The summary depicting best crosses, specific combiners and heterotic hybrids are presented in Table 29.

5.3.3 Estimation of Heterosis over Better Parent, Mid parent and the Standard Checks

Heterosis has been widely used in agriculture to increase yield and to broaden adaptability of hybrid varieties. Extensive work on various aspects of heterosis in vegetable crops has been carried out and tremendous improvement has been made in its exploitation over the past several years. In recent years, lot of emphasis is being laid on the exploitation of heterosis in vegetable crops. The phenomenon of heterosis has proved to be a potential tool in the hands of plant breeders for genetic enhancement of crop cultivars.

5.3.3.1 Plant Height (cm)

In view of productivity and crop management, plant height is important growth parameters. Out of 28 hybrids evaluated, 21 and 25 hybrids exhibited

significant positive heterosis over their better parent and mid parent, respectively. Twenty one and 26 hybrids exhibited significant positive standard heterosis over check hybrid CH-27 and Arka Harita, respectively. The high amount of positive significant heterosis manifested in the F_1 hybrids for plant height indicated the prevalence of dominant gene action in controlling this trait. The hybrids L1 × T4, L4 × T1, L5 × T1 showed high significant negative heterosis for plant height. Shorter plant height is positively associated with early yield. Such genotypes could fit well in multiple cropping systems and escape adverse climatic conditions due to shorter life span.

Earlier, Singh *et al.* (2014) reported the range of better parent heterosis from -3.11 to 32.21% for plant height. Bhutia *et al.* (2015) observed the extent of heterobeltiosis from -39.54 to 2.08%, the highest mid parent heterosis and heterobeltiosis was recorded from the hybrid BCCK Sel-4 × Kashi Anmol (18.30%) and BCCK Sel-4 × Chaitali (2.08%), respectively. Prasath and Ponnuswami (2008) observed the range of standard heterosis from 16.81 to 131.37%. Heterosis over better parent was also reported by Geleta and Labuschagne (2004), Tembhurne and Rao (2012) and Janaki *et al.* (2018). Marame *et al.* (2009) recorded the heterosis for plant height over better parent ranged from -47.70 to 18.24%, -40.80 to 25.65% over mid parent and from -63.07 to 7.29% over the standard check. Generally, chilli F_1 hybrids exhibited positive heterosis for plant height (Patel *et al.*, 1997; Shukla *et al.*, 1999; Nandadevi and Hosamani, 2003; Zate *et al.*, 2005; Shankarnag and Madalageri, 2006; Farag and Khalil, 2007; Chaudhary *et al.*, 2013; Janaki *et al.*, 2018).

5.3.3.2 Primary Branches Plant^{-1}

Primary branches contribute to the fruit yield attributes. The range of positive heterobeltiosis varied from 20.51% in the cross L6 × T1 to 99.17% in the cross L4 × T2 and only four hybrids exhibited significant positive heterobeltiosis. The highest mid parentheterosis was recorded in the hybrid L4 × T2 (103.40%). The highest standard heterosis was recorded from the hybrid L4 × T2 (69.50%)

and L4 × T2 (64.83%) over commercial hybrids CH-27 and Arka Harita, respectively. Bhutia *et al.* (2015) observed the extent of heterosis from -37.50 to 33.33% and -46.41 to 20.05% over mid parentand better parent, respectively. In a cross LCA-466 × LCA-315, Janaki *et al.* (2018) observed the higher magnitude of positive heterosis over better parent (12.69%), mid parent(21.29%) and standard checks Tejaswini (6.34%) and Indam-5 (18.90%). Marame *et al.* (2009b) reported the range of heterosis from -48.20% (P1 × 912) to 95.02% (P3 × P10) over mid parent and from -79.80% (P1 × P7) to 55.63% (P3 × P10) over better parent. The range of economic superiority over standard check ranged from -7.33% (P1 × P12) to 161.00% (P3 × P10).

5.3.3.3 Days to First Flower

For days to flower and days to harvest negative heterosis is desirable. In general, early flowering is an indication of early yield. The positive significant heterobeltiosis was lacking in all the hybrids which has great importance in chilli improvement program to get early flowering hybrids. This indicated the involvement of dominance in controlling this trait and hybrid breeding is effective in improving this trait. The cross combination L1 × T4 showed highest significant negative heterosis of -28.89% over better parent. The range of mid parent heterosis varied from -4.25 to -23.66%. Earlier, Singh *et al.* (2014) reported the heterobeltiosis ranging from -35.77 to -8.14% for days to flowering. Krishnamurthy *et al.* (2013) observed 21 hybrids with significant negative mid parent heterosis. The range of standard heterosis from -3.22 to 13.34% was reported by Prasath and Ponnuswami (2008). Geleta and Labuschagne (2004) observed the range of heterosis over mid parent and high parent from -18.7% (P1× P6) to 1.3% (P3 × P5) and -14.6 (P5 × P7) to 3.1 (P2 × P7), respectively.

The range of standard heterosis over the check hybrid CH-27 varied from -5.00% (L7 × T3) to -28.32% (L1 × T4). These results were in agreement with the findings of Geleta and Labuschagne (2004), they also reported the range of standard heterosis from -9.4% (P3 × P6) to -26.70% (P5 × P7). Significant

negative heterosis for days to flowering was also reported by Meshram and Mukewar (1986), Cao and Su (1988), Shankarnag and Madalageri (2006), Millawithanachchi *et al.* (2006) and Farag and Khalil (2007).

5.3.3.4 Days to First Harvest

An early harvest is profitable as the produce get better price in the market. For days to first harvest, heterobeltiosis ranged from -5.36% (L3 × T3) to -20.69% (L3 × T2) and 24 hybrids showed significant negative heterobeltiosis. Significant mid parent heterosis ranged from -3.64% (L3 × T3) to -19.30% (L3 × T2). Earlier, Singh *et al.* (2014) recorded nine hybrids with significant negative heterosis over better parent and they observed the magnitude of heterobeltiosis from -64.94% to 238.48% for early yield. Krishnamurthy *et al.* (2013) observed 63 hybrids with significant negative mid parentheterosis. Marame *et al.* (2009b) reported the range of heterosis from -29.80% (P5 × 96) to 6.80% (P10 × P12) over mid parentand from -31.50% (P5 × P6) to 6.80% (P10 × P12) over better parent. The range of economic superiority over standard check ranged from -23.59% (P5 × P6) to 11.60% (P7 × P11). Geleta and Labuschagne (2004) observed the range of heterosis over mid parentand better parent from -16.30% (P5× P7) to -0.90% (P4 × P5) and -11.6 (P5 × P7) to 3.1 (P1 × P4), respectively. The range of standard heterosis varied from -27.20% (L1 × T6) to 108.50% (L4 × T6). Recently, Janaki *et al.* (2018) reported the range of heterobeltiosis from -22.66 to 20.93% and mid parent heterosis from -18.21 to 24.92%. They observed the standard heterosis from -12.57 to 24.55% and -23.16 to 9.47% over standard check Tejaswini and Indem-5, respectively.

5.3.3.5 Fruit Length (cm)

Fruit length is an important trait in chilli destined for fresh consumption. The smaller fruits are more suitable for the production of dehydrated products (Klieber, 2001; Lannes *et al.,* 2007). Nineteen hybrids showed significant positive heterosis over better parent and the heterobeltiosis ranged from -24.11% in the

cross L5 × T1 to 74.71% in the cross L6 × T4. Twenty-six hybrids showed significant positive heterosis over mid parent and the hybrid L4 × T4 exhibited highest mid parentheterosis of 87.44%.

Bhutia *et al.* (2015) reported the extent of heterobeltiosis from -64.66 to 6.14% for fruit length while, Payakhapaab *et al.* (2012) observed the range of heterobeltiosis from -12.43 to 40.36%. Singh *et al.* (2014) reported the magnitude of heterobeltiosis from -5.13 to 39.64% and they produced 47 hybrids with significant and positive heterosis over their respective better parent. The range of standard heterosis was observed from -20.59 to 39.85% (Prasath and Ponnuswami, 2008). Under severe leaf curl disease conditions, Butcher *et al.* (2013) reported the significant positive heterobeltiosis in the crosses SP15 × SP128 (24.49%), SP79 × SP2 (23.74%), SP15 × SP5 (21.84%) and SP15 × SP57 (21.21%). Naresh *et al.* (2016) recorded the range of heterobeltiosis from -88.92 to 15.84%. They observed the highest heterosis of 31.36 and 33.33% over better parent and standard check, respectively. Significant positive heterosis for fruit length was also reported by Gopalakrishnan *et al.* (1987), Thomas and Peter (1988), Bhagyalakshmi *et al.* (1991), Singh *et al.* (1992), Patel *et al.* (1997), Ahmed *et al.* (1998), Zate *et al.* (2005), Farag and Khalil (2007), Perez-Grajales *et al.* (2009) and Janaki *et al.* (2018).

5.3.3.6 Fruit Girth (cm)

Fruits with larger girth have more potential to produce fruits with thicker pericarp and higher weight. The high genetic association of fruit weight with fruit width and pericarp thickness was reported by Ben-Chaim and Paran (2000). In the current study, the hybrids which showed higher fruit weight also had larger fruit girth. Thirteen hybrids showed significant positive heterobeltiosis and the range varied from 13.15% (L7 × T1) to 37.58% (L4 × T3). The mid parent heterosis varied from -15.63% (L5 × T2) to 45.39% (L2 × T3). Hybrids L4 × T3 (37.58%), L2 × T3 (32.66%), L6 × T3 (27.94%), L3 × T1 (24.47%) and L4 × T1 (23.83%) exhibited significant high positive heterosis over the better parent. Earlier, Bhutia

et al. (2015) observed the extent of heterobeltiosis and mid parent heterosis from -37.88 to 4.49% and -23.77 to 10.20%, respectively for fruit girth under severe leaf curl disease conditions. Chaudhary *et al.* (2013) identified three best hybrids namely Japanese Longi × DC-16, Japanese Long 1 × Punjab Lal and Kashi Sindhuri × R Line based on heterobeltiosis and mid parent heterosis for fruit width. Naresh *et al.* (2016) observed the range of heterobeltiosis from -32.76 to 21.53% for fruit width and the highest standard heterosis of 165.00% was exhibited by the hybrid IHR 4507 × IHR 3476. Recently, Ganefianti and Fahrurrozi (2018) reported the highest heterosis and better parent heterosis in the hybrids B (KG 2) × E (KG 5) and D (KG 4) × G (KG 7) for fruit length and fruit diameter. Positive as well as negative heterosis for fruit girth and fruit width has been reported by Payakhapaab *et al.* (2012), Singh *et al.* (2014), Prasath and Ponnuswami (2008), Butcher *et al.* (2013), Geleta and Labuschagne (2004) and Shrestha *et al.* (2011).

5.3.3.7 Fruit Weight (g)

Fruit weight contributes directly towards total fruit yield and has a key role in acceptance of chillies by the consumer. Ten hybrids showed significant positive heterosis over the better parent and the highest heterobeltiosis was exhibited by the cross L1 × T2 (51.65%) followed by L1 × T4 (39.47%), L1 × T1 (36.84%) and L6 × T3 (23.17). Heterobeltiosis from -28.65 to 57.52% has been reported by Singh *et al.* (2014), from 49.87 to 111.27 % by Singh and Hundal (2001), from -58.60 to 45.08% by Prasath and Ponnuswami (2008), from -38.63 to 64.96% by Butcher *et al.* (2013) and from -38.19 to 50.29% by Marame *et al.* (2009) for fruit weight. Heterobeltiosis up to 123.33%, up to 87.20% and up to 8.36% has been reported by Chaudhary *et al.* (2013), Shrestha *et al.* (2011) and Doshi and Shukla (2000), respectively.

Twenty-three hybrids showed significant positive heterosis over mid parent and the highest mid parent heterosis was exhibited by the hybrid L2 × T2 (65.27%). Heterosis over mid parent up to 123.33% has been reported by

Chaudhary *et al.* (2013), from -37.42 to 79.46% by Butcher *et al.* (2013) and from -32.94 to 74.29% by Marame *et al.* (2009) for fruit weight. The range of standard heterosis varied from 11.87 to 103.14% and 12.26 to 95.28% over check F_1 CH-27 and Arka Harita, respectively. Marame *et al.* (2009) reported the range of economic superiority over standard check from -50.22 to 1.31%.

5.3.3.8 Fruits Plant^{-1}

In chilli, number of fruits is the most important primary component of yield plant^{-1}. Heterosis for fruit yield has been attributed to heterosis for fruit plant^{-1}. Thus, it is imperative to have acceptable fruit weight coupled with increased fruit number to get higher fruit yield plant^{-1}. The observed range of heterobeltosis among hybrids was -48.49% (L1 × T2) to 64.77% (L7 × T3) and significant positive heterosis was observed in 12 hybrids over better parent. Hybrids L7 × T3 (64.77%), L6 × T1 (37.86%), L3 × T2 (37.33%) and L7 × T1 (33.22%) exhibited high positive significant heterobeltosis. Earlier, the range of heterobeltiosis was reported from 44.77 to 0.29% (Bhutia *et al.*, 2015); from -79.30 to 205.95% (Singh *et al.,* 2014); from -46.06 to 47.06% (Payakhapaab *et al.*, 2012); from -42.40 to 85.40% (Shrestha *et al.,* 2011); from -44.00 to 11.00% (Perez-Grajales *et al.,* 2009); and from -42.86 to 79.61% (Marame *et al.*, 2009b) for number of fruits plant^{-1}.

In the current study, the range of mid parent heterosis varied from -31.87 (L4 × T3) to 79.52% (L7 × T3) and the hybrids L7 × T3 showed highest mid parent heterosis of 79.52%. In chilli, mid parent heterosis for fruits plant^{-1} has been observed from -23.70 to 37.72% by Bhutia *et al.* (2015). The range of standard heterosis varied from -35.13% (L5 × T1) to 79.75% (L6 × T1) and -31.21% (L5 × T1) to 90.60% (L6 × T1) over CH-27 and Arka Harita, respectively. The range of standard heterosis from -22.94 to 137.61 and -37.50 to 136.36% was observed by Prasath and Ponnuswami (2008) and Marame *et al.* (2009b), respectively. Both positive and negative heterosis was recorded for this trait suggested the potentiality of heterosis breeding in chilli.

5.3.3.9 Yield Plant^{1} (g)

In any crop improvement program high fruit yield is one of the most important breeding objectives. Fruit yield is a variable parameter and depends not only on the parental combinations but also on the environmental conditions (Geleta and Labuschagne, 2004). Here, heterobeltiosis was of considerable magnitude ranging from -52.73% to 55.87% for yield plant^{-1}. Thirteen hybrids exhibited significant positive heterobeltiosis and the highest heterobeltiosis was exhibited by the hybrid L3 × T2 (55.87%) followed by L7 × T1 (50.46%), L1 × T1 (41.78%), L6 × T1 (37.03%) and L3 × T1 (23.00%). The high amount of positive heterosis manifested in these F_1 hybrids indicated the predominance of dominance gene action in controlling this trait and importance of heterosis breeding to improve this trait.

Heterobeltiosis to the extent of 71.06% (BCCG Sel-4 × AC-575) has been observed by Bhutia *et al.* (2015), up to 81.36% by Pandey *et al.* (1981), up to 73.03% by Payakhapaab *et al.* (2012), from -71.82 to 331.11% by Singh *et al.* (2014), up to 220.53% by Chaudhary *et al.* (2013), from -24.60 to 119.30 % by Shrestha *et al.* (2011), up to 161.79% by Marame *et al.* (2009) and from -22.00 to 51.00% by Perez-Grajales *et al.* (2009). High magnitude of heterobeltiosis for fruit yield have also been reported by Bhagyalakshmi *et al.* (1991), Ahmed and Muzafar (2000), Pandey *et al.* (2002), Singh and Chaudhary (2005) and Janaki *et al.* (2018).

Twenty-five hybrids showed significant positive mid parents heterosis and the range of mid parent heterosis ranged from -40.87% (L4 × T3) to 99.20% (L3 × T2). Mid parent heterosis from -40.83 to 106.23% was reported by Bhutia *et al.* (2015), from -52.04 to 163.80% by Marame *et al.* (2009b) and up to 264.47% by Chaudhary *et al.* (2013).

The range of standard heterosis varied from -19.37% (L4 × T3) to 148.07% (L3 × T2) and from -19.05% (L4 × T3) to 149.06% (L3 × T2) over check hybrids CH-27 and Arka Harita, respectively. Standard heterosis ranging

from -51.84 to 99.40% was observed by Prasath and Ponnuswami (2008) and from -52.67 to 92.05% by Marame *et al.* (2009b). Shrestha *et al.* (2011) reported the highest standard heterosis in the hybrid 5AVS7 × SP45 for fruit yield over the checks Special (67.50%), Fiesta (79.20%) and President (24.70%).

5.3.3.10 Yield Plot^{-1} (kg/6.48m^2)

The significant heterosis over better parent varied from -53.39% in the cross L4 × T3 to 56.04% in the cross L3 × T2 and 13 hybrids showed significant positive heterosis over the better parent. Highest heterobeltiosis for yield plot^{-1} was recorded in the hybrid L3 × T2 (56.04%). Twenty-one crosses showed significant positive heterosis over mid parent. The hybrid L3 × T2 showed highest heterosis over better parent, mid parent and standard checks. The range of heterosis varied from -19.78% (L4 × T3) to 150.32% (L3 × T2) and -19.46% (L4 × T3) to 151.34% (L3 × T2) over commercial hybrids CH-27 and Arka Harita, respectively. Payakhapaab *et al.* (2012) found heterosis and heterobeltiosis from -44.41 (CA 1449 × CA 1448) to 77.94% (CA 1445 × CA 683) and from -48.35 (CA 1449 × CA 1448) to 72.96% (CA 1445 × CA 683), respectively for green fruit yield. The range of standard heterosis was observed from -40.35 to 126.32% by Prasath and Ponnuswami (2008) for yield ha^{-1} and crosses which showed significant standard heterosis were Arka Abhir × Byadagi Kaddi, Byadagi Kaddi × Co-4, MDU Y × Co-4 and Co-4 × MDU Y.

5.3.3.11 Vitamin C (mg 100 g^{-1})

Chillies are rich in Vitamin C, it helps in forming protein that gives structure to bones, muscle, cartilage and blood vessels, and it also aids in absorption of iron (Legesse and Labuschagne, 2006). The observed range of significant heterobeltiosis among hybrids was -24.11% (L6 × T4) to 23.15% (L4 × T2). The hybrids L4 × T2 (23.15%), L5 × T3 (21.55%) and L4 × T1 (20.47%) exhibited high magnitude of heterobeltiosis. The hybrid L3 × T1 (43.28%) showed highest magnitude of mid parent heterosis. The hybrids L3 × T2, L3 ×

T1, L7 × T1, L4 × T2 and L3 × T3 showed high positive significant heterosis over both checks.

Heterobeltiosis from -69.44% (BCC-1 × AV-575) to 28.93% (BCCH Sel-4 × Chaitali) has been observed by Bhutia *et al.* (2015) and from -63.85 to 75.91% by Butcher *et al.* (2013). For Vitamin C, mid parent heterosis from -51.48% (BCC-1 × AC-575) to 64.64% (BCCH Sel-4 × AC-575) has been observed by Bhutia *et al.* (2015) and from -23.70 to 104.93% by Butcher *et al.* (2013). Geleta and Labuschagne (2004) reported the range of heterosis from -33.40 to 24.40%, -27.00 to 53.10% and -28.50 to 37.20% over better parent, mid parent and standard check, respectively.

5.3.3.12 Carotenoids (mg 100 g^{-1})

Twenty-one and and seven hybrids exhibited significant positive and negative heterobeltiosis, respectively. The range of heterosis over better parent varied from -12.30% in the cross L3 × T4 to 40.98% in the cross L6 × T3. The highest heterobeltiosis was observed in the cross L6 × T3 (40.98%). Naresh *et al.* (2016) observed 11 hybrids with positively significant heterobeltiosis and it ranged from -72.29% (IHR 4506 × IHR 2451) to 112.04% (IHR 4503 × IHR 2451) for total carotenoids.

In the current study, twenty-four hybrids showed significant positive heterosis over mid parent. The hybrid L4 × T2 exhibited highest significant positive mid parent heterosis of 76.82%. The mid parent heterosis up to 477.66% (IHR 4506 × IHR 3476) has been reported by Naresh *et al.* (2016) for total carotenoids. They also observed the standard heterosis up to 155.44% (IHR 4503 × IHR 500) for total carotenoids.

5.3.3.13 Coefficient of Infection (CI)

Out of 28 evaluated hybrids, nine hybrids showed significant negative heterosis over their respective better parents. Top hybrids L7 × T4 (-61.36%), L7 × T3 (-60.88%), L7 × T1 (-59.35%) and L6 × T1 (-56.52%) exhibited high

negative significant heterosis over the better parent. None of the hybrids displayed significant negative mid parent heterosis. Twenty-eight and twelve hybrids exhibited significant and negative standard heterosis over Arka Harita and CH-27, respectively. Hybrids namely L1 × T1, L7 × T4, L7 × T3 and L1 × T4 exhibited high negative significant standard heterosis over both check hybrids.

Bhutia *et al.* (2015) observed three hybrids with negative significant heterobeltiosis and they were BCCH Sel-4 × AC-575 (-47.61%), BCCH Sel-4 × Chaitali (-11.06%) and AC-575 × Chaitali (-3.98%) for PDI of leaf curl disease. They also observed the range of significant negative mid parent heterosis from -4.00% in the cross AC-575 × Chaitali to -65.15% in the cross BCCH Sel-4 × AC-575 for PDI of leaf curl disease. For Vulnerability Index, Muthuswamy (2004) observed top three hybrids *viz.,* Kottikulam local × Haripuram local (-28.21%), Pollakada local × Alampady local (-64.10%) and Pollakada local × Neyyatinkara local with significant negative standard heterosis. Recently, Darshan *et al.* (2017) conducted heterosis studies under severe leaf curl disease conditions in Vellayani and reported significant and negative heterosis of -100.00% over better parent, mid parent and standard check in the hybrids Vellayani Athulya × Pusa Sadabahar, Jwalasakhi × Pusa Sadabahar, Pant C-1 × Vellayani Athulya, Pusa Sadabahar × Ujwala and Pusa Sadabahar × Jwalasakhi.

Out of 28 F1 hybrids, seven hybrids exhibited high heterobeltiosis for yield plant-1. These hybrids were L3 × T2 (55.87%), L7 × T1 (50.46%), L1 × T1 (41.78%), L6 × T1 (37.03%), L3 × T1 (23.00%), L7 × T3 (19.49%) and L3 × T3 (19.28%). All of these hybrids except L3 × T1 and L3 × T3 had significant positive SCA effects along with high *per se* performance suggested the importance of non-additive gene action. The top hybrid L3 × T2 also showed significant and desirable heterobeltiosis for primary branches, days to flower, days to harvest, fruit length, fruits plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection. The second beset hybrid, L7 × T1 showed significant and desirable heterobeltiosis for plant height, days to first flower, days to first harvest,

fruit length, fruits plant^{-1}, fruit weight, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection. Similarly, the other hybrid L1 × T1 had significant and desirable heterobeltiosis for plant height, days to first flower, days to first harvest, fruit length, fruit girth, fruits plant^{-1}, fruit weight, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection. The cross combination L6 × T1 also showed significant and desirable heterobeltiosis for plant height, primary branches plant^{-1}, days to first flower, days to first harvest, fruit length, fruit girth, fruits plant^{-1}, yield plot^{-1}, carotenoids and coefficient of infection. The F1 hybrid, L3 × T1 exhibited significant and desirable heterobeltiosis for plant height, days to first flower, days to first harvest, fruit length, fruit girth, fruits plant^{-1}, fruit weight, yield plot^{-1}, vitamin C and carotenoids. The cross combination, L7 × T3 also exhibited significant and desirable heterobeltiosis for plant height, fruit length, fruits plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection. The F1 hybrid, L3 × T3 exhibited significant and desirable heterobeltiosis for plant height, days to first flower, days to first harvest, fruit length, fruits plant^{-1}, fruit weight, yield plot^{-1} and vitamin C. The hybrids which showed superior performance for yield and yield attributes are presented in the Plate 17a to 17d.

Two hybrids, *viz.*, L4 × T2 and L4 × T1 exhibited high heterobeltiosis for vitamin C and carotenoids. The hybrid L4 × T2 also exhibited significant and desirable heterobeltiosis for plant height, primary branches, days to first flower, days to first harvest, fruit length, fruit girth and fruit weight. The cross combination L4 × T1 exhibited significant and desirable heterobeltiosis for days to first flower, days to first harvest, fruit length and fruit girth.

5.3.4 Incidence of Pest and Disease

5.3.4.1 Incidence of Leaf Curl Disease

All the four testers were symptomless and among seven lines, two were moderately resistant and remaining five were moderately susceptible. For chilli leaf curl disease, Bhutia *et al.* (2015) reported the minimum per cent disease

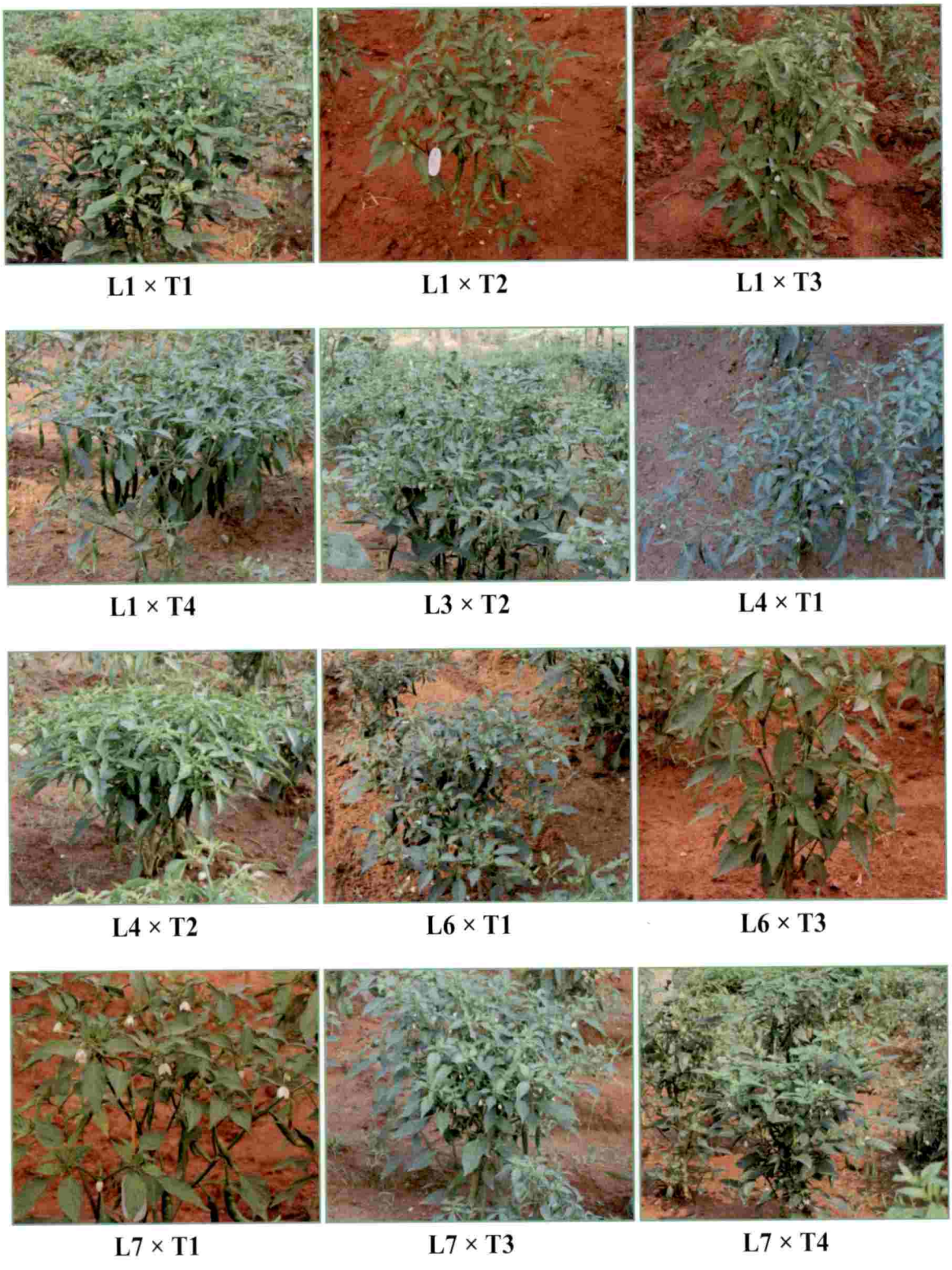


Plate 16. Moderate resistant (MR) reaction of F_1 hybrids under field conditions

(A) (B)

(C) (D)

(E) (F)

Plate 17(a): View of some identified promising crosses of chilli

(A) & (B): L3 (CHIVAR-6) × T2 (Sel-4) (C) & (D): L1 (CHIVAR-3)×T1 (Sel-3)

(E) & (F): L7 (CHIVAR-10) × T1 (Sel-3)

(A) (B)

(C) (D)

(E) (F)

Plate 17(b): View of some identified promising crosses of chilli

(A) & (B): L6 (Keerthi) × T1 (Sel-3) **(C) & (D): L3 (CHIVAR-6)×T3 (Sel-6)**

(E) & (F): L1 (CHIVAR-3)×T4 (CHIVAR-1)

(A)

(B)

(C)

(D)

(E)

(F)

Plate 17(c): View of some identified promising crosses of chilli

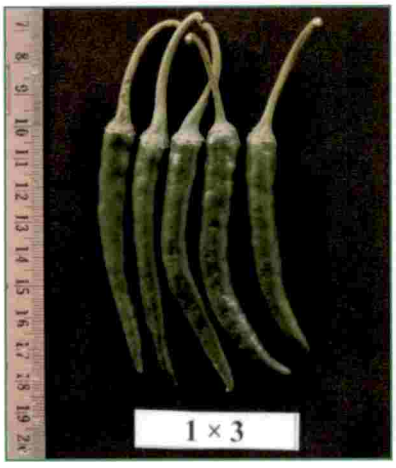
(A) & (B): L7 (CHIVAR-10)×T3 (Sel-6) (C) & (D): L6 (Keerthi) × T3 (Sel-6)

(E) & (F): L4 (CA-32) × T1 (Sel-3)

(A)

(B)

(C)



(D)

(E)

(F)

Plate 17(d): View of some identified promising crosses of chilli

(A) & (B): L4 (CA-32) × T2 (Sel-4) (C) & (D): L1 (CHIVAR-3) × T3 (Sel-6)

(E) & (F): L5 (Vellayani Athulya) × T3 (Sel-6)

index (PDI) of 9.22% in the parent BCCH Sel-4 whereas, maximum PDI was displayed by the parent Kashi Anmol (21.30%).

Among 28 F_1 hybrids, none was completely free from ChiLCV incidence. Twelve hybrids showed moderately resistant reaction and the CI of disease ranged from 13.90 in the cross L3 × T2 to 18.13 in the cross L1 × T3. The crosses which showed moderate resistant reaction to ChiLCV included L1 × T1, L1 × T2, L1 × T3, L1 × T4, L3 × T2, L4 × T1, L4 × T2, L6 × T1, L6 × T3, L7 × T1, L7 × T3, L7 × T4 (Plate 16).

Darshan *et al.* (2017) reported the Vulnerability Index (V.I) for leaf curl disease from 0.00 to 49.29% and 0 to 53.33% for parents and hybrids, respectively. In six hybrids they observed 0.00% V.I. Bandla (2015) observed the V.I range from 0.00 to 98.20% in capsicum germplasm, whereas Muthuswamy (2004) observed the V.I range from 23.33 to 83.33% in hybrids.

The resistant check hybrid CH-27 was moderately resistant with 18.49 CI and the variety Kashi Anmol was highly susceptible. The hybrid Arka Harita showed susceptible reaction.

5.4 GENERATION MEAN ANALYSIS

5.4.1 Estimation of Scaling Test, Gene Effects

5.5.1.1 Plant Height (cm)

Higher plant height and long fruiting duration can lead to higher fruit yield in conducive environment for growth and fruiting over a longer time frame. In cross 1, positive significance was observed for A, B and C scales, of which scale A had highest magnitude which indicated that F_2 plants were longer than backcrosses. All scales (A, B, C and D) were significant in cross 2 of which scale C had highest value which indicated that F_2 produced higher plants than backcross. The additive gene effects were found negative and significant in all three crosses. The dominance gene effects had positive significant values in crosses

1 and 3, while they were negative in cross 2. Cross 1 exhibited dominance [h] gene effects and additive × additive [i] gene interactions in the desirable direction coupled with duplicate epistasis indicating the possibility of heterosis breeding as well as reciprocal recurrent selection and biparental mating followed by selection for desirable segregants in subsequent generations.

Opposite signs for dominance [h] gene effect and dominance × dominance [l] interaction were observed in the cross 1 and cross 2, which implied the presence of duplicate type of gene action. Duplicate epistasis was observed in cross 1 and 2 in which selection should be delayed in the segregating generations. Duplicate type of epistasis will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistasis effects (Dhall and Hundal, 2006). The same signs of [h] and [l] in the cross 3 advocated the presence of complementary type of gene action. Complementary epistasis and significant additive × additive gene action in cross 3 indicated that simple selection may be followed for taller chilli plants.

While working in sweet papper, Devi and Sood (2018) have reported higher magnitude of dominance gene effects and additive × additive [i] gene interactions couple with duplicate type of epistasis in the cross EC-464115 × KS and EC-464107 × SH-1 for plant height. However, Hasanuzzaman and Golam (2011) have reported the involvement of additive, dominance, additive × additive, dominance × dominance gene actions for plant height. They observed the duplicate type of epistasis in the cross CCA 5 × CCA 15.

5.5.1.2 Primary Branches Plant^{-1}

In cross 1 and 2, scale D had highest magnitude which suggested that F_2 is superior to backcrosses. In cross 3, scale D had highest magnitude which implies that F_2 produced more primary branches than parents. For primary branches plant^{-1} six parameter model indicated negative and significant additive [d] gene effects in cross 1 while significant and positive dominance [h] gene effects in cross 3. Additive × additive [i] and additive × dominance [j] gene interactions were

positively significant in cross 3. In cross 2, dominance × dominance [l] gene interaction was positively significant. Additive × dominance [j] and dominance × dominance [l] gene interactions were found positively significant in cross 1. The cross 3 showed the high magnitude of additive × additive [i] gene interaction suggested the importance of progeny selection in this cross. The higher values of 'l' along with duplicate type of epistasis in cross 2 suggested greater role of dominance in expression of this trait, hence selection in the later generations will be effective. The current results were in line with the findings of Navhale *et al.* (2017) who have observed higher values of 'l' with duplicate epistasis gene action in three crosses (Jwala × DPL-C-5, Jwala × Parbhani Tejas and Jwala × AKC-08-95-05). However, Anandhi and Khader (2011) observed complementary type of epistasis in the cross Mavelikkara Local × Jwalasakhi and Nenmara Local × Vellayani Athulya.

5.5.1.3 Days to First Flower

In cross 1, scale A, B and C were significant in favorable negative direction. Scales A, C and D were found negatively significant in cross 2. In cross 3, scales A, B and D were significant, of which scale D was in positive direction. The scale B had highest magnitude in negative direction in the cross 1 and 3 which indicated that F_1 is better than P_2. In cross 2, scale C showed highest magnitude in negative direction which suggested that F_2 is better than parents.

The additive [d] gene effects were negative and significant in the cross 1 and 2. Cross 1 and 3 exhibited significant negative dominance [h] gene effect. For days to first flowering, the cross 1 and 2 showed dominance [h] gene effects and additive × additive [i] gene interaction in desirable direction coupled with presence of duplicate type of epistasis suggested the possibility of heterosis breeding as well as reciprocal recurrent selection and biparental mating followed by selection in getting desirable segregants in subsequent generations. Additive [d], additive × dominance [j] and dominance × dominance [l] type of gene interactions in cross 2 were found to be negatively significant. The early

flowering in this cross could be improved through simple selection, pedigree selection, heterosis breeding and delayed selection as this trait governed by both additive and non-additive gene interactions. Devi and Sood (2018) reported significant negative values for 'h', 'i' and 'j' in the cross EC-464107 × KS; 'h' and 'i' in the cross EC-4641159 × KS; and 'j' and 'l' in the cross EC-464107 × EC-464115. All three hybrids showed duplicate type of epistasis. Hasanuzzaman and Golam (2011) observed high negative significant values for 'i' coupled with duplicate type of epistasis in the cross 2 and 4. For days to first flower, complementary type gene action was observed in the cross Jwala × DPL-C-5 by Navhale *et al.* (2017) and in the cross CCA 5 × CCA 11 by Hasanuzzaman and Golam (2011).

5.5.1.4 Days to First Harvest

The cross 1 and 2 showed high magnitude of scale C in favorable negative direction. This suggested that F_2 is better than parents. The scale B was negatively significant with high magnitude which implies that F_1 is better than P_2. Additive [d] gene effects in the cross 1 and 2; dominance [h] gene effects in all crosses; additive × additive [i] gene interaction in cross 1 and 3; and additive × dominance [j] and dominance × dominance [l] type of gene interactions in all crosses were found significant. The opposite signs of [h] and [l] in all three cross combinations indicated duplicate type of gene interaction. Number of days to harvest could be improved through pedigree selection, simple selection, heterosis breeding and delayed selection as this trait is governed by both additive, non-additive as well as non-allelic gene interactions.

Dhall and Hundal (2006) reported three crosses PBC830 × LLS, PBC830 × Ooty Round and PBC830 × ATG with higher values of dominance gene effects coupled with duplicate type of epistasis for early yield. The complementary type of epistasis was observed in the cross PBC830 × S-2530. They concluded that early yield was controlled by both additive and non-additive gene effects. Hasanuzzaman and Golam (2011) observed high magnitude of dominance [h]

gene effects coupled with duplicate epistasis in four crosses for days to green fruit maturity. Duplicate epistasis was also observed by Navhale *et al.* (2017) in three cross for days to first picking. Whereas, complementary type of epistasis was observed in the cross EC-464107 × EC-464115 and EC-464107 × SH-I for days to first picking by Devi and Sood (2018).

5.5.1.5 Fruit Length (cm)

Fruit length is an important trait in deciding consumer preference. In the cross 1, significance was observed for scales A, B, C and D among which scales A, B and C were in favorable positive direction of which scale C had the highest magnitude which indicated that F_2 produced longer fruits than parents. In cross 2, all four scales were significant of which scale D was in favorable positive direction. This suggested that F_2 fruits are longer than fruits from backcrosses.

In the cross 1 and 3 Additive [d], dominance [h] and additive × additive [i] type of gene interactions were found positively significant. The magnitude of dominance [h] gene action was high in these crosses indicating the probability of heterotic combination for longer fruits. Devi and Sood (2018) also observed high dominance gene effects in the cross EC-464107 × EC-464115.

In the cross 2, additive [d], dominance [h], additive × dominance [j] and dominance × dominance [l] type of gene interactions were positive and significant. The magnitude of dominance × dominance [l] gene interaction was high (with relatively lower magnitude of additive × dominance [j] gene interaction) along with complementary gene action in the cross 2. This indicates the importance of exploiting hybrid vigor in this cross.

Bento *et al.* (2016) observed the involvement of major gene with additive and dominance gene effects for fruit length. Devi and Sood (2018) observed the presence of duplicate type of epistasis coupled with dominance gene effects (negative direction) in the cross EC-464115 × KS and they suggested biparental approach to select desirable segregants with longer fruits. The duplicate type of epistasis coupled with high magnitude of dominance [h] gene effects was

observed in the cross BARI Morich 1 × CCA 19 and CCA 15 × CCA 19 (Hasanuzzaman and Golam, 2011). The complementary type of epistasis was observed in the cross Jwala × Parbhani Tejas, while duplicate epistasis observed in the cross Jwala × DPL-C-5 and Jwala × AKC-08-95-05 (Navhale *et al.*, 2017).

5.5.1.6 Fruit Girth (cm)

Fruit girth is an important character as that of fruit length. In cross 1, positive significance was observed for scales A, B and C of which scale A had highest magnitude which implies that F_1 produced higher fruit girth than P_1. Further analysis showed that additive [d], dominance [h], additive × additive [i] and additive × dominance [j] gene interactions were in favorable positive direction. Among them dominance [h] gene effects had highest magnitude coupled with duplicate epistasis. Hence hybridization followed by selection would improve this trait in the cross 1.

In cross 2, scale D was positively significant which indicates that F_2 is better than backcrosses. In six-parameter model additive [d], additive × dominance [j] and dominance × dominance [l] type of gene interactions were significant in favorable positive direction of which dominance × dominance [l] gene interaction had highest magnitude. This pointed out the possibility of obtaining fruits with maximum girth through hybridization and selection in cross 2.

Scale B was positively significant in the cross 3 suggesting F_1 better than P_2. In this cross, additive [d], dominance [h] and additive × additive [i] gene interactions were positively significant. The magnitude of dominance [h] gene effects and additive × additive [i] gene interaction was high (with relatively low magnitude of additive gene effects). This suggested the involvement of both additive and non-additive gene action in the inheritance of this trait. Hence resorting to recombination breeding would improve the trait.

Bento *et al.* (2016) reported the predominance of additive variance for fruit diameter. Hasanuzzaman and Golam (2011) observed the involvement of

additive, dominance and all type of epistasis in the inheritance of fruit width. Duplicate type of epistasis was observed in three crosses, CCA 5 × CCA 15, BARI Morich 1 × CCA 19 and CCA 5 × CCA 11. Anandhi and Khader (2011) observed high magnitude of 'l' coupled with duplicate epistasis in the cross Mavelikkara Local × Jwalasakhi and Nenmara Local × Vellayani Athulya for fruit width.

5.5.1.7 Fruit Weight (g)

For fruit weight positive significance was observed for all the scales (A, B, C and D) of which scale C had highest magnitude in cross 1. This implies that F_2 is better than parents. In cross 1 additive [d] genic effects and dominance × dominance [l] gene interaction were positively significant with no epistasis. The magnitude of dominance × dominance [l] gene interaction was high compared to additive gene effects. This suggested the predominance of non-additive gene action in the inheritance of fruit weight in the cross 1.

All four scales were significant in cross 2 among which scale C and D were in favorable positive direction. Significant values of C and D scales in cross 2 pointed out the presence of dominance × dominance [l] and additive × additive [i] type of gene interactions, respectively. Additive [d], additive × dominance [j] and dominance × dominance [l] gene interactinos were found positive and significant. Predominance of dominance × dominance [l] gene interaction is evident from the high magnitude of scale C. Predominance of dominance × dominance [l] gene interaction was earlier reported by Hasanuzzaman and Golam (2011) in the cross CCA 5 × CCA 11 and CCA 15 × CCA 19.

In cross 3 additive [d] gene effects and dominance × dominance [l] gene interaction were significant in favorable positive direction. The magnitude of dominance × dominance [l] gene interaction was high compared to additive gene effects indicating a fair chance for development of larger fruits through heterosis breeding.

Earlier, Marame *et al.* (2009a) reported duplicate epistasis in four crosses namely PBC 972 × PBC 223, ICPN 10#5 × PBC 731, Marekofana × PBC 972 and Bakolocal × ICPN 10#5 for fruit weight. The majority of duplicate epistasis in these crosses were due to favorable over-dominance (+h) effects. Dhall and Hundal (2006). observed high magnitude of dominance gene effects coupled with duplicate epistasis in five crosses namely PBC830 × S-2530, PBC830 × LLS, PBC830 × Ooty Round, PBC830 × ATG, PBC830 × Pepsi 7 for fruit weight.

5.5.1.8 Fruits Plant^{-1}

In cross 1, scales A, B, C and D were significant among which scale B was in the positive direction which implies that F_1 is better than P_2. Further analysis showed the significance of additive [d], dominance [h] and dominance × dominance [l] type of gene interactions in positive direction. The dominance × dominance [l] gene interaction had highest magnitude followed by dominance [h] gene effects. This suggested that hybridization followed by selection would improve fruit number plant^{-1} in chilli.

Significance was observed for all scales in cross 2 among which scale C had the highest magnitude. Further analysis showed the significance of additive and non-additive gene actions of which dominance (h) gene effects had the highest magnitude. Significance of dominance (h) gene effects was in corroboration with earlier findings by Devi and Sood (2018) in the crosses EC-464107 × KS, EC-464115 × KS and EC-464107 × SH-I.

In cross 3, all scales were significant among which scale C and D were in positive direction. Additive [d] and dominance [h] gene effects and their interaction components were significant in cross 3 among which additive [d], additive × dominance [j] and dominance × dominance [l] gene interactions were in positive direction. The magnitude of dominance × dominance [l] gene interaction was highest coupled with duplicate epistasis.

Anandhi and Khader (2011) reported high magnitude of 'h' and 'l' with complementary epistasis in the cross Nenmara Local' × 'Vellayani Athulya and

with duplicate epistasis in the cross Mavelikkara Local × Jwalasakhi. The high magnitude of 'h' and 'l' with complementary type gene interaction was observed by Hasanuzzaman and Golam (2011) in the cross CCA 5 × CCA 15 and BARI Morich 1 × CCA 19. Dhall and Hundal (2006) reported duplicate type of epistasis in six cross combinations whereas, Devi and Sood (2018) observed complementary epistasis in the cross EC-464107 × EC-464115. The duplicate epistasis was operative in the cross Jwala × AKC-08-95-05 and Jwala × Parbhani Tejas, complementary epistasis observed in cross Jwala × DPL-C-5 for fruits plant^{-1}(Navhale *et al.*, 2017).

5.5.1.9 Yield Plant^{-1} (g)

The simple additive-dominance model was found inadequate in all the crosses as indicated by significant values of A, B, C and D scales in all three crosses. In the cross 1 and 2 scales C and D were in the favorable positive direction indicated the presence of dominance × dominance [l] and additive × dominance [j] type of interactions, respectively.

In the cross 1 and 2, the magnitude of scale C was high which indicated that F_2 is better than parents. All the genetic components were significant in all three crosses. In the cross 1 and 2, additive [d], dominance [h] and dominance × dominance [l] gene interactions were in the favorable positive direction of which dominance × dominance [l] gene interaction had the highest magnitude coupled with complementary epistasis. This suggested the usefulness of exploiting hybrid vigor in these crosses.

In the cross 3, scale D magnitude was highest which suggested that F_2 is better than backcrosses. Additive [d] and dominance × dominance [l] gene interactions were in the favorable positive direction of which dominance × dominance [l] gene interaction had the highest magnitude coupled with duplicate epistasis. This indicated the possibility of heterosis breeding and recurrent selection to get desirable segregants with high fruit yield in subsequent generation.

Anandhi and Khader (2011) reported high magnitude of dominance gene effects with complementary epistasis in the cross Nenmara Local' × 'Vellayani Athulya and Mavelikkara Local × Jwalasakhi. The duplicate epistasis in the cross Jwala × DPL-C-5 and Jwala × Parbhani Tejas was observed by Navhale *et al.* (2017) for green fruit yield plant^{-1}. The high magnitude of dominance [h] and dominance × dominance [l] gene interactions coupled with complementary epistasis was observed in the crosses CCA 5 × CCA 15, BARI Morich 1 × CCA 19 and CCA 5 × CCA 11 for yield plant^{-1} (Hasanuzzaman and Golam, 2011). Devi and Sood (2018) observed dominance [h] gene effects in the crosses EC-464107 × KS, EC-464115 × KS and EC-464107 × SH-I, while in the cross EC-464107 9 EC-464115 dominance [h] and dominance × dominance [l] gene interactions were predominant.

5.5.1.10 Yield Plot^{1} (kg/6.48m^{2})

For yield plot^{-1} A, B, C and D scales were significant in the cross 1 and 2 among which scale A, B and C were in positive direction. The scale C had the highest magnitude which implies that F_2 is better than parents. In the cross 3, scale D was significant and positive which implies that F_2 is better than backcrosses.

All genetic components were significant in all three crosses. Additive [d], dominance [h] and dominance × dominance [l] gene interactions were in the favorable positive direction of which dominance [h] and dominance × dominance [l] gene interactions were having high magnitude coupled with complementary epistasis in all three crosses. In chilli predominance of non-additive gene action was also reported by Payakhapaab *et al.* (2012) for yield and by Prasath and Ponnuswami (2008) for dry yield ha^{-1}.

5.5.1.11 Vitamin C (mg 100 g^{-1})

In the cross 1, significance was observed for the scales A, B, C and D among which scale C and D were in the favorable positive direction implies the

presence of dominance × dominance [l] and additive × dominance [j] type of interactions, respectively. Scale D had the highest magnitude in the cross 1 indicating that F_2 is better than backcrosses. In cross 1, all genetic components displayed significance among which additive [d] and dominance × dominance [l] gene interactions were found to act in positive direction. The highest magnitude was exdpressed by dominance × dominance [l] gene interaction.

In the cross 2, scale D was significant and positive which indicated that F_2 is better than backcrosses. All genetic components were significant, of which dominance × dominance [l] gene interaction was in favorable positive direction.

Significance was observed for all the scales in the cross 3 among which scale B, C and D were in positive direction and the scale C had highest magnitude in the cross 3 which indicated that F_2 is better than parents. All genetic components displayed significance, among which additive [d] and dominance × dominance [l] gene interactions were found to act in positive direction. Dominance × dominance [l] gene interaction had highest magnitude. In all three crosses, dominance × dominance [l] gene interaction was predominant coupled with duplicate epistasis. Dominance gene action played an important role in the inheritance of this trait. Hence heterosis breeding and delay selection would be effectively used in these crosses. The predominance of non-additive gene action for the control of Vitamin C (Rohini *et al.,* 2017; Bhutia *et al.,* 2015) has also been noted. The additive gene action in controlling the Vitamin C content was reported by Khalil and Hatem (2014) and do Nascimento *et al.* (2014).

5.5.1.12 Carotenoids (mg 100 g^{-1})

All four scales were significant in all three crosses. In cross 1, scale A, B and C were in positive direction of which scale B had the highest magnitude which implied that F_1 is better than P_2. Dominance [h] gene effects and additive × additive [i] gene interaction were significant and positive of which dominance [h] gene effects had highest magnitude coupled with duplicate epistasis. Heterosis breeding would improve the trait in this cross.

In the cross 2, all four scales were significant among which scale B and C were in positive direction. Dominance [h], additive [d] and additive × additive [i] gene interaction were significant and positive of which dominance [h] gene effects had highest magnitude coupled with duplicate epistasis. Presence of epistatic variance indicated that recombination breeding could improve the trait in the cross 2.

Significance of scale C and D in cross 3 pointed out the presence of dominance × dominance [l] and additive × additive [i] type of gene interactions, respectively. The scale D had highest magnitude which indicated that F_2 is better than backcrosses. In the cross 3, dominance [h] gene effects and dominance × dominance [l] gene interaction were positively significant of which dominance × dominance [l] gene interaction had the highest magnitude. Predominance of non-additive gene effects coupled with duplicate epistasis indicated that heterosis breeding could improve the trait in the cross 3. Earlier, Maradana *et al.* (2016) observed high magnitude of dominance × dominance [l] gene interaction in the cross LCA-764 × LCA-315 for total carotenoids. They reported duplicate epistasis in the cross LCA-710 × HC-28 and LCA-712 × HC-28 and complementary epistasis in the cross LCA-712 × LCA-710 and LCA-764 × LCA-315.

5.5.1.13 Coefficient of Infection (CI)

Significance of scale C and D in all three cross indicated the presence of dominance × dominance [l] and additive × dominance [j] type of interactions, respectively. In the cross 1, dominance [h] gene effect, additive × additive [i] and additive × dominance [j] gene interactions were in favorable negative direction of which additive × additive [i] gene interaction had the highest magnitude coupled with duplicate epistasis. Improvement of this trait could be through recombination breeding or recurrent selection

In cross 2 and 3, scales A, B, C and D were significant. All genetic components were significant among which dominance [h] gene effect, additive ×

additive [i] and additive × dominance [j] gene interactions were in favorable negative direction in the cross 2 and 3. Duplicate nature of epistasis in all the three crosses were indicated by the opposite signs of dominance [h] and dominance × dominance [l] effects. This indicated the possibility of heterosis breeding as well as reciprocal recurrent selection for desirable segregants with low Coefficient of Infection in subsequent generations.

All genetic components were significant and coupled with complementary epistasis in the cross Mavelikkara Local × Jwalasakhi and duplicate epistasis in the cross Nenmara Local × Vellayani Athulya for leaf curl virus scores under leaf curl disease severity conditions in Vellayani (Anandhi and Khader, 2011). Based on predictability ratio (< 0.60) Bhutia *et al.* (2015) observed the involvement of non-additive gene effects in conditioning of PDI of leaf curl virus. Muthuswamy (2004) observed significance of both additive and non-additive gene interactions in desirable direction for leaf curl incidence (V*ulnerability Index*) and they recommended recombination breeding or recurrent selection for the improvement of this trait. Presence of non-additive gene action was also reported earlier by Darshan *et al.* (2017) under severe leaf curl disease severity conditions.

Table 28: Summary depicting best parent and general combiner

Characters	Best parent *Per se*	Best general combiners
Plant height (cm)	L6 (56.00), L2 (51.76), L7 (48.00) and T1 (55.03)	L7 (10.91), L2 (4.31) and T1 (2.14)
Primary branches plant^{-1}	L6 (4.33cm), L5 (3.80), T1 (4.22) and T3 (4.11)	L3 (0.34) and T1 (0.49)
Days to first flower	L5 (26.79), L4 (28.74), T3 (33.27) and T2 (34.32)	L5 (-2.92), L4 (-1.90) and T1 (-0.83)
Days to first harvest	L4 (48.00), L5 (48.00), T3 (54.00) and T4 (56.00)	L5 (-3.31) and L4 (-2.07)
Fruit length (cm)	L5 (8.43), L4 (6.35), T3 (6.10) and T2 (5.52)	L4 (2.30), L5 (0.38) and T2 (0.65)
Fruit girth (cm)	L5 (4.12), L7 (3.42), T2 (3.64) and T3 (3.11)	L4 (0.34), L6 (0.32), L5 (0.24) and T3 (0.27)
Fruit weight (g)	L5 (7.45), L4 (4.60), T2 (4.40) and T3 (4.25)	L1 (0.72), L5 (0.55) and T2 (0.47)
Fruits plant^{-1}	L1 (148.00), L6 (133.00), L2 (132.00) and T3 (84.00)	L3 (23.64), L6 (17.14) and T1 (22.04)
Yield plant^{-1} (g)	L4 (584.15), L1 (580.22), L3 (545.00), L6 (544.50) and T3 (349.67)	L3 (128.41), L1 (91.23) and T1 (108.17)
Yield plot^{-1} (kg)	L4 (16.16), L1 (16.05) and T3 (9.50)	L3 (3.57), L1 (2.56) and T1 (3.03)
Vitamin C (mg100^{-1} g)	L3 (114.67), L7 (112.00) and T4 (93.67)	L3 (17.76), L7 (10.43) and T1 (9.31)
Carotenoids (mg100^{-1} g)	L2 (272.00), L4 (263.00), L7 (250.67) and T4 (222.67)	L4 (75.35), L2 (34.46) and T1 (5.82)
Coefficient of infection (%)	L4 (16.92), L1 (18.85), T1 (0.00), T2 (0.00), T3 (0.00) and T4 (0.00)	L1 (-11.96), L4 (-5.47), T3 (-4.05) and T1 (-2.80)

Table 29: Summary depicting best crosses, F_1s specific combiners and heterotic hybrids

Characters	Best crosses *Per se*	Best specific combiners	Best heterotic hybrids over better parent	Best heterotic hybrids over check (CH-27)
Plant height (cm)	L7 × T3 (70.70 cm), L7 × T2 (67.73 cm), L7 × T1 (65.75 cm), L2 × T3 (64.56 cm) and L7 × T4 (63.73 cm)	L1 × T2 (7.50**), L1 × T1 (6.25**), L3 × T1 (5.35**), L2 × T3 (5.26**) and L7 × T3 (4.81**)	L7 × T3 (47.30%), L7 × T2 (41.10%), L7 × T4 (32.70%), L1 × T2 (31.45%) and L2 × T3 (24.74%)	L7 × T3 (22.53%), L7 × T2 (17.37%), L7 × T1 (13.94%), L2 × T3 (11.88%) and L7 × T4 (10.44%)
Primary branches plant^{-1}	L4 × T2 (5.31), L3 × T2 (5.25), L6 × T1 (5.22) and L3 × T1 (4.75)	L4 × T2 (1.29**), L3 × T2 (1.08**), L6 × T1 (0.71**) and L2 × T4 (0.46**)	L4 × T2 (99.17%), L3 × T2 (49.18%), L7 × T2 (26.73%) and L6 × T1 (20.51%)	L4 × T2 (69.50%), L3 × T2 (67.59%), L6 × T1 (66.67%), L3 × T1 (51.49%), L6 × T3 (40.78%) and L7 × T1 (40.43%)
Days to first flower	L1 × T4 (25.69), L5 × T1 (27.02), L3 × T2 (27.12) and L4 × T1 (27.83)	L1 × T4 (-4.95**), L3 × T2 (-2.83**), L3 × T4 (-2.48**), L6 × T2 (-2.22**) and L7 × T1 (-1.73**)	L1 × T4 (-28.89%), L3 × T2 (-26.18%), L5 × T1 (-24.40%), L3 × T4 (-23.59%) and L4 × T1 (-22.13%)	L1 × T4 (-28.89%), L3 × T2 (-26.18%), L5 × T1 (-24.40%), L3 × T4 (-23.59%) and L4 × T1 (-22.13%)
Days to first harvest	L5 × T1 (46.00), L3 × T2 (46.00), L1 × T4 (46.00), L5 × T2 (47.00) and L4 × T3 (47.00)	L1 × T4 (-5.36**), L3 × T2 (-3.22**), L7 × T1 (-2.11**), L4 × T3 (-1.77**) and L6 × T2 (-1.72**)	L3 × T2 (-20.69%), L5 × T1 (-19.30%), L5 × T2 (-18.97%), L1 × T4 (-17.86%) and L4 × T1 (-15.79%)	L1 × T4 (-14.81%), L3 × T2 (-14.81%), L5 × T1 (-14.81%), L4 × T3 (-12.96%), L4 × T1 (-11.11%), L5 × T3 (-11.11%) and L5 × T4 (-11.11%)

Table 29 (Contd.)

Characters	Best crosses *Per se*	Best specific combiners	Best heterotic hybrids over better parent	Best heterotic hybrids over check (CH-27)
Fruit length (cm)	L4 × T2 (10.40 cm), L4 × T1 (9.37 cm), L4 × T4 (9.20 cm) and L1 × T2 (9.17 cm)	L1 × T2 (1.36**), L7 × T1 (1.09**), L6 × T3 (1.03**), L3 × T3 (0.84**), L6 × T4 (0.79**) and L2 × T2 (0.72**)	L6 × T4 (74.71%), L1 × T2 (66.16%), L4 × T2 (63.78%), L1 × T4 (48.12%) and L4 × T4 (44.88%)	L4 × T2 (140.00%), L4 × T1 (116.15%), L1 × T2 (111.54%), L4 × T4 (112.31%), L4 × T3 (99.23%) and L5 × T2 (92.31%)
Fruit girth (cm)	L5 × T3 (4.33), L4 × T3 (4.29), L6 × T3 (4.22), L5 × T4 (4.13) and L2 × T3 (4.12)	L2 × T3 (0.49**), L7 × T2 (0.42**), L3 × T1 (0.43**) and L5 × T4 (0.42**)	L4 × T3 (37.58%), L2 × T3 (32.66%), L6 × T3 (27.94%), L3 × T1 (24.47%) and L4 × T1 (23.83%)	L5 × T3 (29.78%), L4 × T3 (28.53%), L6 × T3 (26.33%), L5 × T4 (23.82%) and L2 × T3 (23.51%)
Fruit weight (g)	L1 × T2 (6.90 g), L7 × T1 (6.00 g), L5 × T2 (5.78 g), L6 × T3 (5.32 g) and L1 × T4 (5.30 g)	L7 × T1 (1.17**), L6 × T3 (1.13**), L1 × T2 (0.95**) and L3 × T3 (0.37**)	L1 × T2 (51.65%), L1 × T4 (39.47%), L1 × T1 (36.84%) and L6 × T3 (23.17%)	L1 × T2 (103.14%), L7 × T1 (76.64%), L5 × T2 (70.17%), L6 × T3 (56.53%), L1 × T4 (56.04%), L7 × T2 (54.07%) and L5 × T4 (54.17%)
Fruits plant^{-1}	L6 × T1 (189.33), L3 × T2 (168.10), L7 × T3 (163.67), L1 × T1 (161.10) and L2 × T1 (152.67)	L3 × T2 (38.17**), L7 × T3 (34.95**), L6 × T1 (32.38**), L4 × T1 (18.38**) and L1 × T1 (17.21**)	L7 × T3 (64.77%), L6 × T1 (37.86%), L3 × T2 (37.33%), L5 × T2 (23.08%), L5 × T3 (19.28%) and L3 × T1 (16.08%)	L6 × T1 (79.75%), L3 × T2 (59.49%), L7 × T3 (55.38%), L1 × T1 (52.85%), L2 × T1 (44.94%) and L3 × T1 (34.81%)

Table 29 (Contd.)

Characters	Best crosses *Per se*	Best specific combiners	Best heterotic hybrids over better parent	Best heterotic hybrids over check (CH-27)
Yield plant^{-1} (g)	L3 × T2 (849.47 g), L1 × T1 (822.67 g), L7 × T1 (774.73 g), L6 × T1 (746.13 g) and L3 × T1 (670.33 g)	L3 × T2 (185.13**), L5 × T3 (88.05**), L2 × T4 (82.52**), L1 × T1 (81.20**) and L5 × T4 (80.63**)	L3 × T2 (55.87%), L7 × T1 (50.46%), L1 × T1 (41.78%), L6 × T1 (37.03%) and L3 × T1 (23.00%)	L3 × T2 (148.07%), L1 × T1 (140.24%), L7 × T1 (126.24%), L6 × T1 (117.89%), L3 × T1 (95.76%), L2 × T1 (81.57%), L1 × T4 (80.18%) and L7 × T3 (79.67%)
Yield plot^{-1} (kg)	L3 × T2 (23.50 kg), L1 × T1 (22.89 kg), L7 × T1 (21.49 kg) and L6 × T1 (20.69 kg)	L3 × T2 (5.14**), L5 × T3 (2.40**), L5 × T4 (2.28**), L2 × T4 (2.28**) and L1 × T1 (2.28**)	L3 × T2 (56.04%), L7 × T1 (51.17%), L1 × T1 (42.31%) and L6 × T1 (37.52%)	L3 × T2 (150.32%), L1 × T1 (143.23%), L7 × T1 (128.93%), L6 × T1 (120.40%) and L3 × T1 (97.06%)
Vitamin C (mg100^{-1} g)	L3 × T2 (134.00), L3 × T1 (133.00), L7 × T1 (129.67), L4 × T2 (122.33) and L3 × T3 (120.67)	L5 × T4 (11.55**), L3 × T2 (9.33**), L5 × T3 (9.26**), L1 × T1 (7.61**) and L2 × T1 (7.52**)	L4 × T2 (23.15%), L5 × T3 (21.55%), L4 × T1 (20.47%), L4 × T3 (17.45%) and L3 × T1 (15.99%)	L3 × T2 (35.63%), L3 × T1 (34.62%), L7 × T1 (31.24%), L4 × T2 (23.82%), L3 × T3 (22.13%), L4 × T1 (21.12%) and L7 × T3 (20.78%)
Carotenoids (mg100^{-1} g)	L4 × T1 (363.67), L4 × T2 (348.33), L4 × T3 (332.00), L2 × T4 (327.33) and L4 × T4 (324.00)	L6 × T3 (41.86**), L3 × T2 (30.29**), L3 × T1 (29.43**), L2 × T4 (26.76**) and L7 × T4 (21.18**)	L6 × T3 (40.98%), L4 × T1 (38.28%), L4 × T2 (32.45%), L1 × T1 (28.30%) and L4 × T3 (26.24%)	L4 × T1 (53.66%), L4 × T2 (47.18%), L4 × T3 (40.28%), L2 × T4 (38.31%), L4 × T4 (36.90%), L2 × T3 (29.15%) and L7 × T4 (25.49%)
Coefficient of infection (%)	L3 × T2 (-16.56), L6 × T1 (-14.90), L5 × T4 (-13.29) and L6 × T3 (-12.86)	L3 × T2 (-16.56**), L6 × T1 (-14.90**), L5 × T4 (-13.29**), L6 × T3 (-12.86**) and L4 × T2 (-11.51**)	L7 × T4 (-61.36%), L7 × T3 (-60.88%), L7 × T1 (-59.35%), L6 × T1 (-56.52%) and L6 × T3 (-53.69%)	L1 × T1 (-46.59%), L7 × T3 (-45.04%), L7 × T4 (-45.71%), L1 × T4 (-44.29%), L6 × T1 (-41.05%), L3 × T2 (-41.59%) and L7 × T1 (-42.88%)

Summary

6. SUMMARY

The investigation entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" was carried out at the Department of Vegetable Science, College of Agriculture, Vellayani, during the period of 2015-2018. The objectives of the study were to identify the sources for ChiLCV resistance in a collection of germplasm through natural and artificial screening; to identify potential parents for ChiLCV resistant hybrid breeding based on mean performance and general combining ability (GCA) effects; to identify superior performing ChiLCV resistant hybrids on the basis of expressed heterosis and specific combining ability (SCA) effects; and to study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and for ChiLCV resistance using generation mean analysis.

The investigation was conducted in four experiments. In experiment I (a), seventy germplasm collections or accessions were evaluated for yield and quality attributes during summer 2016. Significant difference was observed among the genotypes with respect to all the characters studied. The best genotypes based on *per se* performance were CHIVAR-9 (T_{58}) for plant height (73.33), CHIVAR-4 (T_{51}) for primary branches plant^{-1} (4.77), Jwalasakhi (T_{19}) for days to first harvest (42.00 days), CHIVAR-7 (T_{53}) for fruits plant^{-1}(137.33), Vellayani Athulya (T_{10}) for days to first flower (26.94 days), fruit weight (7.57 g), fruit length (8.50 cm) and fruit girth (4.78 cm), CA-32 (T_{32}) for yield plant^{-1} and yield plot^{-1} (587.33 g and 16.10 kg, respectively), Punjab Sindhuri (T_8) for Vitamin C (120.33 mg 100 g^{-1}) and Byadagi Kaddi (T_{18}) for Carotenoids (331.33 mg 100 g^{-1}). Selection index were computed based on yield and quality traits for 70 genotypes. Seven genotypes *viz.*, CHIVAR-3 (L1), CHIVAR-7 (L2), CHIVAR-6 (L3), CA-32 (L4), Vellayani Athulya (L5), Keerthi (L6) and CHIVAR-10 (L7) were selected based on selection index ranking and were utilized as lines in hybridization program (Experiment III (a)).

The field screening was undertaken to evaluate 70 chilli germplasm against chilli leaf curl disease under natural epiphytotic condition during summer season of 2016 (Experiment I (b)). On the basis of Coefficient of Infection (CI) all the genotypes were assigned specific disease reaction. To facilitate the attack of chilli leaf curl disease in the experiment, plant protection measures were not used for proliferation of the vector whitefly.

Out of 70 genotypes screened, ten genotypes were found to be completely free from ChiLCV infection and were regarded as symptomless (SL) genotypes. The genotype which showed symptomless reaction to ChiLCV included Sel-3 (T_2), Sel-4 (T_3), Sel-6 (T_5), CHIVAR-1 (T_{46}), CHIVAR-3 (T_{50}), CHIVAR-8 (T_{57}), VS-9 (T_{63}), Sel-40 (T_{65}), Sel-7-1 (T_{66}) and Sel-36-1 (T_{67}). Five genotypes showed highly resistant (HR) reaction included CHIVAR-4 (T_{51}), Japani Longi (T_{60}), Perennial (T_{61}), PLS-3-1 (T_{68}) and Sel-20-1 (T_{69}). In these genotypes the days to first disease symptom appearance varied from 45 DAT (T_{51}) to 60 DAT (T_{60}, T_{61}, T_{68} and T_{69}). Six genotypes *viz.*, T_4, T_6, T_{23}, T_{28}, T_{58} and T_{64} showed resistant (R) reaction. The first disease symptom appeared within 15 DAT in T_6; 30 DAT in T_{23}; 45 DAT in T_4, T_{28}, T_{58}; and 60 DAT in T_{64}. The remaining genotypes were moderately resistant (11), followed by moderately susceptible (12), susceptible (12) and highly susceptible (2). In order to establish true resistance, the genotypes that were symptomless and highly resistant under field conditions were subjected to artificial screening.

To find out true resistance, selfed progenies of 10 symptomless (SL) genotypes (T_2, T_3, T_5, T_{46}, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67}) and five highly resistant (HR) genotypes (T_{51}, T_{60}, T_{61}, T_{68} and T_{69}) under field conditions were subjected to artificial screening (Experiment II (a)) by using whitefly mediated inoculation and graft inoculation. In whitefly mediated inoculation single plant inoculation technique was used, where the individual seedling was inoculated at two true leaves stage by 10 viruliferous whiteflies after acquiring virus from ChiLCV infected chilli source. The severity of infection was categorized on visual basis.

After six weeks of visual observation, six genotypes *viz.*, T_2, T_3, T_5, T_{46}, T_{50} and T_{57} were remained symptomless. Two genotypes T_{63} and T_{67} were resistant and the first disease symptoms were appeared 23.67 and 22.33 DAT, respectively. The genotype T_{65} and T_{66} were found highly resistant, and the first symptom development starts 26.67 and 27.67 DAT, respectively. Three genotypes *viz.*, T_{60}, T_{61} and T_{69} expressed resistant reaction and two T_{51} and T_{68} expressed moderate resistant reaction.

Graft inoculation was also carried out under greenhouse condition to identify true source of resistance from 10 symptomless (SL) genotypes (T2, T3, T5, T46, T50, T57, T63, T65, T66 and T67) and five highly resistant (HR) genotypes (T51, T60, T61, T68 and T69) under field conditions. Here, the ChiLCV infected plant was used as rootstock and the test plant as scion. Out of 10 symptomless genotypes under field conditions, four genotypes *viz.*, T_2, T_3, T_5 and T_{46} showed highly resistant reaction and the first disease symptoms appeared 32.00, 34.33, 33.33 and 34.33 DAT, respectively. Remaining six genotypes *viz.*, T_{50}, T_{57}, T_{63}, T_{65}, T_{66} and T_{67} showed moderate resistant reaction with the days to first appearance of disease from 25.67 (T_{50}) to 27.33 (T_{67}). The genotypes which showed highly resistant reaction under field conditions were moderately susceptible (T_{51}, T_{60}, T_{61}, T_{68}, and T_{69}) under artificial graft inoculation.

To confirm the virus presence in artificially inoculated plants, the DNA from the top young leaves from these plants were subjected to Polymerase Chain Reaction (PCR) using geminivirus universal primers (AV494/AC1048) for confirmation of ChiLCV [experiment II (b)]. Out of six symptomless genotypes after whitefly inoculation, four genotypes namely T_2, T_3, T_5 and T_{46} did not show any amplification for presence of virus, confirming the absence of viral genome in the inoculated plants. However, two genotypes T_{50} and T_{57} showed the presence of viral genome. Under graft inoculation, all tested genotypes (4 highly resistant and 6 moderately resistant) showed presence of viral genome. Since virus was present in all the graft inoculated plants but the apparent symptoms

varied with genotypes, there was a better resistance mechanism working in the four highly resistant genotypes. Hence, the four highly resistant genotypes *viz.*, Sel-3, Sel-4, Sel-6 and CHIVAR-1 were used as testers (male parent) for line × tester analysis in the experiment III (a).

Homology check of the amplified sequence (Begomovirus Vellayani isolate) showed 93 % similarity with *Tomato leaf curl Karnataka virus.* This isolate could be considered as a strain of *Tomato leaf curl Karnataka virus*. This suggested the possibility in the predominance of the stain of *Tomato leaf curl Karnataka virus* (India: Kerala: 2016-KX246859.1-ToLCKaV-(IN:Ker:16)) under Vellayani region.

Seven genotypes (lines) with high yield and quality attributes from experiment I (a) were crossed with four highly resistant genotypes (testers) in line (L) × tester (T) mating design in experiment III (a) to produce 28 F_1 hybrids. These hybrids were evaluated along with parents and two checks (CH-27 and Arka Harita) for yield and quality attributes and ChiLCV resistance during summer in 2017 [experiment III (b)].

The ANOVA for the experimental design revealed that the mean squares (MS) due to genotypes were highly significant ($P \leq 0.01$) for all 12 characters *viz.*, plant height, primary branches plant^{-1}, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C and carotenoids. This indicated that there were significant differences among the genotypes that included parents, their one-way F_1 hybrids and the two commercial checks for all the traits evaluated. The ANOVA for combining ability revealed that MS due parents, lines and testers, hybrids and parent vs crosses were significant for all the characters. Lines vs testers showed significant differences for all the characters except for plant height. This suggested considerable differences exist among genotypes i.e. parents (lines and testers) and their 28 F_1 hybrids.

The MS due to GCA of lines and SCA of crosses were significant at $P \leq$

0.01 for all traits studied. The GCA of testers were observed to be significant for all the traits except for days to first harvest. Highly significant variation due to GCA of lines and GCA of testers, and SCA of crosses indicated the importance of additive as well as non-additive types of gene effects in inheritance of the traits studied. This suggested that genetic improvement of chilli for the traits under study could be achieved both by hybrid development and pure line breeding. The analysis further revealed that the σ^2GCA/σ^2SCA ratio was less than unity for all the studied traits which indicated the predominance of non-additive gene effects for these traits. The contribution of lines were more as compared to testers for all the characters except for the primary branches plant^{-1}.

Heterosis was observed for all the characters studied. The best crosses based on *per se* performance was L7 × T3 for plant height (70.70 cm), L4 × T2 for primary branches plant^{-1} (5.31), L1 × T4 for days to first flower (25.69 days), L1 × T4, L3 × T2 and L5 × T1 for days to first harvest (46.00 days). L4 × T2 for fruit length (10.40 cm), L5 × T3 for fruit girth (4.33 cm), L1 × T2 for fruit weight, L6 × T1 for fruits plant^{-1} (189.33), L3 × T2 for yield plant^{-1} and yield plot^{-1} (849.47 g and 23.50 kg, respectively), L3 × T1 for vitamin C (134 mg 100 g^{-1}) and L4 × T1 for carotenoids (363.67 mg 100^{-1} g).

Heterosis studies revealed that 21 hybrids exhibited significant positive heterosis over better parent for plant height, four hybrids for primary branches plant^{-1}, 19 hybrids for fruit length, 13 hybrids for fruit girth, 12 hybrids for fruits plant^{-1}, 10 hybrids for fruit weight, 13 hybrids for yield plant^{-1} and yield plot^{-1}, 14 hybrids for vitamin C and 21 hybrids for carotenoids. Twenty-two hybrids exhibited significant negative heterosis over better parent for days to first flower, 24 hybrids for days to first harvest and nine hybrids showed heterosis for coefficient of infection. Over the check hybrid CH-27 F_1, eight hybrids exhibited significant positive heterosis for plant height, 28 hybrids for fruit length, 15 hybrids for fruit girth, 17 hybrids for fruits plant^{-1}, 27 hybrids for fruit weight, 25 hybrids for yield plant^{-1} and yield plot^{-1}, 16 hybrids for vitamin C and 17 hybrids

for carotenoids. Twenty-five hybrids exhibited significant negative heterosis over check hybrid CH-27 F_1 for days to first flower, 17 hybrids for days to first harvest and 12 hybrids for coefficient of infection.

The high magnitude of heterosis over better parent was exhibited by the cross L3 × T2 for yield plant^{-1} (55.87%), yield plot^{-1} (56.04%), days to first harvest (-20.69), days to first flower (-26.18%), primary branches plant^{-1} (49.18%), vitamin C (16.86%), fruits plant^{-1} (37.33%) and coefficient of infection (-53.42%); by cross L7 × T1 for yield plant^{-1} (50.46%), yield plot^{-1} (51.17%), vitamin C (15.77%) and coefficient of infection (-59.35%); by cross L1 × T1 for yield plant^{-1} (41.78%), yield plot^{-1} (42.31%), carotenoids (28.30%), fruit weight (36.84), coefficient of infection (-30.25%); by cross L6 × T1 for yield plant^{-1} (37.03%), yield plot^{-1} (37.52%), fruits plant^{-1} (37.86%), primary branches plant^{-1} (20.51%) and coefficient of infection (-56.52%); by cross L3 × T1 for yield plant^{-1} (23.00%), vitamin C (16.86%), fruits plant^{-1} (16.08%) and fruit girth (24.47%); by cross L1 × T4 for fruit weight (39.47%), fruit length (48.12%), days to harvest (-17.86%) and days to flower (-28.89%); by cross L6 × T3 for fruit weight (23.17%), carotenoids (40.98%), fruit girth (27.94%) and coefficient of infection (-53.69%); by cross L4 × T2 for vitamin C (23.15%), carotenoids (32.45%), primary branches plant^{-1} (99.19%) and fruit length (48.12%); by cross L4 × T1 for days to flower (-22.13), days to harvest (-15.79%), fruit girth (23.83%), vitamin C (20.47%) and carotenoids (38.28%); by cross L1 × T2 for fruit weight (51.65%), fruit length (66.16%) and plant height (31.45%); by cross L7 × T3 for fruits plant^{-1} (64.77%), plant height (47.30%) and coefficient of infection (-60.88%); by cross L4 × T3 fruit girth (37.58%) and carotenoids (26.24%); by cross L5 × T1 for days to first flower (-24.40%) and days to first harvest (-18.97%); by cross L5 × T2 for fruits plant^{-1} (23.08%) and days to first harvest (-18.97%); by cross L5 × T3 for fruits plant^{-1} (19.28%), vitamin C (21.55%) and coefficient of infection (-27.12%); and L7 × T4 for coefficient of infection (-61.36%) and plant height (32.70%).

High magnitude of standard heterosis over the check hybrid CH-27 F_1 was exhibited by the cross L3 × T2 for yield plant^{-1} (148.07%), yield plot^{-1} (150.32%), days to first harvest (-14.81), days to first flower (-26.18%), primary branches plant^{-1} (67.59%), vitamin C (35.63%), fruit weight (53.09%), fruits plant^{-1} (59.49%) and coefficient of infection (-41.59%); by cross L1 × T1 for yield plant^{-1} (140.24%), yield plot^{-1} (143.23%), fruit weight (53.09%), fruits plant^{-1} (52.85%) and coefficient of infection (-46.59%); by cross L7 × T1 for yield plant^{-1} (126.24%), yield plot^{-1} (143.23%), vitamin C (31.24%), fruit weight (76.64%), primary branches plant^{-1} (40.43%), plant height (13.94%) and coefficient of infection (-42.88%); by cross L6 × T1 for yield plant^{-1} (117.89%), yield plot^{-1} (128.93%), primary branches plant^{-1} (66.67%), fruits plant^{-1} (79.75%) and coefficient of infection (-41.05%); by cross L3 × T1 for yield plant^{-1} (95.76%), yield plot^{-1} (97.06%), vitamin C (31.24%), fruits plant^{-1} (34.81%) and primary branches plant^{-1} (51.49%), by cross L6 × T3 for fruit weight (56.53%), fruit girth (26.33%), yield plant^{-1} (77.70%), primary branches plant^{-1} (40.78%) and coefficient of infection (-37.20%); by cross L7 × T3 for fruits plant^{-1} (55.38%), plant height (22.53%), yield plant^{-1} (79.67%), vitamin C (20.78%) and coefficient of infection (-45.04%); by cross L7 × T2 for plant height (17.37%) and fruit weight (54.07%), by cross L4 × T1 for yield plant^{-1} (72.10%), vitamin C (21.12%), carotenoids (53.66%), fruit length (116.15%), days to first harvest (-11.11%), days to first flower (-22.13%) and coefficient of infection (-40.99%); by cross L4 × T2 for fruit length (140.00%), vitamin C (23.82%), carotenoids (47.18%), primary branches plant^{-1} (69.50%) and coefficient of infection (-37.61%); by cross L5 × T2 for fruit weight (70.17%) and fruit length (92.31%); by cross L4 × T3 for days to first harvest (-12.96%), fruit length (99.23%), fruit girth (28.53%) and carotenoids (40.28%); by cross L1 × T4 for days to first flower (-28.89%), days to first harvest (-14.81%), yield plant^{-1} (80.18%) and coefficient of infection (-44.29%); by cross L5 × T3 for days to first harvest (-

11.11%) and fruit girth (29.78%); and by cross L5 × T4 for days to first harvest (-11.11%) and fruit girth (23.82%).

Based on general combining ability (GCA) effects, the line L1 was identified as good general combiner for fruit weight, yield plant^{-1}, yield plot^{-1} and coefficient of infection; L2 for plant height and carotenoids; L3 for fruits plant^{-1}, yield plant^{-1}, yield plot^{-1} and vitamin C; L4 for days to first flower and harvest, fruit length, fruit girth, carotenoids, vitamin C and coefficient of infection; L5 for days to first flower and harvest, fruit length, fruit girth and fruit weight; L6 for plant height, fruit girth and fruits plant^{-1}; L7 for plant height, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C and coefficient of infection. Among four testers, T1 was identified as good general combiner for plant height, primary branches plant^{-1}, days to first flower, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, carotenoids, vitamin C and coefficient of infection; T2 for fruit length, fruit weight and vitamin C; T3 for fruit girth, vitamin C and coefficient of infection.

The superior crosses identified on the basis of high SCA effects included L3 × T2 for primary branches plant^{-1}, days to first flower, days to first harvest, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1}, vitamin C, carotenoids and coefficient of infection; cross L1 × T1 for plant height, fruits plant^{-1}, yield plant^{-1}, yield plot^{-1} and vitamin C; cross L7 × T1 for fruit length, fruit weight, days to first flower, days to first harvest, yield plant^{-1}, yield plot^{-1} and coefficient of infection; cross L4 × T2 for primary branches plant^{-1}, vitamin C, fruit length, fruits plant^{-1}, yield plant^{-1}, carotenoids and coefficient of infection; cross L4 × T1 for primary branches plant^{-1}, yield plant^{-1}, yield plot^{-1}, carotenoids and coefficient of infection; L6 × T3 for coefficient of infection, fruit length, fruit weight, yield plant^{-1} and yield plot^{-1} and carotenoids; cross L1 × T4 for days to first flower, days to first harvest, yield plant^{-1} and yield plot^{-1}; cross L6 × T1 for coefficient of infection, primary branches plant^{-1}, fruits plant^{-1}, yield plant^{-1} and yield plot^{-1}; cross L5 × T3 for yield plant^{-1}, yield plot^{-1}, vitamin C, fruits plant^{-1} and coefficient of infection; cross L5 × T4 for coefficient of infection, vitamin C, yield plant^{-1}, yield plot^{-1}, fruit girth and fruits

plant^{-1}; cross L7 × T3 for fruits plant^{-1}, plant height, yield plant^{-1}, yield plot^{-1}, vitamin C and coefficient of infection; cross L2 × T4 for primary branches plant^{-1}, yield plant^{-1}, yield plot^{-1}, carotenoids and fruits plant^{-1}; and cross L3 × T3 for fruit weight and fruit length.

All the four testers were symptomless to ChiLCV under field conditions and among seven lines, two were moderately resistant and remaining five were moderately susceptible. Among 28 F_1 hybrids, 12 showed moderately resistant reaction, 11 were moderately susceptible and five showed susceptible reaction. The check hybrid CH-27 F_1 was moderately resistant and the hybrid Arka Harita showed susceptible reaction.

To study the nature of gene action governing vegetative, flowering, yield and quality attributes and ChiLCV resistance. Three superior crosses identified from line (L) × tester (T) analysis *viz.,* cross 1 (L1 × T1), cross 2 (L3 × T2) and cross 3 (L7 × T1) were utilized for generation mean analysis. The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three crosses were developed and evaluated during 2018 summer in experiment IV (b). The estimation of simple scaling tests revealed that additive-dominance model was inadequate (significance of any one scale A/B/C/D) in all three crosses for entire characters and the presence of inter allelic interaction. In addition, all three cross combination for entire characters had significant joint scaling test value (χ^2) in three parameter model indicating inadequacy of additive-dominance model and need for fitting six-parameter model in all crosses to estimate the probable epistatic components present.

Fitting of six parameter model revealed predominance of dominance gene action for most of the characters in all three crosses. The sign of dominance (h) and dominance × dominance (l) gene effects were opposite in case of plant height, days to first flower, days to first harvest, fruit length, fruit girth, vitamin C and carotenoids (cross 1); plant height, primary branches plant^{-1}, days to first harvest, fruit girth, fruit weight, fruits plant^{-1}, vitamin C and carotenoids (cross 2); primary branches plant^{-1}, days to first flower, days to first harvest, fruit girth, fruit weight,

fruits plant^{-1}, yield plant^{-1}, vitamin C and carotenoids (cross 3) suggesting duplicate type of interaction in these traits. In these crosses selection in the early generation for a character would be ineffective. Duplicate epistasis could be exploited by biparental mating between recombinants in early segregating generation (F_2) and delaying the selection to the advanced generations. The heterosis breeding and reciprocal recurrent selection would be helpful in improvement of this trait due to presence of duplicate epistasis coupled with high magnitude of 'h' and 'l' epistasis.

Additive × additive [i] gene interaction for fruit girth and additive gene action [d] for fruits plant^{-1} was predominant in cross 3. Days to first flowering in cross 2 was controlled by additive gene action. The sign of 'h' and 'l' gene effects were same in the case of fruits plant^{-1}, yield plant^{-1} and yield plot^{-1} (cross 1); fruit length, yield plant^{-1} and yield plot^{-1} (cross 2); plant height and yield plot^{-1} (cross 3) indicating the presence of complementary type of interaction for this traits. The additive, additive × additive or complementary gene interactions are fixable which could be exploited effectively for the improvement of the traits through simple selection or pedigree method of selection. For ChiLCV resistance, dominance (h) gene action, additive × additive (i), additive × dominance (j) and dominance × dominance (l) type of gene interactions were significant. Among them, the former three were in negative desirable direction.

From the present investigation it is concluded that, ten genotypes were symptomless and five genotypes were highly resistant under natural field conditions. Out of these, four genotypes were highly resistant under artificial inoculated conditions. The identified begomovirus sequence under field conditions showed 93 % similarity with *Tomato leaf curl Karnataka virus* (ToLCKV) suggested that, it could be a strain of ToLCKV responsible for ChiLCV disease. The hybrids *viz.,* L3 × T2, L7 × T1, L1 × T1, L6 × T3, L1 × T4, L4 × T2 and L7 × T3 were the most promising with desirable SCA effects, heterosis and *per se* performance for yield and quality attributes and they were moderately resistant to

ChiLCV. The dominance (h) gene action and dominance × dominance (l) epistasis were predominant for yield and quality traits indicating the importance of heterosis breeding in varietal improvement of chilli. For ChiLCV resistance, the genetic components 'h', 'i' and 'j' were significant and in negative direction implying that the ChiLCV resistance could be improved through recombinant breeding or recurrent selection.

6.1 FUTURE LINE OF WORK

a) The identified four highly resistant genotypes under artificial inoculated conditions could be used as potential parents for ChiLCV resistance breeding programme.

b) Begomovirus species specific screening of *Capsicum* germplasm needed.

c) The lines with good GCA effects may be hybridized and selection can be practiced in segregating generations to develop advance generation lines resistant against ChiLCV with desirable horticultural traits.

d) The hybrids performing better than commercial checks needs to be further tested for stability under different agro-climatic situations.

e) There is a need to develop multiple virus resistant hybrids/varieties.

f) Development of ChiLCV resistant lines using marker assisted backcrossing.

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DEVELOPMENT OF CHILLI (*Capsicum annuum* L.) HYBRIDS WITH LEAF CURL VIRUS RESISTANCE, HIGH YIELD AND QUALITY

by

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ABSTRACT

The investigation entitled "Development of chilli (*Capsicum annuum* L.) hybrids with leaf curl virus resistance, high yield and quality" was carried out at the Department of Vegetable Science, College of Agriculture, Vellayani, during the period of 2015-2018. The study was aimed at identification of sources for chilli leaf curl virus (ChiLCV) resistance, development of chilli hybrids with ChiLCV resistance, high yield and quality and studying the gene action of ChiLCV resistance.

The investigation was conducted in four experiments. In experiment I (a), 70 chilli genotypes were evaluated for yield and quality traits. The best genotypes based on *per se* performance were CHIVAR-9 for plant height (73.33 cm), CHIVAR-4 for primary branches plant^{-1} (4.77), Jwalasakhi for days to first harvest (42.00 days), CHIVAR-7 for fruits plant^{-1}(137.33), Vellayani Athulya for days to first flower (26.94 days), fruit length (8.50 cm), fruit girth (4.78 cm) and fruit weight (7.57 g), CA-32 for yield plant^{-1} and yield plot^{-1} (587.33 g and 16.10 kg/6.48m^2 respectively), Punjab Sindhuri for vitamin C (120.33 mg 100 g^{-1}) and Byadagi Kaddi for carotenoids (331.33 mg 100 g^{-1}). Seven genotypes *viz.,* CHIVAR-3 (L1), CHIVAR-7 (L2), CHIVAR-6 (L3), CA-32 (L4), Vellayani Athulya (L5), Keerthi (L6) and CHIVAR-10 (L7) were selected based on selection index ranking for utilization as lines in line (L) × tester (T) analysis.

Among the 70 genotypes screened against ChiLCV under field condition [experiment I (b)], 23 were moderately susceptible, 12 each were susceptible and moderately resistant, ten were symptomless, six were resistant, five were highly resistant and two were highly susceptible. The selected ten symptomless and five highly resistant genotypes were subjected to artificial screening by using whitefly mediated and graft inoculations in experiment II (a). Six genotypes were symptomless under whitefly mediated inoculation, among which, four genotypes *viz.,* Sel-3, Sel-4, Sel-6 and CHIVAR-1 showed highly resistant reaction under graft inoculation.

The resistant genotypes identified under artificial inoculation by Polymerase Chain Reaction (PCR) using universal primers (AV494/AC1048) for the confirmation of ChiLCV.

All the graft inoculated genotypes showed presence of virus. However, in the whitefly mediated inoculation, four genotypes *viz.*, Sel-3 (T1), Sel-4 (T2), Sel-6 (T3) and CHIVAR-1 (T4) did not show any amplification for presence of virus. Hence, they were used as testers (male parent) in line (L) × tester (T) analysis. The overall disease score was higher with graft inoculation than whitefly mediated inoculation. The BLAST analysis of the amplified sequence showed 93 per cent similarity to *Tomato leaf curl Karnataka virus* (ToLCKV).

Seven genotypes (lines) with high yield and quality attributes were crossed with four highly resistant genotypes (testers) in line (L) × tester (T) mating design in experiment III (a) to produce 28 F_1 hybrids. These hybrids were evaluated along with parents and two checks (CH-27 and Arka Harita) for yield and quality attributes and ChiLCV resistance during summer in 2017 [experiment III (b)].

Based on *per se* performance most promising hybrids were L3 × T2, L6 × T1, L1 × T1, L7 × T1 and L3 × T1 for yield traits and L4 × T1, L4 × T2, L4 × T3 and L7 × T1 for quality traits. The superior crosses based on heterobeltosis, standard heterosis and SCA effects were L3 × T2, L1 × T1, L7 × T1, L6 × T1, L3 × T1, L2 × T4, L4 × T1, L5 × T3 and L5 × T4 for yield attributes; L4 × T1, L4 × T2, L3 × T1, L7 × T1, L3 × T2, L6 × T3 and L1 × T1 for quality traits; L6 × T1, L7 × T4, L3 × T2, L7 × T1 and L7 × T3 for ChiLCV resistance.

Lines vs. testers showed significant differences for all the characters except for plant height. The GCA effects for testers were significant for all the traits except for days to first harvest. The ratio of σ^2GCA/σ^2SCA was less than unity for all the characters, which indicated the predominance of non-additive gene effects in the inheritance of these traits. The contribution of lines were more compared to testers for all the characters except for primary branches plant^{-1}. The superior lines based on GCA effects were L1, L3, L7 and L6 for yield attributes; L2, L3, L4 and L7 for quality traits and L1, L2 and L4 for

ChiLCV resistance. Among testers, T1 and T2 were best general combiners for yield and quality traits, and T1 and T3 for ChiLCV resistance.

The hybrids *viz.,* L3 × T2, L7 × T1, L1 × T1, L6 × T3, L1 × T4, L4 × T2, L5 × T3, L5 × T4, L7 × T3 were most promising with desirable SCA effects, heterosis and *per se* performance for yield and quality attributes and they were moderately resistant to ChiLCV except L5 × T3 and L5 × T4. The hybrid L1 × T1 and L7 × T1 had both parents with high GCA effects for yield plant^{-1}. All the four testers were symptomless and among seven lines, two were moderately resistant and five were moderately susceptible. Among 28 F_1 hybrids, 12 showed moderate resistant reaction, 11 were moderately susceptible and five susceptible. The check hybrids CH-27 and Arka Harita were moderately resistant and susceptible respectively.

Three superior crosses identified from line (L) × tester (T) analysis *viz.,* cross 1 (L1 × T1), cross 2 (L3 × T2) and cross 3 (L7 × T1) were utilized for generation mean analysis. The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three crosses were developed and evaluated during 2018 summer. Both simple and joint scaling tests were significant for all the characters in all the crosses indicating the inadequacy of additive-dominance model and involvement of digenic or higher order non-allelic gene interactions.

Duplicate type of epistasis was observed for plant height, days to first flower, days to first harvest, fruit length, fruit girth, vitamin C, carotenoids and ChiLCV resistance (cross 1); plant height, primary branches plant^{-1}, days to first harvest, fruit girth, fruit weight, fruits plant^{-1}, vitamin C, carotenoids and ChiLCV resistance (cross 2); primary branches plant^{-1}, days to first flower, days to first harvest, fruit girth, fruit weight, fruits plant^{-1}, yield plant^{-1}, vitamin C, carotenoids and ChiLCV resistance (cross 3). These crosses can be improved by biparental mating between recombinants in early segregating generation and delaying the selection in the advanced generations.

Complementary type of epistasis was noticed for fruits plant^{-1}, yield plant^{-1} and yield plot^{-1} (cross 1); fruit length, yield plant^{-1} and yield plot^{-1} (cross 2); plant height and yield plot^{-1} (cross 3). Additive, additive × additive or complementary gene interactions are fixable, thus, these crosses can be

exploited effectively through pedigree method of selection. For ChiLCV resistance dominance (h) gene action, additive × additive (i), additive × dominance (j) and dominance × dominance (l) type of gene interactions are significant. Among them, the former three are in negative desirable direction.

The four ChiLCV resistant genotypes identified in this study could be used as potential parents for ChiLCV resistance breeding programme. The 93 per cent similarity of the amplified sequence to ToLCKV suggests that, it could be a strain of ToLCKV responsible for ChiLCV disease. The parents L1, L3, T1 and T3 were superior on the basis of GCA effects for most of the economic traits studied. The hybrids L3 × T2, L7 × T1, L1 × T1, L6 × T3, L1 × T4, L4 × T2 and L7 × T3 were most promising for yield and quality traits, and were moderately resistant to ChiLCV. The dominance (h) gene action and dominance × dominance (l) epistasis were predominant for yield and quality traits indicating the importance of heterosis breeding in varietal improvement of chilli. The ChiLCV resistance could be improved through recombinant breeding or recurrent selection.

Appendices

APPENDIX 1

PHYSICO-CHEMICAL PROPERTIES OF SOIL

Parameter	**Value**	**Rating**
pH	5.60	Moderately acid
Electrical conductivity (dSm^{-1})	0.074	Normal
Organic carbon (%)	1.10	Medium
Available P ($kg\ ha^{-1}$)	43.20	High
Available K	405.00	High
Exchangeable Ca (ppm)	250.00	Deficient
Exchangeable Mg (ppm)	60.00	Deficient
Available S (ppm)	25.20	Sufficient
Available Fe (ppm)	26.60	Sufficient
Available Mn (ppm)	39.30	Sufficient
Available Zn (ppm)	6.50	Sufficient
Available Cu (ppm)	1.00	Sufficient
Available B (ppm)	0.52	Sufficient

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