

**GENETICS OF DROUGHT AND TOMATO YELLOW
LEAF CURL VIRUS TOLERANCE IN TOMATO**
(Solanum lycopersicum L.)

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**GENETICS OF DROUGHT AND TOMATO YELLOW
LEAF CURL VIRUS TOLERANCE IN TOMATO
(*Solanum lycopersicum* L.)**

Thesis submitted to the
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By
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CERTIFICATE

This is to certify that the thesis entitled “**GENETICS OF DROUGHT AND TOMATO YELLOW LEAF CURL VIRUS TOLERANCE IN TOMATO (*Solanum lycopersicum* L.)**” submitted in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY (HORTICULTURE)** to the University of Horticultural Sciences, Bagalkot, is a record of bonafide research work carried out by **Mr. VIJEETH CHIDANANDA HEGADE** under my guidance and supervision and that no part of the thesis has been submitted for the award of any other degree, diploma, associateship, fellowship or other similar titles.

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(V. C. HEGADE)

**Affectionately Dedicated to
The Indian Farming Community
and Scientists**

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1. INTRODUCTION

Tomato (*Solanum lycopersicum* L.), is one of the most important Solanaceous vegetable crops of Peru-Ecuador origin (Rick, 1969). It is an important source of minerals and vitamins (Vitamin A and C). Because of high nutritional quality, tomatoes are being used directly as raw vegetable in sandwiches, salads *etc.* Several processed products like paste, puree, soup, juices, ketchup, drinks, whole peeled tomatoes *etc.*, are prepared on large scale and enjoy high acceptance as food ingredients. Thus, today it is one of the important raw materials for multimillion food industries.

Worldwide, the aggressive exploitation of natural resources has endangered water resources, biodiversity and soil quality. More than 1.2 billion people in over 110 countries are already affected by the social and environmental effects of the land degradation in dry lands (Schuster, 2003), which leads to declining biological and economic productivity. Indian agriculture is highly dependent on climatic conditions. Acute shortage of irrigation water, global warming, outbreak of pests and diseases are adversely affecting the crop production in general and vegetable production in particular. Drought and disease stress during vegetative or early reproductive growth largely reduces yield in number of crops and tomato is not an exception for that.

The Portuguese merchants and the English traders of East-India Company introduced tomato to India. In India, it has become a very popular vegetable. The fruit is available in the market throughout the year (Choudury and Khanna, 1972).

Tomato is grown throughout the country; both under rainfed and irrigated conditions and ranks second among vegetables next to potato in area and production. It occupies an area of 6.34 lakh hectares with an annual production of 124.33 lakh metric tonnes accounting to an average productivity of 15.9 tonnes per hectare contributing 7.7 per cent of the total vegetable production. In Karnataka, tomato ranks third in area and second in production of among the vegetables with an area of 48.3 thousand hectares and annual production of about 15.8 lakh tonnes and an average productivity of 20.91 tonnes per hectare (Anon, 2014).

Tomato is considered as an important source of dietary antioxidants, its components such as lycopene, phenols, flavonoids and vit-C are responsible for the antioxidants activity of fresh and processed form of tomato products. Epidemiological studies have shown that high consumption of tomato fruit is consistently correlated with a reduced risk of prostate cancer and may account for a low incidence of heart disease. Acidosis is quite common in our society leading to many ailments, aches and loss of calcium from the bones. Thus, these problems can be prevented by adding tomatoes to diet as they have an alkali power (Anon., 2009).

If we look into the evolution of earth, we find drought as a recurrent phenomenon. Plants have evolved diverse adaptive strategies to cope with water-limited environments. These mechanisms range from cellular level tolerance to adaptation in response to stress and/or specific growth behaviours and morphological characteristics (inherent traits) that avoid stress effects. These diverse plant physiological mechanisms have their relevance in enhancing stress adaptation. However, from the agronomic perspective, mechanisms that can sustain growth under water limited environment need greater emphasis. Furthermore, the drought tolerance mechanisms and their relevance at specific target environment depend on intensity, magnitude and frequency of occurrence. Therefore, the key to progress towards breeding for drought tolerant crops requires understanding the stress responses of crop plant to identify the relevant drought adaptive mechanisms and/or traits. Hence, the major focus has been to devise strategies for achieving the formidable challenge of precise phenotyping for drought adaptive traits and introgress them through strategic molecular breeding program to improve drought stress tolerance of crops.

Tomato leaf curl virus was reported to be a serious disease on tomato throughout India. The disease may cause up to 75 per cent or more reduction in fruit yield and due to its devastating nature it has become a national problem (Sastry and Singh, 1973; Saikia and Muniyappa, 1989). Today we have achieved many mile stones in the field of crop breeding. Even though, till today, management of TyLCV is solely depending upon the control of insect vector (*Bamisia tabaci*). Extensive use of crop protecting chemicals is also becoming a cause for environmental pollution. These are also causing imbalance in ecology. The residual chemicals in food products are hazardous to human health. The only solution for this is to breed resistant or

tolerant varieties and/or hybrids which can yield more. Plenty of resistant sources are available in natural germplasm. The knowledge of genetic nature of genes pertaining to the resistance or tolerance will lead us to reach our goal.

Varieties with multiple resistances are proving to be the best now a day. Proper understanding of the nature of inheritance of genes governing the resistant traits is the prerequisite for breeding such a variety. Hence, the present research work is aimed at tracing out the genetics of drought and TyLCV tolerance in tomato. The objectives of the research are as follows:

1. Evaluation and selection of tomato genotypes for TyLCV and drought tolerance
2. Development of hybrids
3. Studies on genetics of TyLCV and drought tolerance
4. Evaluation of hybrids for tolerance against TyLCV and drought

2. REVIEW OF LITERATURE

There is no kitchen where tomato is not cut. Tomato has place in almost all types of culinary preparations. It is consumed as fresh, salad and also for preparation of many value added products. Compilation of recently available research reports on the topic are presented in this chapter. Review of literature is done under the following headings:

2.1 Tomato Yellow Leaf Curl Virus (TyLCV)

2.2 Drought tolerance studies in tomato

2.3 Variability studies in tomato

2.4 Genetic divergence in tomato

2.5 Heterosis in tomato

2.6 Combining ability reports in tomato

2.1 Tomato Yellow Leaf Curl Virus (TyLCV)

2.1.1 A brief history of TyLCV disease

The natural occurrence of tobacco leaf curl virus was observed on tomato in India by Pruthi and Samuel (1939). Serious nature of leaf curl disease of tomato was reported in Northern India by Vasudeva and Samraj (1948) and later from Coimbatore (Ramakrishnan *et al.*, 1964), Delhi (Vasudeva, 1959; Naraini, 1968), Hisar (Varma and Poonam, 1977; Varma *et al.*, 1986), Karnataka (Govindu, 1964; Sastry and Singh, 1971; Muniyappa and Veeresh, 1984), Kanpur (Singh and Lal, 1964), Kerala (Nair and Wilson, 1969), Lucknow (Srivastava *et al.*, 1975), Maharashtra (Varma, 1959; Mote, 1976; Mayee *et al.*, 1974; Datar, 1981), Punjab (Butter and Rataul, 1973) and Pantnagar, UP (Saklani and Mathai, 1978).

Besides India, tomato leaf curl virus was reported from Sudan (Cowland, 1932), Srilanka (Shivanathan, 1983), Egypt (Nour-Eldin *et al.*, 1969), Philippines (Retuerma *et al.*, 1971), Somalia (Castelloni *et al.*, 1981), Thailand (Thanapase *et al.*, 1983) and Taiwan (Green *et al.*, 1987).

Tomato yellow leaf curl virus (TyLCV) closely resembling ToLCV has been reported from Israel (Cohen and Nitzany, 1966; Nitzany, 1975), Jordan (Makkouk, 1978), Lebanon (Makkouk *et al.*, 1979) Saudi Arabia (Mazyad *et al.*, 1979) and Thailand (Alathom and Sutabutra, 1986).

2.1.2 Importance of TyLCV disease

Tomato leaf curl virus was reported to be a serious disease on tomato throughout India. The disease may cause up to 75 per cent or more reduction in fruit yield and due to its devastating nature it has become a national problem (Sastry and Singh, 1973; Saikia and Muniyappa, 1989).

Sastry and Singh (1973) reported that TyLCV infected plants produced very few fruits when infected within 20 days after planting and resulting up to 92.3 per cent yield loss. Plants infected 35 and 50 days after transplanting resulted in 74 and 22.9 per cent yield loss respectively. An average of 39 per cent losses in tomato yield due to TyLCV was reported annually from Somalia (Castellani *et al.*, 1981).

Banerjee and Kalloo (1987b) reported that major constraint in the cultivation of tomato was the outbreak of TyLCV during summer in South India and autumn in North-India.

Saikia and Muniyappa (1989) studied in detail the incidence of TyLCV in some tomato growing areas of Karnataka and reported that the incidence ranged from 17-53 per cent in July-November to 100 per cent during February – May grown crop resulting in heavy yield losses.

TyLCV can result up to 75 per cent or more reduction in fruit yield (Yasin and Nour, 1965). Its devastating nature posed national problem in Sudan.

2.1.3 Symptomology

The symptoms of tomato leaf curl virus (TyLCV) included vein clearing, reduction in leaf size, stunted growth, deformation of leaf lets, inward and outward curling and puckering of leaf lets. The infected plants produced few fruits in case of late infection and no fruits, if infected at very early stage. The diseased plants usually developed purple patches especially on older leaves (Vasudeva and Samraj 1948;

Sastry and Singh, 1973, Saklani and Mathai, 1977; Raychoudhari and Naraini, 1977; Reddy, 1978; Capoor, 1981; Saikia and Muniyappa, 1989).

Yassin and Nour (1965) described tomato leaf curl symptoms viz., leaf curling, stunting of plants, thickening, greening of the veins of leaves. Similar symptoms were described by Vasudeva and Samraj (1948).

Gevorkyan *et al.* (1976) reported that the growth and development of tomato plants infected by leaf curl virus were considerably delayed. The disease accompanied by a decreased content of green and yellow pigments and increased total nitrogen and accumulation of hexose and saccharose.

2.1.3.1 Host range of TyLCV

Vasudeva and Samraj (1948) reported that TyLCV exhibited leaf curl symptoms on *Nicotiana tabaccum* L. (cv. white barley, samsun and Harrison's species), *N. sylvestris* L. (cv. Spegas), *N. glutinosa* L., *Solanum tuberosum* L. (cv. Craig defiance) and *Datura stramonium* L. when inoculated by grafting. Varma (1959) transmitted TyLCV by *B. tabaci* to *N. rustica* L., *Zinnia elegans* Jacq., *Datura stramonium* L., *Salvia splendens* L., *Althea rosea* Cav., *Petunia hybridavilm*, *Euphorbia geniculata* L. and *Cassia tora* L.

Ramakrishnan *et al.* (1964) transmitted TyLCV to *Althea rosea* Cav., *Carica papaya* L., *Petunia hybridavilm*, *Sesame orientale* L., *Nicotiana tabaccum* L. and *Zinnia elegans* Jacq. using *B. tabacci* Genn.

Naraini (1968) also transmitted TyLCV by *B. tabaci* to tobacco, *Datura stramonium* L. and *Capsicum annum* L.

Natural hosts of tobacco leaf curl virus include : *Ageratum conyzoides* L. (Pruthi and Samuel, 1942), *Acanthospermum hispidum* DC., *Blocrivillae rhombaridae* L. (Mariappan and Narayanaswamy, 1972), *Crotolaria juncea* L., *Euphorbia hirta* L., *Lycopersicon esculentum* Mill., *Launca asphenifolia* L., *Scoparia dulcis* L., *Solanum nigrum* L., *Vernonia cinerea* Less. (Pruthi and Samuel, 1942) *Carica papaya* L. (Naraini, 1956), *Flaveria australisica* Hook (Mariappan and Narayanaswamy, 1977) and *Withania somnifera* Dunn (Pathak and Raychaudhari, 1967).

Nitzany (1975) reported that *Malva nicaensis* and *D. stramonium* L. serves as an alteranate hosts for TyLCV. *Datura stramonium* L and okra were reported to serve as virus sources for TyLCV (Yassin and Nour, 1965).

Sastry (1984) reported that weed hosts such as *Acanthospermum hispidum*, *Ageratum conyzoides*, *Parthenium hysterophorus*, *Datura stramonium*, *E. geniculata* and *Gynandropisis pentaphylla* as sources of inoculums for tomato leaf curl virus disease.

Saikia and Muniyappa (1989) transmitted TyLCV by *B. tabaci* Genn to *A. hispidum* DC., *A. conyzoides* L., *Bidens biternata*, *C. anthelmintium* (L.) Kuntze, *Conyza stricta*, *Garhinsoga parviflora* Cav., *Sonchus brachyotis* L., *Synedrella nodiflora* (L.) Gaertn., *Z. elegans* Jacq, *E. geniculata* L., *A. rosea* Cav., *Oxalis acetosella* L., *C. annuum* L., *D. stramonium* L., *L. esculentum* L., *L. glandulosum* L., *L. hirsutum* L., *L. peruvianum* L., *N. benthamiana* L., *N. glutonasa* L., *N. tabacum* L., *Phasalis minima* L. and *S. nigrum* L.

Valand (1990) reported the transmission of tobacco leaf curl virus on tomato, produced symptoms of mild curling of leaves, vein thickening and greening of veins followed by dark green sessile enations. Further, tobacco leaf curl virus was transmitted to potential weeds viz., *Croton bonplandiamum* L., *E. geniculata* L., *A. conyzoides* L., *A. hispidum* DC, *Parthenium hysterophorus* L., *D. stramonium* L., *Nicandra physaloides* Gaertn and *Galingosa parviflora* cav.

Mandal and Muniyappa (1991) reported transmission of CVYMV to tomato through *B. tabaci* at 9-13 days of inoculation and described the various kinds of symptoms such as curling of newly emerged leaves, leathery and reduction in leaf size. The virus caused 100 per cent infection on tomato varieties viz., Arka Vikas, Pusa Ruby and Arka Saurabh.

Valand and Muniyappa (1992) studied the host range of tobacco leaf curl virus and found virus was transmissible to nine crop plants, eight ornamental plants and eighteen weed hosts.

Naik (2001) reported the natural occurance of TyLCV on several weeks viz., *A. hispidum* DC., *A. conyzoides* L., *Oxalis acetosella* L., *Oxalis corniculata* L.,

Euphorbia geniculata L., *Synedrella hodiflora* (L.) Gaertn. *Galinsoga parviflora* Cav., *Solanum nigrum* L., *Cassia uniflora* L., *Parthenium hysterophorus* L. and *Walteria americana* L. in all the seasons with high disease incidence during summer compared to *Kharif* and *rabi*. The highest TyLCV incidence (37.68%) was recorded on *Euphorbia geniculata* L., reported to be one of the reservoir hosts for TyLCV.

Khan *et al.* (2002) reported a severe virus-like disease affected 80-90 per cent of sunnhemp plants in experimental plots at the NBRI, Lucknow. Whiteflies (*Bemisia tabaci*) transmitted the associated virus from diseased to healthy sunnhemp plants. The PCR amplification of its DNA with begomovirus specific primers and its strong hybridization with a DNA-A probe of Indian tomato leaf curl virus strongly indicate that it is a begomovirus.

2.1.4 Transmission

2.1.4.1 Vector transmission

Gennadius (1889) first identified the holotype specimen of whitefly *Bemisia tabaci* Genn. in tobacco from Greece. Insect classified under the order Homoptera, family Aleyrodidae and sub family Aleyrodinae (Mohanty and Basu, 1986; Martin, 1987), reported as the only known vector of TyLCV (Vasudev and Raj, 1948; Ramakrishnan *et al.*, 1964; Yassin and Naur, 1965, Retuerma *et al.*, 1971; Butter and Rataul, 1973; Reddy and Yaraguntaiah, 1981; Castellani *et al.*, 1981; Saikia 1985; Zouba, 1995 and Muniyappa *et al.*, 2000).

The whitefly *B. tabaci* with piercing and sucking type of mouth parts was reported to carry plant viruses on the stylet. The minimum acquisition and inoculation feeding period required by *B. tabaci* to transmit tomato leaf curl virus was found to be 30 minutes each. After acquisition the vector required 6 h. to become viruliferous. Single whitefly was able to transmit the virus; the whiteflies remained infective throughout their life span, the virus was not transmitted to the progeny of the whitefly (Butter and Rataul, 1973; Reddy and Yaraguntaiah, 1981; Saikia, 1985).

Muniyappa and Reddy (1976) reported that whiteflies required a minimum of 30 minutes AAP to transmit Horse gram yellow vein mosaic virus.

Ioannou (1987) reported that minimum acquisition and inoculation – feeding periods for the vector, *Bemisia tabaci* to transmit yellow leaf curl virus was 20 and 30 minutes, respectively. The latent period was 21-24 h. The vector was infective for about 12 days, but there was no transovarial transmission.

Brown and Nelson (1988) studied the virus vector relationship of tomato leaf curl virus, a whitefly transmitted geminivirus from Sinaloa, Mexico. Minimum acquisition access period and inoculation access period were 1h. (22% transmission) and 2 h. (8.3% transmission), respectively. A latent period of 17-22 h was demonstrated. The vector retained the virus for 4.5 and 7.3 days after 24 and 72 h AAP, respectively. Relative efficiencies for 1, 5, 10 and 20 *B. tabaci* were 15, 49, 84 and 100 per cent transmission, respectively.

Mathew and Muniyappa (1991) found that an AAP of 10 minutes by *B. tabaci* was sufficient for successful transmission of Indian Cassava mosaic virus.

Mansour and Al-musa (1992) reported that a single whitefly (*B. tabacci*) was able to transmit the virus (TyLCV). The minimum AAP and IAP were 60 minutes and 30 minutes respectively and latent period was 20-24 h. The virus was retained by *B. tabaci* for 11 days.

Ramappa (1993) reported that five adult whiteflies were required for 100 per cent transmission of TyLCV, when AAP and IAP were 24 h. each. The minimum acquisition access and inoculation access periods were 10 and 20 minutes, respectively. Further he reported that the rate of transmission of TyLCV by *B. tabaci* from tomato to tomato was 90.28 per cent, when single whitefly was used per seedling and survived 24 h. after inoculation. The female adults were more efficient in transmission (92-100%) than males (23-28%).

2.1.4.2 Biotypes of *B. tabaci*

Bird (1957) first demonstrated the existence of phenotypes of *B. tabaci* species complex in Puerto Rico. Russell (1975) reported strictly monophagous behaviour as exemplified by *Jatropha* race or a moderate host range phenotype for *Sida* race was inconsistent with widely held notion that, *B. tabaci* colonized over 300 host species. Therefore, it was a highly polyphagous pest having an identical host range phenotype worldwide, regardless of environmental, geographic and other differences.

B-biotype introduced into Caribbean Basin and US and inadvertently distributed into vegetable and cotton growing areas throughout the region, beginning in about 1986. Subsequently from 1986 to present, the B-biotype has distributed nearly worldwide on ornamental plants.

The discovery of the B-biotype in the Sunbelt states of the US and the Caribbean basin involved in the ornamental plants industry was correlated with geminivirus. Incited epidemics rampant in those same locations or the first time in the history of the region. Economic disaster was at large in cotton and vegetable except in the US Sunbelt states and in Puerto Rico, Northern Mexico and the Dominion Republic and in certain locations in Central America and the Eastern Caribbean countries. At present, the B-biotype is well established in both green house and field crops throughout the world (Bedford, *et al.*, 1994; Brown and Costa, 1994).

2.1.4.3 Biological characterization of *B. tabaci* B-biotype

Bedford *et al.* (1994) reported that, recent and unprecedented change in the status of *B. tabaci*, as a globally important virus vectors underscored for the need to study *B. tabaci* complex in relation to virus-vector interactions and whitefly host specificity. Shortly after the discovery of the B-biotype, many laboratories undertook studies to investigate the fundamental biology of B-biotype. These efforts had obvious relevance in implementing control strategies based on sound biological information.

As such, definitive characteristics are now recognized which rapidly permit differentiation of the indigenous and B-biotypes. In contrast to the indigenous biotype, the biotype has the ability to induce phytotoxic like disorders in various host species, *i.e.*, squash silver leaf (SSL) and tomato uneven ripening. B-biotype has a high degree of fecundity and can disperse across relatively great distances in desert environments, a broader host range and resistance to certain insecticides. However, both indigenous and B-biotypes can transmit gemini viruses from eastern and western hemisphere provided they are fed on the virus source plant (Burger *et al.*, 1988).

2.1.4.4 Biology of *Bemisia tabaci*

Pruthi and Samuel (1942) described the duration of various instars of *B. tabaci* on tobacco plant. Incubation period of the egg was 3-4 days in April-July, 3-10 days

in August to March, the longest period observed 7-10 days in December. Young nymphs cast their first moult in 3-5 days in August-September, 8-10 days in December-January and 3-5 days in August-September, 8-10 days in December-January and 3-5 days in May-June. Second instar moults were observed in 2-6 days in August-September, 6-9 days in December-January and 2-4 days in April-May. Pupal period was 2-5 days in August-September, 4-6 days in December and 3-6 days in January. A freshly formed pupae was thin and flat, sub elliptical, light yellow but soon become convex and yellow with margins broadly crenellate. Average duration of each of the three nymphal instars was 4-5 days. Total period of three instars was 12-21 days in August-March, 10-14 days in April-May and 18-24 days in October-December.

Butler *et al.* (1983) observed the development of *B. tabaci* on cotton seedlings in constant temperature cabinets. The duration of egg stage varied from 22.5 days at 16.7⁰C to 5 days at 32.5⁰C whereas, eggs failed to hatch at a constant temperature of 36⁰C. Total development time from egg to adult varied from 16.6 days at 30⁰C to 65.1 days at 49.1⁰C. Development took longer time and there was evidence of aestivation at temperature fluctuating between 27 and 43⁰C. Average number of eggs laid per female was 81 at 26.7⁰C. Males lived an average of 7.6 and 11.70 days and female lived an average of 8.0 and 10.4 days at 26.7 and 32.2⁰C respectively. Emergence of adults from pupae occurred between 6 and 9 am.

Saikia (1985) described that the eggs were elliptical, white and turned brown after one or two days. Eggs hatched into nymphs, which were oval, light yellow with functional legs. They moved for some time and then settled to feed. The second instars were sedentary and oval in shape, third instar closely resembled second instar except in size. The total development period from eggs to adults varied from 16 to 28 days during April-May while during November-December it took 25-42 days. Whitefly, *B. tabaci* activity depends on temperature and light. It was found that temperature from 27 to 28⁰C increased the activity of identify but did not induce flight, as soon as additional light was given to this temperature range, flight started. Additional light had only a slight influence on flight activity when temperature was lower than 27⁰C. Adult whiteflies exhibited a significant preference for feeding and oviposition on the lower surface of top, young leaves. Usually the female whitefly

deposited its first eggs on the lower surface of the cotton leaf on which it emerges, but soon it moved to the top young leaves of the some plant or another neighboring plant where more eggs were laid. The attraction of white flies to the upper leaves was possibly by a combination of negative geotropism and nutritional selection for feeding and breeding site (Gameel, 1972).

2.1.4.5 Host preference of *B. tabaci*

Venkatesh (2000) reported that *B. tabaci* preferred TyLCV infected than healthy *Euphorbia geniculata* for oviposition. Number of eggs laid on infected plants in generation-I was significantly high (216.27) compared to healthy plants (149.9). Number of *B. tabaci* developmental stages on infected plants (1320/plants) in generation-II were more than the double of developmental stages on healthy plants (583/plant).

Naik (2001) reported that *B. tabaci* preferred brinjal host for oviposition compared to cucumber, cotton, sunflower, *Salvia farnecia* R. Br., *Solanum viraum*, *S. khasianum* L., Marigold, *Datura metel* L. and cowpea.

2.1.5 Epidemiology

2.1.5.1 Weather parameters

Pruthi and Samuel (1942) studied the population of whitefly on tobacco crop in Northern India at different months of the year. They reported that the population was highest in autumn up to middle of November and decreased in winter and again increased in March. Further the incidence of tobacco leaf curl disease was found to dependent on vector population.

Varma (1959) reported that the incidence of tomato leaf curl virus on tomato was directly related to the population of the vector *B. tabaci*. The vector population developed during January when incidence of the disease also began to increase.

Yassin and Naur (1965) showed that during March - September 304 out of 577 (52%) tomato seedlings, which were exposed to virus carrying white flies developed leaf curl symptoms. Similarly, in the cooler months of December-February, 132 out of 367 (35.9%) exposed seedlings became infected.

Cohen *et al.* (1974) reported that TyLCV spread was significantly correlated with the population size of its vector, *B. tabaci*. An increase in the vector population and in TyLCV infection was found in tomato plots surrounded by wind breaks.

Yassin (1975) reported the negative correlation between TyLCV incidence and wind direction when observations were made in Sudan for five growing seasons and the highest rate of natural spread of TyLCV in the early stages of growth, usually within 7-10 weeks after planting.

Nitzany (1975) reported that in Israel TyLCV outbreaks always followed in months with a mean relative humidity less than 60 per cent and mean maximum temperature of 30⁰C. However, in Lebanon (Makkouk *et al.*, 1979). TyLCV outbreaks were reported only in the coastal region with a mean relative humidity more than 60 per cent.

Saklani and Mathai (1977) reported that October to Mid December was the most effective time for planting of tomato followed by January to first March in Pantnagar (U.P). Further, they added that tomato leaf curl virus disease appeared very early (25 to 45 days) when the crop was planted between 16th March to 16th September and there was delayed appearance (132 to 162 days) of the disease between October to Mid December.

Mazyad *et al.* (1979) reported that in tomato growing areas of Saudi Arabia TyLCV caused severe epidemics in summer and early autumn owing to optimum conditions and an abundance of the vector, *B. tabaci*, winter planting showed only low infection with mild symptoms. Tomato cultivars varied in their susceptibility to the virus infection.

Ohnesorge (1981) studied the population dynamics of *B. tabaci* in the winter months, when the density of the pest was lowest. Of the immature stages, eggs and young larvae were most abundant during this period. A high mortality rate resulted from the asynchrony of the development of the insect and ageing of plant leaves. When the temperatures were low, a large part of the pest population was unable to complete lifecycle before ageing and deterioration of the food plants. On early transplanted tomatoes very few insects completed their development.

Shanab and Award-Allah (1982) studied the seasonal population fluctuations in *B. tabaci* on tomato in relation to temperature and relative humidity in Egypt. Whitefly population first appeared in May, were lowest from July to October when the daily mean temperature was 20.86 – 27.58°C and the relative humidity 58.96 – 66.66 per cent and reached peak number in September.

The effect of daily mean temperature on population in summer was insignificantly negative in first year and significantly positive in second year, while in autumn it was highly significant positive during both the years. The effect of daily mean relative humidity in summer was highly significantly positive during both years, while in autumn it was insignificantly negative during both years.

Shaheen (1983) found *B. tabaci* attacking tomato in April-November with infestation peak in August-October. Early sown tomato in February was seldom infested, but that sown in April became severely infested throughout the flowering and fruiting stage resulting in 40 per cent crop loss. Severe infestation at the seedling stage resulted in complete yield loss on autumn crops sown in August.

Saikia and Muniyappa (1989) reported that tomato plants susceptible to infection by TyLCV at all stages of their growth. 50 to 70 per cent yield loss was observed in tomato Cv. Pusa Ruby in February – May. A strong correlation was obtained between the percentage incidence of TyLCV and whitefly (*Bemisia tabaci*) number.

Anitacherian (1998) reported that tomato nursery raised without nylon net covering resulted in TyLCV incidence in early weeks of transplanting which reached hundred per cent by fourth and fifth week.

Arsenio *et al.* (2002) reported that in the winter/spring season, the *B. tabaci* or TyLCV complex is a minor problem because of the low populations of *B. tabaci* and the climatic conditions.

Ramos *et al.* (2002) recorded in Algarve during 1997-98, 1998-99 and 2000 that the population counts of *B. tabaci* were high in the first months of autumn and then decreased until January, when numbers of *T. vaporariorum* became higher. The counts of *B. tabaci* then increased again.

2.1.6 Screening for resistance

Success of disease resistance breeding solely depends on the evaluation tests employed. It is important to employ most reliable tests of resistance when dealing with destructive diseases like TyLCV.

Som and Choudhary (1976) examined for resistance source by growing plants in summer using *Bemisia tabaci* for inoculation and graft transmission. Hassan *et al.* (1984) employed vector inoculation graft transmission and progeny tests for screening TyLCV resistant lines.

Many workers have evaluated for TyLCV reaction the basis of visual symptoms of the disease either by observing under field conditions (Yassin, 1985; Zidan *et al.*, 1993) or after vector inoculation (Pilowsky and Cohen, 1990; Kaloo and Banerjee, 1990; Forgette *et al.*, 1996) or both (Naraini and Vasudeva, 1963; Banerjee and Kallo, 1987b, Muniyappa *et al.*, 1991a; Kheyrpour *et al.*, 1994).

To assess the resistance of a given line symptom severity grades, designated with numerical values of 0-4 has been given on the basis of visual inspection (Som and Choudhary, 1976; Joshi and Choudhary, 1981; Banerjee and Kalloo, 1987a; Kallloo and Banerjee, 1990). Similarly four grades were adopted by Hassan *et al.* (1984) and Muniyappa *et al.* (1991a), Yassin (1985) and Pilowsky and Cohen (1990) scored reaction of test lines as diseased and healthy.

Bisht *et al.* (1989) in India screened 88 germplasm collections of different species and reported that all collections from *Lycopersicon hirsutum* and *L. peruvianum* had high degree of resistance while *L. pimpinellifolium* lines did not show any marked resistance.

Muniyappa *et al.* (1991a) reported that the adult whiteflies died within three days after release on to resistant lines, while they survived upto 25 days on susceptible cultivars. In field conditions 0-4 adult whiteflies on resistant lines and 5-25 adult whiteflies on susceptible lines were observed.

Dharmatti *et al.* (1996) reported that, few genotypes derived from tester (Alcobosa) x line crosses had potato leaf characters which carried genes for field resistance to TyLCV. The crosses 20/6 Alcobosa x L-58, 20/5 Alcobasa x N – 2298-MF-F6 and 20/4 Alcobasa x L- 58 showed negative heterosis for TyLCV and whitefly with high yield which can be exploited as hybrids in summer.

Singh *et al.* (1999) reported that Pusa Ruby was outstanding in all characters and was relatively less susceptible to jassids, whiteflies and TyLCV compared to all other varieties. Whitefly population played an important role in TyLCV incidence.

Nainar and Pappiah (2002) reported two accessions *viz.*, IIHR.1942 (*L. pimpinellifolium*) and LE. 1118 (*L. hirsutum*) did not exhibit infection (TyLCV) up to 75 days after transplanting under field conditions. Among the accessions screened, six were susceptible, seven were moderately susceptible, five were moderately resistant and two were resistant.

Ali *et al.* (2002) screened ten tomato cultivars of the determinate type, the results showed that 45 days after planting (DAP) was the critical time for viral infection in the plants in relation to yield. The cultivar Punjab Chhuhara was the most resistant, followed by Sel-7. A correlation between whitefly (*Bemisia tabaci*) and disease incidence was observed at different days after planting.

Maruthi *et al.* (2003) screened a total of 34 tomato genotypes resistant/tolerant to TyLCV-Is and for resistance to TyLCV-[Ban4] under glasshouse and field conditions, accessions of wild species, *Lycopersicon hirsutum*, LA 1777 and PI 390659 were the best sources of resistance to both viruses. Lines 902 and 910, which were, resistant to TyLCV-Is were only tolerant to TyLCV-[Ban4] and accession *Lycopersicon peruvianum* CMV Sel. INRA, resistant to TyLCV-[Ban4], was only tolerant to TyLCV-Is.

Rai *et al.* (2001) screened twenty tomato genotypes for resistance to tomato leaf curl virus (TyLCV) and found that high temperature and humidity increased TyLCV incidence and maximum infection was obtained at 25⁰C and 79.73 per cent relative humidity. None of the cultivars were highly resistant to the virus, but cultivars Hisar Anmol and Hisar Gaurav were found to be resistant with disease incidences of 6.52 and 7.63 per cent, respectively.

Sankari *et al.* (2002) screened 36 F₁ hybrids and 13 parents of tomato for their resistance to TyLCV by graft inoculation under glasshouse conditions. The hybrids FLCR5 x MLCR4 and FLCR5 x MLCR1 and the parents FLCR1, FLCR3, FLCR5, MLCR4, MLCR5 and MLCR6 recorded the lowest disease incidence.

2.1.7 Exploitation of natural resistance

Breeding for resistance to TyLCV has been undertaken in several institutes throughout India. Various methods have been employed to screen systemically the *Lycopersicon* germplasm for resistance viz., subjecting the plants to natural epidemics, artificial inoculation by grafting or by whiteflies.

Different *Lycopersicon* accessions with resistance or tolerance to TyLCV reported from India are presented in Table 1.

2.2 Drought tolerance studies in tomato

Worldwide, the aggressive exploitation of natural resources has endangered water resources, biodiversity and soil quality. More than 1.2 billion people in over 110 countries are already affected by the social and environmental effects of the land degradation in dry lands (Schuster, 2003), which leads to declining biological and economic productivity. India is also one of the countries, which have agriculture system challenged with climate change. Acute shortage of irrigation water is adversely affecting the crop production in general and vegetable production in particular. Water stress during vegetative or early reproductive growth usually reduces yield in number of crops and tomato is not an exception for that.

The tomato is a major vegetable crop and grown all over the world in outdoor fields, greenhouses and net houses. Aside from being tasty, tomatoes are a very good source of vitamins A and C (Farooq *et al.*, 2005).

2.2.1 Morphological modification in plant body by drought effect

Adequate water supply is very important for proper growth of plants. Insufficient availability of water during early and mid growth phase has been proven to affect vegetative growth of plants. The bad effect on vegetative growth will reflect in yield of crops.

Table 1. List of *Lycopersicon* accession with resistance or tolerance to TyLCV reported from India

Sr. No.	Species and lines	Reference
1	<i>L. esculantum</i>	
A	EC 104395	Varma <i>et al.</i> , 1986
B	Nova, Nematex, HS10	Mayee <i>et al.</i> , 1974
2	<i>L. chilense</i>	
A	Line 414-2 x 414-ISIB, LA-267, 55L-Antogogster, chileLine, 1986-22 x 986-24 SIB, LA 458, 63 L-Tacna, Peru	Joshi and Choudhary, 1981
3	<i>L. glandulosum</i>	
A	EC 66003, E.C. 66002	Varma <i>et al.</i> , 1986
4	<i>L. pimpinellifolium</i>	
A	LA1921, XXXII-354-A-Silvestra	Banerjee and Kalloo, 1987b, Som, 1973
B	SI – 496, PRSP13 (2247), XXXII-354-4Silvestra	Joshi and Choudhary, 1981
5	<i>L. hirsutum</i>	
A	LA-386, LA1777, PI 390658, PI 390659, PI 390513, PI 127826, PI 390658, PI 390659	Muniyappa <i>et al.</i> , 1991a
B	PI 390513	Saikia and Muniyappa, 1989
C	PI 127826	Banerjee and Kalloo, 1987b
6	<i>L. hirsutum f. glabratum</i>	
A	B 6013	Banerjee and Kalloo, 1987b
7	<i>L. hirsutum f. typicum</i>	
A	LA 1921	Banerjee and Kalloo, 1987b
B	XXXII-354-A-Silvesta, SI-496	Som, 1973
C	PRS, P13 (2247), XXXII-354-A-Silvestra	Joshi and Choudhary, 1981
8	<i>L. peruvianum</i>	
A	EC 65980, EC 65968, EC 148898, EC 148897	Varma <i>et al.</i> , 1986
B	B 6022/77	Banerjee and Kalloo, 1987b
C	PI 127830, PI 127831	Saikia and Muniyappa, 1989; Muniyappa <i>et al.</i> , 1991a
D	Line 996-92 x 996-24SIB, LA444, 63L-Chincha, Peru	Joshi and Choudhury, 1981
9	<i>L. peruvianum f. glandulosum</i>	
A	B 6005	Banerjee and Kalloo, 1987a
10	<i>L. peruvianum var regulare</i>	
A	49B-295	Joshi and Choudhary, 1981

2.2.1.1 Vegetative growth - Stem and branches

Imposition of water stress caused a significant reduction in plant height of treated plants as compared to control plants. Well watered plants produced the taller plants as compared to rest of the treatments. However, late stress had much less effects on plant height and it produced taller plants than early and middle stress (Pervez *et al.*, 2009). They have also reported reduction in number of branches in stressful conditions. Main shoot found to dominate over the side branches, although the plant height was found to lesser compared with the irrigated genotypes.

Salt stress also has similar effects to that of drought stress, which limits water availability for plant growth. Increased salinity level was accompanied by significant reduction in growth. Plant height and stem girth were drastically reduced when tomato genotypes were exposed to salt stress (Mohammad *et al.*, 1998).

Among the 42 pigeonpea genotypes studied, Narina *et al.* (2014) noticed the shortest five were tolerant to drought. Plant height among these genotypes did not differ significantly between different levels of drought and with the normal irrigated condition. They have attributed this to the capacity of those tolerant genotypes to maintain proper cell elongation in stressful conditions.

Significant reduction in plant height was noticed in chickpea cultivars exposed to drought stress. Imposition of drought during vegetative growth phase was reflected in number of branches (Mafakheri *et al.*, 2010).

2.2.1.2 Vegetative growth - Leaves

Many factors influence crop yield, of which radiation is one of the very important factor, as it supplies energy required for photosynthesis, the basic production process in plants. Part of radiation intercepted by leaves is responsible for photosynthesis. Heuvelink *et al.* (2005) demonstrated the importance of number of leaves and leaf area in yield of tomato. They opined that by plant yield can be enhanced by increasing the area of light interception.

The leaf is the most adaptable organ in its response to environmental conditions (Marchi *et al.*, 2008; Nevo *et al.*, 2000).

The water stress significantly reduced leaf numbers per plant as compared to control. The late stressed plants produced comparatively more leaves as compared to early and middle stress (Pervez *et al.*, 2009).

Drought tolerance was prominently noticed in those pigeonpea genotypes which had more number of leaves per stem. These genotypes were reported to have narrower leaves with more waxy coating on them, compared to the other non-tolerant genotypes. This was attributed that these morphological adjustments enabled those genotypes to lose more heat and reduce transpirational losses (Narina *et al.*, 2014).

Reduced plant height and number of leaves was noticed in rice genotypes resistant to water deficit. Decrease in leaf number and plant height may be an adjustment mechanism of the rice genotypes to reduce water loss through transpiration (Chaum *et al.*, 2013). Similar kind of results were reported in *P. vulgaris* (Xian and Rajashekhar, 1999), soybean (Agboma *et al.*, 1997) and maize (Li *et al.*, 2011).

Water deficit decreased individual leaf area significantly in olive cultivars. Cultivars with smaller leaves were better adapted to drought. The area of leaves produced during drought stress reduced up to 25 per cent in tolerant cultivars (Ennateh *et al.*, 2010).

2.2.1.3 Vegetative growth - Root and its importance in drought tolerance

The importance of root growth for maintaining crop yields is becoming recognized and of increasing interest to plant breeders (Gewin, 2010). Extensive root systems are vital when plants are grown in soils containing insufficient supplies of water or nutrients. With the demand for food escalating globally and variable soil water regimes associated with changing weather patterns, it is particularly important that we have a good understanding of the processes affecting root growth.

Adequate root elongation is important for plant growth, especially in soil where resources of water and nutrients are scarce. Roots elongate more slowly in drying soil due to a combination of water stress and mechanical impedance. Recent evidence shows that penetrometer resistances in excess of 2 MPa occur even in many relatively moist soils (*e.g.* matric potentials of –100 kPa to –200 kPa) and that this is

sufficient to slow root elongation to less than half of its unimpeded rate. Root tip traits beneficial to root penetration include traits that decrease cavity expansion pressure, frictional resistance, or axial cell wall tension. In soil containing macropores and channels, the ability of roots to exploit such channels may also be of significant benefit and root hairs are probably sufficiently strong to aid root tip anchorage significantly. It is essential to consider root responses to soil strength when developing strategies to breed drought-resistant crops and, to address this adequately, may require the development of some novel screening approaches (Bengough *et al.*, 2011).

Drought resistance can be enhanced by improving the ability to mine water from soil (Wright and Nageswara Rao, 1994). This might be achieved by selection for large root systems for better adaptation to drought conditions (Passioura, 1983; Turner, 1986; Ludlow and Muchow, 1990; Rucker *et al.*, 1995; Matsui and Singh, 2003; Taiz and Zeiger, 2006; Songsri *et al.*, 2008). Information on the ability of drought resistant peanut genotypes to alter their root systems contributing to high yield under water stress might reveal avoidance mechanisms and could result in the development of improved breeding strategies for drought resistance in peanut (Songsri *et al.*, 2008).

Songsri *et al.* (2009) revealed that long root system contributed to high vegetative growth in peanut genotypes. The sink competition between harvestable and root sink should be considered when devising breeding strategies to improve drought resistance.

Increase in fibrous roots with enhanced root volume was reported in rice cultivars resistant to water deficit (Chaum *et al.*, 2013). This characteristic of number of fibrous roots and root volume was attributed to pump more water from soil which is water deficit.

2.2.1.4 Effect of water stress on number of stomata

When faced with drought, plants adopt one of two strategies: drought avoidance, or drought tolerance. The avoidance of dehydration is associated with a variety of adaptive traits to minimize water loss and maximize water uptake. Both can be brought about by a combination of morphological, anatomical and physiological

adaptations. In contrast, drought tolerance refers to the ability of a plant to maintain its normal functions during periods of low tissue water potential. It involves specific metabolic and biochemical reactions at the sub-cellular level.

A fundamental response to drought by plants is to conserve water through stomatal regulation. Stomata are pores found in the epidermis of the leaf that allow for an influx of CO₂ for photosynthesis and consequently water loss through transpiration. These pores are flanked by specialized cells, known as guard cells. Within these guard cells, the plant hormone abscisic acid (ABA) is one of the most important chemical signals that triggers a signaling cascade leading to stomatal closure under abiotic conditions such as drought. Guard cell control of transpiration and water loss is strongly associated with drought tolerance (Tuberosa, 2012).

Olive trees are able to delay the onset of water stress (*i.e.*, adopt drought avoidance) both by controlling transpiration and by increasing water uptake through having a large and deep root volume. Furthermore, olive trees are able to tolerate dehydration and thus sustain a large internal water deficit, yet maintain sufficient metabolic activity for survival (Connor, 2005; Ennajeh *et al.*, 2008; 2009). Significant increase in stomatal density was reported in olive cultivars as an adjustment criteria against drought stress. This increase help the plants to assimilate more CO₂ from atmosphere in stress. Loss of water through transpiration was managed by increased number of trichomes (Ennateh *et al.*, 2010).

Hopper *et al.* (2014) reported that grapevine can bring some changes in stomatal response to cop up with drought stress. Stomata of drought resistant species and varieties of grapevine are very sensitive and close immediately on water shortage. Stomatal density of the resistant cultivars found to be lower compared to the susceptible ones.

2.2.1.5 Effect of water stress on number of pubescence

Plant leaf hairs play important physiological and ecological roles. They are often implicated in plant protection from abiotic stresses including: UV damage (Skaltsa *et al.*, 1994; Karabourniotis *et al.*, 1995), drought tolerance (Grammatikopoulous and Manetas, 1994; Espigares and Peco, 1995), radiation heat load reduction (Ehleringer, 1984) and the sequestration of toxins (Yaniv and Werker,

1983). Leaf hairs are also implicated in plant protection from biotic stresses: they can decrease pathogen germination rates by decreasing leaf wettability (Brewer and Smith, 1997) and leaf hairs can protect plants from damage by herbivores (Hagley *et al.*, 1980; Sharma and Agarwal, 1983; Wellso, 1986; Bauchan, 1987; Doss *et al.*, 1987; Tomkins *et al.*, 1991; Agren and Schemske, 1993; Paliniswamy and Bodnaryk, 1994). Leaf hairs do not always protect against herbivores (Lange and Jochemsen, 1987) and hairs may interfere with plant protective parasitoids (Van Lenteren *et al.*, 1995). Because leaf hairs are ecologically important to plants, in both negative and positive ways, it is important for ecologists to understand the factors that influence leaf hair density. Leaf hair density is often under some genetic control; species within a genus typically differ in hairiness (Paliniswamy and Bodnaryk, 1994; Upadhyaya and Furness, 1994; Fortner *et al.*, 1995) and within species there is often genetic variation for leaf hair density (Zaiter *et al.*, 1990; Agren and Schemske, 1993; Stoner, 1992). However, as is so often the case with plants, leaf hair density can also respond in a plastic way to environmental influences (Upadhyaya and Furness, 1994; Fortner *et al.*, 1995; Wilkens *et al.*, 1996). For example, when individuals of four species of *Arctic festuca* were grown under different combinations of temperature and water supply, the mean leaf hair density of each species depended on the environment (Fortner *et al.*, 1995). It is not known how water supply and temperature influenced leaf hair density in the *A. festuca* experiment and this question has rarely been addressed.

Olive cultivars showed highly significant variation for trichome density (TD). This variability can be attributed to efficacy of the defense mechanisms used by these cultivars. The cultivars which were tolerant to drought stress found to increase TD to 25 per cent when exposed drought stress. The increase in TD around stomata resulted in reduced water loss due to transpiration (Ennateh *et al.*, 2010).

2.2.1.6 Effect of water stress on yield

Pervez *et al.* (2009) reported significant reduction in tomato fruits up on water stress. The control plants, with normal irrigation produced significantly higher yields than the stressed. Average fruit weight also found to be significantly lower in stressed tomato genotypes.

Significant yield reduction, ranging from 45 to 61 per cent, was reported in chickpea cultivars exposed to water stress. Drought imposition in vegetative phase reflected in anthesis and hence reduced number of filled pods and 1000 grain weight. The decrease in yield was largely due to the decrease in average pod weight (Mafakheri *et al.*, 2010).

2.2.1.7 Biochemical changes in plant by drought

2.2.1.7.1 Chlorophyll: The photosynthetic pigment

Chlorophyll and higher carotenoids are proved to be associated with stress tolerance. It is reliable to measure the changes chlorophyll, the photosynthetic pigment to analyse the effect of different environmental stress on plant physiology (Kraus *et al.*, 1995). Chlorophyll is one of the basic pigments in plants whose reduction in concentration causes chlorosis and reduction of growth and yield (Khosh and Ando, 1995).

Water is very important in synthesis of chlorophyll. After a heavy rain the amount of chlorophyll is increased, but in the arid time its value decreases. On the other hand, if the soil is water saturated, leaves chlorophyll content decreases. Leaf water content to maintain the maximum amount of chlorophyll should be high (Bohrani and Habili, 1992). During environmental stress, the chlorophyll content in plant tissue reduces in susceptible cultivars and it increases in resistant or tolerant cultivars. Rapid loss of chlorophyll is reported in cold sensitive plants which have resulted in decreased photosynthetic activity (Hendry *et al.*, 1987).

Songsri *et al.* (2009) demonstrated higher total chlorophyll content in leaves were responsible for greater amount of photosynthesis and dry matter production in peanut. Peanut genotypes with higher total chlorophyll content showed significant positive correlation with total dry matter production.

Leaves of resistant wheat cultivars showed an increase in chlorophyll content compared to other cultivars when exposed to cold stress. Activity of superoxide dismutase was reported to increase in these cultivars when the stress was induced. This prevented the damage of chloroplasts by free radicals and thus increasing the chlorophyll content. Yield of these cultivars were significantly higher compared to other 25 wheat cultivars tested for stress tolerance (Shriari *et al.*, 2009).

Severe drought stress in pea plants inhibited the photosynthesis by causing changes in chlorophyll content and by damaging the photosynthetic apparatus (Ormaetxe *et al.*, 1998). Ommen *et al.* (1999) reported that leaf chlorophyll content decreases as a result of drought stress. Drought stress caused a large decline in the chlorophyll *a* content, the chlorophyll *b* content and the total chlorophyll content in all sunflower varieties investigated (Manivannan *et al.*, 2007). The decrease in chlorophyll under drought stress is mainly the result of damage to chloroplasts caused by active oxygen species (Smirnoff 1995).

Mafakheri *et al.* (2010) imposed drought stress on three chickpea cultivars and found a significant reduction in chlorophyll *a*, chlorophyll *b* and total chlorophyll content. Chlorophyll *a/b* ratio revealed lack of effect of drought on chlorophyll *b* content. Similar kind of reduction of chlorophyll content was reported by Nyachiro *et al.* (2001) in *T. aestivum* cultivars. Decreased or unchanged chlorophyll level during drought stress has been reported in other species, depending on the duration and severity of drought (Kpyoarissis *et al.*, 1995). A decrease of total chlorophyll with drought stress implies a lowered capacity for light harvesting. Since the production of reactive oxygen species is mainly driven by excess energy absorption in the photosynthetic apparatus, this might be avoided by degrading the absorbing pigments (Herbinger *et al.*, 2002).

Salami and Saadat (2013) reported that drought stress damaged chloroplast and reduced chlorophyll content in maize cultivars. The resistant cultivars were potential yielders and had higher amount of chlorophyll. Decline in concentration of chlorophyll *a*, *b* and total chlorophyll was reported in rice also by Chaum *et al.* (2013).

2.2.1.7.2 Proline: The osmoregulator

In response to water deficit/ drought conditions, maintenance of cellular osmotic pressure/osmoregulation is the major mechanism (Serraj and Sinclair, 2002; Thapa *et al.*, 2011). Earlier studies have reported that molecules like glycine betaine, proline, mannitol, sorbitol and trehalose act as osmoprotectants under water stress and help to maintain plant growth and development (Valliyodan and Nguyen, 2006; Hadiarto and Tran, 2011).

Plants can partly protect themselves against mild drought stress by accumulating osmolytes. Proline is one of the most common compatible osmolytes in drought stressed plants. For example, the proline content increased under drought stress in pea (Sanchez *et al.*, 1998; Alexieva *et al.*, 2001). Proline accumulation can also be observed with other stresses such as high temperature and under starvation (Sairam *et al.*, 2002). Proline metabolism in plants, however, has mainly been studied in response to osmotic stress (Verbruggen and Hermans, 2008). Proline does not interfere with normal biochemical reactions but allows the plants to survive under stress (Stewart, 1981). The accumulation of proline in plant tissues is also a clear marker for environmental stress, particularly in plants under drought stress (Routley, 1966). Proline accumulation may also be part of the stress signal influencing adaptive responses (Maggio *et al.*, 2002). The purpose of the present study was to contribute to a better understanding of the physiology responses of chickpea plants to drought stress. The increase in proline content due to drought stress was more severe at flowering stage than at the vegetative stage. The proline content depends on plant age, leaf age, leaf position or leaf part (Chiang and Dandekar, 1995). Under vegetative stage, drought stress increased proline content about tenfold, this increasing roles as an osmotic compatible and adjust osmotic potential which resulted in drought stress avoidance in chickpea (Mafakheri *et al.*, 2010). Proline accumulation is believed to play adaptive roles in plant stress tolerance (Verbruggen and Hermans 2008). Accumulation of proline has been advocated as a parameter of selection for stress tolerance (Yancy *et al.*, 1982; Jaleel *et al.*, 2007).

Chaum *et al.* (2013) reported enhanced proline accumulation due to water deficit in rice cultivars. It was reported that proline accumulation in water deficit plants play a key role in osmoregulation defense mechanism under drought stress. Similar kind of increase in accumulation of proline was reported in tobacco (Ma *et al.*, 2007), papaya (Mahouachi *et al.*, 2012) and in sunflower (Iqbal *et al.*, 2011).

Leaf proline content increase significantly under mild and severe drought stress in comparison with control in a trial conducted on tomato genotypes. However stem proline content was not significantly affected by the stress imposed (Ghorbanli *et al.*, 2012). Higher accumulation of proline under stress protects cell membrane and

total proteins. Proline acts as an osmolite beside enzymes and other macromolecules and therefore, protects the plant against low water potential and causes osmotic regulation in plant organs. Also proline can act as an electron receptor preventing photosystems injuries in dealing with ROS function. Proline accumulation facilitates the permanent synthesis of soluble substances in closing stomata. This process is different in various plants. Proline accumulation in foliage was seen in olive cultivars (*Olea europea* L.) in low water condition (Bacelar *et al.*, 2009).

2.3 Variability studies in tomato

A critical estimate and study of genetic variability is pre-requisite for initiating appropriate breeding procedures in crop improvement programmes, which demands wide range of variability in a population. The determination of genetic variability and its partitioning into various components in crop plants is necessary to have an insight into genic nature of yield and its components. The degree to which variability of a character may be transmitted to the progeny is referred to as its heritability. The heritable variation is marked by non-heritable components hence, it is necessary to split the overall heritability using genetic parameters.

According to Hanson *et al.* (1956), heritability in broad sense is the ratio of genotypic variance to total variance in non-segregating population. A high heritability is not always accompanied by high genetic advance but, in the presence of fixable gene effects high genetic advance should be expected (Panse and Sukhatme, 1967). Genetic advance under selection is the improvement in the mean genotypic value of the selected families over base population which depends upon the genetic variability existing in the population, the heritability of the character under selection and the intensity of selection. Hence, the components of variances and heritable components with genetic parameters, such as genetic coefficient of variation, heritability estimate and genetic advance are important tools for the breeders to plan suitable breeding strategy.

Many researchers have studied the variability in tomato. Recent reports on variability, heritability, genetic advance and genetic advance over mean are given in Table 2.

Table 2. Recent reports on variability, heritability, genetic advance and genetic advance over mean in tomato

Sl. No.	Character	PCV %	GCV %	h^2	GA	GAM %	References
1	Plant height	17.90	17.60	96.90	39.10	-	Singh <i>et al.</i> (2000)
		38.36	34.05	78.82	-	62.28	Joshi and Singh (2003)
		28.07	26.81	91.20	28.43	52.73	Mohanty (2003)
		12.16	6.90	32.20	6.91	8.06	Prashanth (2003)
		19.74	14.97	57.50	28.36	23.37	Joshi <i>et al.</i> (2004)
		19.37	17.95	85.80	18.42	34.25	Prashanth (2004)
		21.74	19.54	80.80	34.07	36.17	Veershetty (2004)
		32.01	31.77	98.50	47.75	64.93	Singh (2005)
		33.07	32.63	97.33	52.67	66.10	Tiwari and Lal (2005)
		31.26	28.78	84.80	35.77	-	Upadhyay <i>et al.</i> (2005)
2	Number of branches per plant	-	-	98.80	69.80	-	Prasanna <i>et al.</i> (2005)
		11.70	11.00	89.80	1.80	-	Singh <i>et al.</i> (2000)
		24.59	16.20	43.37	-	21.97	Joshi and Singh (2003)
		15.28	8.36	29.90	1.02	9.41	Prashanth (2003)
		36.93	30.98	70.40	8.70	53.53	Veershetty (2004)
		23.49	22.58	92.40	2.39	44.67	Singh (2005)
		24.79	23.41	89.22	4.57	45.47	Tiwari and Lal (2005)
		16.12	10.68	43.90	1.37	14.57	Kumar <i>et al.</i> (2006)
		17.91	16.41	84.00	-	31.04	Mehta and Asati (2008)

Contd.....

Sl. No.	Character	PCV %	GCV %	h^2	GA	GAM %	References
		35.93	24.72	47.33	14.87	-	Upadhyay <i>et al.</i> (2005)
		45.40	42.29	86.78	3.84	81.16	Revanasiddappa (2008)
		28.36	26.60	93.76	3.20	54.79	Sivaprasad (2008)
3	Stem girth	38.24	19.88	27.00	6.06	21.29	Veershetty (2004)
		18.59	18.29	96.80	11.60	37.07	Singh (2005)
		72.71	70.94	95.19	34.51	142.30	Tiwari and Lal (2005)
		55.56	51.84	87.05	33.08	-	Upadhyay <i>et al.</i> (2005)
		52.74	47.23	80.20	34.69	87.14	Prashanth <i>et al.</i> (2006)
		25.06	20.10	64.40	14.32	33.23	Kumar <i>et al.</i> (2006)
		24.74	18.29	54.70	-	27.86	Mehta and Asati (2008)
		169.15	167.85	98.47	89.95	343.13	Revanasiddappa (2008)
		43.90	37.32	85.00	20.78	76.88	Sivaprasad (2008)
4	Number of fruits per plant	35.50	35.40	99.20	32.90	-	Singh <i>et al.</i> (2000)
		-	-	98.90	79.60	-	Parasanna <i>et al.</i> (2005)
		61.21	44.05	51.77	-	65.24	Joshi and Singh (2003)
		31.79	30.29	90.80	27.30	59.46	Mohanty (2003)
		52.15	44.70	73.40	14.06	78.93	Joshi <i>et al.</i> (2004)
5	Average fruit weight	24.79	24.49	97.53	49.81	-	Parvindarsingh <i>et al.</i> (2002)
		38.96	37.91	94.70	38.94	75.98	Mohanty (2003)
		28.71	27.27	90.20	34.85	53.35	Prashanth (2004)
		41.71	34.73	69.30	30.95	59.59	Joshi <i>et al.</i> (2004)

Contd....

Sl. No.	Character	PCV %	GCV %	h^2	GA	GAM %	References
		21.50	16.58	59.50	13.25	26.34	Veershetty (2004)
		5.57	4.97	79.70	3.15	9.14	Singh (2005)
		31.07	29.82	92.09	22.43	58.90	Tiwari and Lal (2005)
		38.57	38.10	97.60	68.15	77.52	Prashanth <i>et al.</i> (2006)
		29.89	24.11	65.10	-	40.08	Mehta and Asati (2008)
		49.19	46.19	89.18	35.77	89.33	Revanasiddappa (2008)
		24.79	19.33	77.98	15.68	39.82	Sivaprasad (2008)
6	Yield per plant	24.70	24.10	95.70	655.30	-	Singh <i>et al.</i> (2000)
		17.65	16.85	91.13	-	37.13	Parvindarsingh <i>et al.</i> (2002)
		38.63	20.84	29.10	-	23.16	Joshi and Singh (2003)
		24.31	23.22	91.20	0.96	45.93	Prashanth (2004)
		20.64	15.43	55.90	180.59	23.77	Joshi <i>et al.</i> (2004)
		35.14	18.41	27.40	185.94	20.00	Veershetty (2004)
		57.48	55.05	90.90	0.87	106.60	Tiwari and Lal (2005)
		48.34	45.38	88.14	13.26	-	Upadhyay <i>et al.</i> (2005)
		34.83	28.27	65.90	1.16	47.07	Prashanth <i>et al.</i> (2006)
		31.23	29.41	88.70	-	57.23	Mehta and Asati (2008)
		97.22	92.77	91.06	1846.48	182.36	Revanasiddappa (2008)
		48.26	39.51	81.85	855.04	81.39	Sivaprasad (2008)

2.4 Genetic divergence in tomato

Planning and execution of breeding program for the improvement of quantitative attributes depends to a great extent, upon the magnitude of genetic variability and divergence existing in the material. Statistical techniques such as Mahalanobis's D^2 , which quantify the differences among the several quantitative traits is an efficient method to gauge the extent of diversity among the genotypes. D^2 statistic as a measurable genetic divergence was used for the first time in the field of plant breeding by Nair and Mukherjee (1960) in classifying teak. Importance of genetic divergence to yield and heterosis in tomato has been emphasized by several workers.

Genus *Lycopersicon* possess a wealth of genetic diversity. Complexity of forms in the genus *Lycopersicon* include several cultivated and wild progenitors. Phenomenon of introgression between species has further enriched the diversity.

Sachan and Sharma (1971) while studying the multivariate analysis of genetic divergence in tomato reported its use in selecting genetically diverse parents for a successful hybridization programme out of total 20 varieties belonging to diverse genetic and geographical origins. These varieties were grouped in to four clusters and also found that the maximum contribution to total divergence was by stem length followed by number of branches, number of inflorescence and number of fruits per plant. Khanna and Misra (1977) grouped 50 varieties into ten clusters on the basis of intra and inter cluster similarity with respect to plant height, fruit number per plant, number of branches, number of locules, number of days to flowering, total soluble solids and fruit yield in tomato, while TSS, locule number and fruit number per plant were the major determinants of D^2 values.

Bhattacharya *et al.* (1979) attempted to know the species differentiation in tomato based on the results of genetic divergence by D^2 statistics using 50 tomato genotypes including four wild collections. These genotypes were grouped in to 16 clusters on the basis of relative magnitude of D^2 values. Four wild collections of which three belonged to *Lycopersicon peruvianum* and one to *L. pimphenellifolium*

Mill. were grouped in to three distinct clusters which were highly diverse from all other clusters comprising only the common cultivars.

Singh and Singh (1980) studied 21 Indian and nine foreign varieties of tomato using Mahalanobis's D^2 statistics. Maximum divergence was noticed from the number of fruits, fruit size and number of branches per plant and varieties were grouped in to eight clusters. Patil (1984) studied the genetic divergence in 55 genotypes which were grouped in to nine clusters. Among six characters, average fruit weight and plant height contributed 82.90 per cent to the total D^2 statistic.

Kurian and Peter (1994) reported that genetic diversity in a population of 64 tomato lines assessed using D^2 value indicated considerable diversity and were grouped into eight clusters. Maximum contribution to the total genetic divergence was made by locules per fruit.

Dharmatti *et al.* (2001) studied genetic divergence for 402 summer tomato lines using multivariate analysis ethod. The 402 lines were grouped into 4 clusters based on similarities of D^2 values. Considerable diversity within and between the clusters were observed and the characters like tomato leaf curl virus resistance, fruit yield per plant and number of white flies per plant contributed maximum to the divergence.

Sharma and Verma (2001) reported 18 genotypes of tomato were studied for genetic divergence. The genotypes were grouped in cluster irrespective of geographic divergence indicating no parallelism of fruit genetic divergence and geographical divergence. The characters like fruit yield per plant, pericarp thickness and fruit diameter lays an important role in divergence between the population.

A study was conducted with 23 genotypes of Tomato in Meghalaya. There was considerable diversity among genotypes for 8 morphological characters. among them plant height, fruit number and fruit size contributed to the divergence. Crosses involving L-964 and L-154 with Arka Abha and LE-79 were recommended for improved yield and better fruit size as reported by Parthasarathy and Aswath (2002).

Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and they grouped genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes, cluster 5 having 6 genotypes. The mean fruit yield per plant (1034 g/plant) and average fruit weight (102.76 g) were the highest in cluster 5 and 3 respectively. The plant height (135.91 cm), harvest duration (37.77 days) were maximum in cluster 15 and lowest number of leaves (20280) was recorded in cluster 9 and cluster 6 consists of highest number of fruits per cluster (4.90).

Sixty-seven genotypes of tomato were grouped into seven clusters by following Mahalanobis's D^2 analysis. The cluster IV showed maximum intra cluster distance and the maximum inter-cluster distance was observed between cluster V and VI. Among the 21 characters included in D^2 analysis, number of seeds per fruit contributed maximum to genetic diversity followed by average fruit weight, number of fruits per plant and fruit volume (Prashanth, 2003).

Veershetty (2004) reported divergence for 32 tomato genotypes by following Mahalanobis's D^2 analysis for 16 productivity traits. The traits like number of fruits per cluster, plant height and number of clusters per plant contributed greatly towards divergence.

Ten hybrids were evaluated for genetic diversity and grouped into three clusters by using Mahalanobis D^2 statistics for eleven traits. Among the traits studied, average fruit weight and total soluble solids contributed maximum towards genetic divergence followed by number of flowers per cluster, plant height and number of locules per fruit (Sekar *et al.*, 2008).

2.5 Heterosis in tomato

Superiority of F_1 over parents is called heterosis. Exploitation of heterosis provides an excellent opportunity for deciding efficient traits in crops like tomato. Commercial F_1 s of tomato are now gaining popularity among the growers due to their higher yielding potential along with better quality attributes. Superiority of F_1 s over mid and better parent is reviewed in Table 3.

Table 3. Recent reports on heterosis in tomato

Sl. No.	Character	Range Per cent of heterosis over		References
		Mid parent	Better Parent	
1	Plant height	-10.98 to -37.18	14.29 to 27.73	Baishya <i>et al.</i> (2001)
			-24.22 to -25.76	Fageria <i>et al.</i> (2001)
		-6.33 to -38.59	-17.21 to -28.56	Mahendrakar (2004)
			-2.36 to -40.94	Sajjan (2001)
		-18.94 to -20.45	15.71 to 129.67	Sharma <i>et al.</i> (2001)
			-20.98 to 17.57	Joshi and Thakur (2003)
		-21.54 to -55.05	-27.93 to 34.62	Kulkarni (2003)
			-45.90 to 37.50	Prashanth (2004)
		-32.70 to -47.60	-43.98 to -14.43	Tiwari and Lal (2004)
			37.28	Premalakshmi <i>et al.</i> (2006)
		-33.82 to -20.16	2.28 to -74.91	Asati <i>et al.</i> (2007)
			-34.44 to -43.67	Singh <i>et al.</i> (2007)
		-22.52 to -44.19	117.29	Sharma and Thakur (2008)
			-35.99 to -26.02	Singh <i>et al.</i> (2008)
2	Number of branches per plant	-53.85 to -34.02	-25.35 to -1.01	Yashavantakumar (2008)
			-57.4 to -30.49	Santosh and Manish (2011)
		25.60 to -50.80	-18.90 to -38.90	Sajjan (2001)
			-14.35 to -18.66	Kulkarni (2003)
			-19.27 to -35.21	Tiwari and Lal (2004)

Contd.....

Sl. No.	Characther	Range Per cent of heterosis over		References
		Mid parent	Better Parent	
			48.93 155.80 -38.07 to -55.52	Asati <i>et al.</i> (2007) Singh <i>et al.</i> (2008) Yashavantakumar (2008)
3	Number of fruits per plant	-4.27 to -137.82 -27.78 to -181.52 0.90 to 248.90 -15.52 to -213.52 -18.45 to -232.37	-16.93 to 87.32 -27.69 to 49.37 -40.50 to 123.39 -24.17 to 52.28 25.90 to 153.80 -56.81 to 77.90 6.96 to 210.70 38.96 165.43 -30.37 to 215.77	Sajjan (2001) Joshi and Thakur (2003) Kulkarni (2003) Mahendrakar (2004) Tiwari and Lal (2004) Duhan <i>et al.</i> (2005) Premalakshmi <i>et al.</i> (2006) Asati <i>et al.</i> (2007) Singh <i>et al.</i> (2008) Yashavantakumar (2008)
4	Average fruit weight	-11.93 to -120.00 -103.83 to -205.17 -70.83 to -53.65 -45.73 to -57.59 -42.54 to -52.92 -61.49 to -45.01	-36.36 to -96.88 -7.33 to -26.79 -80.59 to 80.63 -76.29 to -42.40 -44.07 to -59.49 -45.73 to -57.59 -29.66 to -45.97 -44.05 to -73.64 -62.50 to -40.31 42.87	Baishya <i>et al.</i> (2001) Fageria <i>et al.</i> (2001) Sharma <i>et al.</i> (2001) Sajjan (2001) Kulkarni (2003) Mahendrakar (2004) Prashanth (2004) Duhan <i>et al.</i> (2005) Premalakshmi <i>et al.</i> (2006) Asati <i>et al.</i> (2007)

Contd.....

Sl. No.	Characther	Range Per cent of heterosis over		References
		Mid parent	Better Parent	
		-30.50 to -30.50	-21.60 to -23.52 2.04 to 40.00 -30.05 to -37.76 12.50 to 14.30	Sharma and Thakur (2008) Singh <i>et al.</i> (2008) Yashavantakumar (2008) Rahmani <i>et al.</i> (2010)
5	Yield per plant	-41.85 to -129.67 -57.22 to -172.52 -40.74 to -93.13 0.47 to 120.41 65.80 to 402.70 -0.06 to -179.45 -30.94 to -333.45	-80.92 to 113.03 17.28 to 48.21 15.44 to 58.59 -70.48 to -108.60 -41.30 to 87.41 -10.22 to 42.49 2.92 to 54.17 -46.01 to 91.63 16.60 to 222.60 -52.33 to -116.03 -38.99 to -177.84 75.68 72.90 to 75.53 75.00 to 87.00 -29.04 to -40.74 210.45 -43.67 to -310.91 24.00 to 34.90 29.82 to 62.31	Baishya <i>et al.</i> (2001) Fageria <i>et al.</i> (2001) Sharma <i>et al.</i> (2001) Sajjan (2001) Kulkarni (2003) Joshi and Thakur (2003) Bhatt <i>et al.</i> (2004) Mahendrakar (2004) Tiwari and Lal (2004) Duhan <i>et al.</i> (2005) Premalakshmi <i>et al.</i> (2006) Asati <i>et al.</i> (2007) Hannan <i>et al.</i> (2007) Roy (2007), Sharma and Thakur (2008) Singh <i>et al.</i> (2008) Yashavantakumar (2008) Rahmani <i>et al.</i> (2010) Ahmad <i>et al.</i> (2011)

2.6 Combining ability reports in tomato

Combining ability studies furnish useful information regarding selection of suitable genotypes for effective hybridization and at the same time to elucidate the nature and magnitude of different types of generation. The magnitude of variances due to gca (σ^2_g) indicated the preponderance of non-additive gene action for yield and other horticultural traits. σ^2_{gca} more than σ^2_{sca} for particular trait reveals predominance of additive generation over other dominance and epistasis gene action. The review of literature related to combining ability effects were given in Table 4.

Table 4. Recent reports on combining ability in tomato

Sl. No.	Character	Combinig ability variance and effect	Gene action		References
			Additive	Non Additive	
1	Plant height	Significant GCA and SCA variance SCA >GCA variance GCA > SCA variance Significant gca and sca effects Higher sca effect	 + 	 + +	Yashavantakumar (2008) Bhatt <i>et al.</i> (2001), Kulkarni (2003), Prashanth(2004), Pandey <i>et al.</i> (2006), Kavitha <i>et al.</i> (2007), Mahendrakar <i>et al.</i> (2007), Singh <i>et al.</i> (2008) Sajjan (2001), Rai <i>et al.</i> (2003) Bhatt <i>et al.</i> (2004), Singh <i>et al.</i> (2005) Kulkarni (2003), Mahendrakar (2004), Prashanth (2004), Singh <i>et al.</i> (2005), Premalakshmi <i>et al.</i> (2006) Asati <i>et al.</i> (2007), Singh <i>et al.</i> (2008), Yashavantakumar (2008), Sharma and Sharma (2010)
2	Number of fruits per plant	Significant of GCA> SCA variance SCA variance > GCA variance Significant gca and sca effects and higher sca effects Higher gca effect	 + +	 + +	Sajjan (2001), Joshi and Thakur (2003) Bhatt <i>et al.</i> (2001), Kulkarni (2003), Mahendrakar (2004), Pandey <i>et al.</i> (2006), Kavitha <i>et al.</i> (2007), Singh <i>et al.</i> (2008), Yashavantakumar (2008) Kulkarni (2003), Joshi and Thakur (2003), Bhatt <i>et al.</i> (2004), Mahendrakar (2004), Premalakshmi et al . (2006), Ahmad <i>et al.</i> (2009), Ravindra <i>et al.</i> (2013) Asati <i>et al.</i> (2007)

Contd.....

Sl. No.	Character	Combinig ability variance and effect	Gene action		References
			Additive	Non Additive	
3	Average fruit weight	Higher GCA variance > SCA variance SCA variance > GCA variance Significant gca and sca effects Higher sca effects	+	+	Chadha <i>et al.</i> (2002), Rai <i>et al.</i> (2003), Joshi and Thakur (2003), Bhatt <i>et al.</i> (2004), Mahendrakar (2004) Singh <i>et al.</i> (2005) Sajjan (2001), Patil (2003), Pandey <i>et al.</i> (2006), Yashavantakumar (2008) Chadha <i>et al.</i> (2002), Kulkarni (2003), Joshi and Thakur (2003), Mahendrakar (2004), Prashanth (2004), Singh <i>et al.</i> (2005), Premalakshmi <i>et al.</i> (2006), Asati <i>et al.</i> (2007), Kavitha <i>et al.</i> (2007), Singh <i>et al.</i> (2008), Yashavantakumar (2008), Ravindra <i>et al.</i> , (2013) Sharma and Sharam (2010)
4	Yield per plant	Significant GCA and SCA variance High GCA variance High SCA variance Significant gca and sca effects High sca effects			Rai <i>et al.</i> (2003), Asati <i>et al.</i> (2007), Yashavantakumar (2008) Bhatt <i>et al.</i> (2001), Sajjan (2001), Kulkarni (2003), Prashanth (2004), Pandey <i>et al.</i> (2006), Kumari and Srivastava (2007) Kavitha <i>et al.</i> (2007), Mahendrakar <i>et al.</i> (2007), Singh <i>et al.</i> (2008) Ahmad <i>et al.</i> , (2009), Akram <i>et al.</i> , (2012) Singh <i>et al.</i> , 2010, Sharma and Sharam (2010)

3. MATERIAL AND METHODS

3.1 Experimental site

The experiment was conducted in experimental field of Department of Crop Improvement and Biotechnology, Kittur Rani Channamma College of Horticulture, Arabhavi, Gokak taluk, Belgaum district, Karnataka. Arabhavi is situated in North Eastern dry zone of Karnataka state at 16°15' N altitude, 75°45' E longitude and at an altitude of 612.03 meters above MSL. Arabhavi comes under dry zone 3 of region 2 of agro-climatic zones of Karnataka. The meteorological data during the period of experiment as recorded at meteorological observatory of Agricultural Research Station, Arabhavi are presented in Appendix I. The experimental site consisted of medium deep black soil.

3.2 Details of experiment

3.2.1 Screening tomato genotypes for TyLCV tolerance

3.2.1.1 Experimental site

The experiment was laid out in a complete randomized block design with hundred genotypes and three replications. The genotypes were collected from AVRDC, Taiwan and other leading research institutes from India (Appendix II). To screen the genotypes on their performance against TyLCV, the experiment was conducted in *rabi* 2011. The experimental field was brought to fine tilth by repeated ploughing. Farmyard manure was incorporated in the soil at the rate of 20 tonnes per hectare. Regular irrigation and hand weeding operations were carried out. Three week transplanted plants were supported by staking. Other cultural operations were carried out as per recommended package of practices University of Agricultural Sciences, Dharwad (Anon., 2009).

3.2.1.2 Fertiliser application

Fertilisers at the rate of 60 kg N, 50 kg P₂O₅ and 30 kg K₂O per hectare were applied uniformly to all genotypes. Half dose of N and full dose of P and K were

applied before transplanting and remaining half dose of N was applied four weeks after transplanting.

3.2.1.3 Experimental plot size

Each genotype was planted in 60 cm x 90 cm spacing. Twenty plants per genotype were planted with three replications and 10.8m² plot was allotted per genotype.

3.2.1.4 Nursery rising of seedlings

Seeds of collected genotypes were sown in nursery trays (14 x 7 cells) in coco peat, soil and sand media (40:30:30). Nursery was laid out in an insect proof polyhouse and care was taken to grow healthy seedlings for transplanting in the main field. 30 days old seedlings were transplanted in the main field.

3.2.1.5 Crop cultivation

Mechanical support was given to the crop three weeks after transplanting to assure proper growth. Regular irrigation and weeding was carried out. No pesticide sprays were applied to ensure high vector population and spreading of TyLCV.

3.2.1.6 Collection of experimental data

Five random plants were selected for recording experimental data. Mean value of these five plants was considered for statistical analysis. Parameters on which observations recorded are given below.

3.2.1.6.1 Morphological parameters

3.2.1.6.1.1 Plant height (cm)

Height of plant was measured from ground to tip in centimetres. This observation was recorded at 45, 60 and 90 days after planting (DAT).

3.2.1.6.1.2 Number of branches

Number of primary branches on main stem was recorded at 45, 60 and 90 DAT.

3.2.1.6.1.3 Stem girth (cm)

Girth of main stem was measured at ground level using measuring tape at 45, 60 and 90 DAT.

3.2.1.6.1.4 Number of leaves

Total number of compound leaves present on plant at 45, 60 and 90 days were counted.

3.2.1.6.1.5 Leaf area per plant (cm²)

Five randomly selected compound leaves from each plant were mounted on graph sheet and the area occupied by each leaf was counted. Mean area was calculated and was considered as single leaf area. This was multiplied to the total number of leaves to get total leaf area per plant. This observation was recorded at 45, 60 and 90 DAT.

3.2.1.6.1.6 Root length (cm)

Plants were uprooted carefully to not to disturb roots. Length was measured from the collar region to tip of root and recorded in centimetres.

3.2.1.6.1.7 Root volume (cc)

Water of known volume is taken in a measuring cylinder. Root portion of plant is immersed completely till the collar level. The volume of water displaced by root is recorded as root volume in cubic centimetres.

3.2.1.6.2 Disease assessment

3.2.1.6. 2.1 Per cent plant survival

Total number of plants which were not infected by leaf curl disease was recorded at 30, 45, 60, 75 and 90 DAT and the plant survival was expressed in percentage using the following formula.

$$\text{Per cent plant survival} = \frac{\text{Number of plants without disease}}{\text{Total number of plants}} \times 100$$

3.2.1.6.2.2 Disease severity index for vegetative growth

Disease progress was monitored fortnightly after 30 DAT (30, 45 and 60 DAT). Disease severity was observed on visual symptoms. Each plant was assigned a disease rate according to Pico *et al.* (1998). The disease scoring is as follows:

Score	Class	Symptoms
0	Tolerant	No visible symptoms
1	Slightly susceptible	Slight marginal yellowing and curling
2	Moderately susceptible	Slight marginal/interveinal yellowing; moderate puckering and curling
3	Severely susceptible	Sever marginal/interveinal yellowing; moderate puckering and curling
4	Highly susceptible	Foliar symptoms similar to 3 accompanied by reduction in leaf size, branching and severe stunting

Individual plant scoring for each cultivar and accession were added and divided by the number of infected plants to obtain the corresponding severity index.

3.2.1.6.2.3 Disease severity index for flowering and fruit setting

Observations were recorded as same as 3.3.1.6.6.1. The scoring was assigned according to Pico *et al.* (1998) on flowering and fruiting characters. The scoring is as follows:

Score	Class	Symptoms
0	Tolerant	No visible symptoms
1	Slightly susceptible	Slight flower shedding
2	Moderately susceptible	Slight flower abortion and shedding. Fruit set slightly reduced.
3	Severely susceptible	Moderate flower abortion and shedding. Fruit set Moderately reduced
4	Highly susceptible	Severe flower abortion and shedding. Fruit set severely reduced

Individual plant scoring for each cultivar and accession were added and divided by the number of infected plants to obtain the corresponding severity index.

3.2.1.6.2.4 Vector population count

Number of whiteflies on top three compound leaves was recorded from each plant in the morning hours without disturbing the plants.

3.2.1.6.3 Yield parameters

3.2.1.6.3.1 Number of fruits per plant

Number of fruits harvested from five tagged plants at each picking (harvest) were counted and total number of fruits per plant was calculated.

3.2.1.6.3.2 Average fruit weight (g)

Average fruit weight was calculated by dividing the final yield by the total number of fruits harvested.

3.2.1.6.3.3 Yield per plant (kg)

Total weight of fruits harvested from the selected plants from all the harvests were added and average yield per plant was worked out. This value was expressed in kilograms per plant.

3.2.1.7 Statistical analysis

All the data collected for different growth, disease assessment and yield parameters were subjected to basic analysis and following statistical parameters were worked out.

3.2.1.7.1 Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) was done separately for each character for all treatments. The model of the analysis of variance is given below.

Source	d.f.	Expected values of M.S.S.	MSS	Calculated Value of (F)
Replication	r-1	MSSr (M_1)	-	(M_1/M_3)
Genotype	g-1	MSSg (M_2)	$\sigma^2_e + \sigma^2_g$	-
Error	(r-1) (g-1)	MSSe (M_3)	σ^2_e	-
Total	(rg-1)	$M_1 + M_2 + M_3$	$M_1 + (M_2/M_3)$	-

Where,

r = Number of replications

g = Number of genotypes

MSSr = Mean sum of squares due to replication

MSSg = Mean sum of squares due to genotypes

MSSe = Mean sum of squares due to error

σ^2_e = Error variance

σ^2_g = Genotypic variance

The standard error was calculated as $SE_m = \frac{\sqrt{EMSS}}{r}$

Significance of treatments mean squares and replication mean squares were tested by comparing with error mean squares referring to 'F' table value at 5 per cent level of probabilities.

3.2.1.7.2 Variability studies

3.2.1.7.2.1 Estimation of genetic parameters

Genotypic and phenotypic variances and coefficient of radiances were computed based on the expected mean sum of squares from ANOVA table as follows.

The treatment mean sum of squares due to genotypes is made up of environmental variance along with 'r' times the genetic variances ('r' being number of replications).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{TMSS} - \text{EMSS}}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

$$\text{Error variance } (\sigma^2_e) = \text{EMSS}$$

Where,

TMSS - Mean sum of squares for treatments

EMSS - Mean sum of squares for error

3.2.1.7.2.2 Genotypic and phenotypic coefficients of variation

Genotypic and phenotypic coefficients of variation were calculated according to Burton (1952).

$$\text{PCV (\%)} = \frac{\sqrt{\text{Phenotypic Variance of Germplasm}}}{\text{General Mean of Character}} \times 100$$

$$\text{GCV (\%)} = \frac{\sqrt{\text{Genotypic Variance of Germplasm}}}{\text{General Mean of Character}} \times 100$$

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as follows.

0 – 10%	- Low
10-20	- Moderate
20% and above	- High

3.2.1.7. 3 Heritability

The broad sense heritability (h^2_{bs}) was estimated by following the procedure suggested by Weber and Moorthy (1952) as indicated here below.

$$\text{Heritability (\%)} = \frac{V_g}{V_p} \times 100$$

Where, V_p is the phenotypic variance and V_g is the genotypic variance of respective germplasm.

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1994)

0 – 10%	- Low
10-20%	- Moderate
>20%	- High

3.2.1.7. 4 Genetic advance

It was predicted by using the formula provided by Johnson *et al.* (1955).

$$GA = h^2_{bs} \times \sigma_p \times k$$

Where,

h^2_{bs} = Heritability in broad sense

σ_p = Phenotypic standard deviation of the trait

k = Standard selection differential which is 2.06 at 5 per cent selection intensity

Genetic advance as per cent mean (GAM)

It was computed by the formula.

$$GAM(\%) = \frac{\text{Genetic Advance}}{\text{General Mean of the Character}} \times 100$$

The genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

0 – 10%	- Low
10-20%	- Moderate
>20%	- High

3.2.1.8 Genetic diversity

Mahalanobis D² analysis

Mahalanobis's (1936) D² - statistic analysis was used for assessing the genetic divergence among the test entries. The generalized distance between any two population is given by formula,

$$D^2 = \sum_{ij} \sum_{ij} s_i s_j$$

Where,

D^2 = Square of generalized distance

$\sum_{ij}$ = Reciprocal of the common dispersal matrix

$$s^{ai} = (\mu_i - \mu)^2$$

$$s^{aj} = (\mu_j - \mu)^2$$

μ = General mean

Since the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character means (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two genotypes (Rao, 1952).

Clustering of D^2 values

All then $n(n-1)/2$ D^2 values were clustered using Tocher's method as described by Rao (1952).

Intra cluster distance

The intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Square of intracluster distance} = \frac{\sum D_i^2}{n}$$

Where, D_i^2 - sum of distance between all possible combinations.

n - Number of all possible combinations

Inter cluster distance

The inter cluster distance were calculated by the formulae described by Singh and Chaudhary (1977).

$$\text{Square of intracluster distance} = \frac{\sum D_i^2}{n_i n_j}$$

Where,

? D_i^2 is the sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.2.1.9 Selection of parents for hybridization

Based on the *per se* performance of genotypes in the TyLCV screening, two genotypes each were selected which were tolerant and susceptible to the disease. These genotypes were used as parents in further hybridization work.

3.2.2 Screening tomato genotypes for drought tolerance

This was done to screen the tomato genotypes for drought tolerance. The experimental site, fertiliser application, experimental plot size, nursery raising of seedlings and crop cultivation (same as 3.3.1.1, 3.3.1.2, 3.3.1.3, 3.3.1.4 and 3.3.1.5) were maintained same as in screening for TyLCV tolerance. The same 100 genotypes used in 3.3.1 were used to screen for drought also. This experiment was laid out in randomized block design. Genotypes and irrigation treatments were considered as two factors for the screening. This screening was conducted in *Summer* 2012.

3.2.2.1 Drought imposition in field

Two sets of these 100 genotypes were transplanted in the main field with three replications. One set was provided with normal irrigation and for the other set irrigation was restricted to once in two weeks to impose drought condition. The seedlings in the second set were allowed to acclimatize in the main field for two week and then the drought condition was imposed.

3.2.2.2 Collection of experimental data

Five random plants were selected for recording experimental data. Mean value of these five plants was considered for statistical analysis. Observations recorded are given below.

3.2.2.2.1 Morphological parameters

Observations for the plant morphological parameters viz., plant height, number of branches, stem girth, number of leaves, leaf area per plant, root length and root volume were recorded in the same way as in 3.3.1.6.1.

3.2.2.2.2 Plant growth parameters

3.2.2.2.2.1 Absolute growth rate

It is the dry matter production per unit time (g.day^{-1}) and was calculated by using the following formula.

$$\text{AGR} = \frac{(W_2 - W_1)}{(t_2 - t_1)}$$

Where,

W_1 - Dry weight of plant at t_1

W_2 - Dry weight of plant at t_2

3.2.2.2.2.2 Relative growth rate

It is the rate of increase in the dry weight per unit dry weight ($\text{mg. m}^{-2}.\text{day}^{-1}$) already present and was calculated by using the formula of Blackman (1919).

$$\text{RGR} = \frac{\log_e W_2 - \log_e W_1}{t_2 - t_1}$$

Where,

W_1 - Dry weight of plant at t_1

W_2 - Dry weight of plant at t_2

3.2.2.2.3 Crop growth rate

It is the rate of dry matter production per unit ground area per unit time. It was calculated by using the formula given by Watson (1952) and expressed as $\text{g.m}^{-2}.\text{day}^{-1}$.

$$\text{CGR} = \frac{W_2 - W_1}{t_2 - t_1} \times \frac{1}{A}$$

Where,

W_1 - Dry weight of plant at t_1

W_2 - Dry weight of plant at t_2

A - Land area

3.2.2.2.3 Yield parameters

Observations for the plant yield parameters viz., number of fruits per plant, average fruit weight and yield per plant were recorded in the same way as in 3.3.1.6.3.

3.2.2.3 Statistical analysis

Fisher's method of analysis of variance was applied for the analysis and interpretation of the experimental data as given by Panse and Sukhatme (1967). The level of significance used in the "F" and "t" tests was of $P=0.05$. The results were presented and discussed in the text at this probability level.

3.2.2.4 Selection of parents for hybridization

Based on the *per se* performance of genotypes in the drought screening, two genotypes each were selected which were tolerant and susceptible to drought. These genotypes were used as parents in the further hybridization work.

3.2.3 Hybridization

The selected genotypes from the screening experiment were used for making half diallel crosses. Unpaired parents planting arrangement was followed for this experiment to make crosses. Emasculation of was carried out in the evening one day prior to pollination with the help of forceps. Anthers were collected in the previous

day of pollination, dried and pollen was collected from these anthers. The pollen was brushed on the receptive stigma at the time of anthesis. Crossed fruits were retained on the plant up to maturity stage. Later, the fruits were harvested and seeds were extracted by fermentation method.

3.2.4 Evaluation of parents and hybrids for TyLCV tolerance

Eight parents and twenty eight hybrids were evaluated for their tolerance to TyLCV during *rabi* 2012. Crop cultivation and management practised carried out were same as those done during the previous screening. No crop protection spray was taken to assure vector population build up and disease spread. Arka Vikas was used as commercial check for evaluation of hybrids and parents.

3.2.5 Evaluation of parents and hybrids for drought tolerance

The same eight parents and twenty eight hybrids were used to evaluate for drought tolerance. This experiment was conducted in *Summer* 2013. Crop cultivation practices were same as those in previous screening. Drought imposing was also as same as 3.3.2.1. The crop was taken in pot culture in departments polyhouse to tune up the evaluation.

3.2.5.1 Observations recorded

The morphological, plant growth and yield parameters were recorded as in 3.3.1.6.1., 3.3.2.2.2 and 3.3.1.6.3 respectively. Few more morphological and biochemical parameters were added to enhance the screening are as follows.

3.2.5.1.1 Morphological parameters

3.2.5.1.1.1 Number of stomata

Five leaves mature leaves (fifth from terminal) were collected from the randomly selected plants in the forenoon of bright sunny day. Stomatal impressions were taken from the middle portion of lower surface of leaves by using adhesive celluloid tape. The tape was then fixed on clean glass slide and observed under microscope.

3.2.5.1.1.2 Number of pubescence

Pubescence count was done as given by Maiti and Bidinger (1979). Healthy leaf was taken and chlorophyll was bleached out using DMSO (dimethyl sulphoxide). Intact leaf sample was kept in 7 ml of DMSO for 3 hr. at 65°C. Then leaf was removed from the DMSO and leaf was made into pieces of 0.5 x 0.5 cm then observed under microscope of area 0.284 cm² and pubescence was counted both on adaxial and abaxial leaf surface and expressed as number of pubescence per cm².

3.2.5.1.2 Biochemical parameters

3.2.5.1.2.1 Proline content (µg of fresh weight)

Leaf sample (250 mg) was taken in pestle and mortar and 10 ml of 3 per cent sulphosalicylic acid was added and crushed and filtered through What Man No. 2 filter paper. Extraction procedure was repeated once again. From the extract 2 ml was pipette into a test tube, to which 2 ml of glacial acetic acid and 2 ml of acid ninhydrin was added. Then test tube was boiled on hot water bath at 100°C for one hour. Then transfer the test tube to ice bath to terminate the reaction. Then 4 ml of toluene was added and shaken the test tube gently and transferred the content to the separating funnel and collected pink coloured layer. Optical density of the extract was read at 520 nm. A blank was maintained with the reactants except the leaf extract Proline content of the sample was calculated by using the formula given by Bates *et al.* (1973).

$$\text{Proline content (}\mu\text{g g}^{-1}\text{ of fresh weight)} = \frac{36.23 \times \text{Optical Density} \times \text{Volume of aliquot taken}}{\text{Fresh weight of the sample}}$$

Where, 115.5 is the molecular weight of proline.

3.2.5.1.2.2 Chlorophyll content (mg/g fresh weight)

Chlorophyll content of leaf tissue was estimated as suggested by Hiscox and Israelstom (1979).

100 mg of freshly harvested and cleaned leaf was taken and cut in to small pieces. Cut pieces were transferred in to test tube containing 7 ml of DMSO and heated to 65°C for three hour in water bath. Extract was collected by discarding the

leaf sample. Then volume was made up to 10 ml with DMSO. Optical density of the extract was measured at 645 and 663 using DMSO as blank.

Chlorophyll a, chlorophyll b and total chlorophyll were calculated using the following formulae.

$$\text{Chlorophyll a} = \{(12.7 \times A_{663}) - (2.69 \times A_{645})\} \times \frac{v}{100 \times w \times a}$$

$$\text{Chlorophyll b} = \{(22.9 \times A_{645}) - (4.68 \times A_{663})\} \times \frac{v}{100 \times w \times a}$$

$$\text{Total Chlorophyll} = \{(20.2 \times A_{645}) - (8.02 \times A_{663})\} \times \frac{v}{100 \times w \times a}$$

Where,

v - Final volume of plant extract in ml

w - Fresh weight of the sample in g

a - Path length of light (1 cm)

3.2.6 Statistical analysis

The data on various observations such as growth, yield and quality parameters were tabulated and subjected to statistical analysis as described by Griffing's (1956).

3.2.6.1 Combining ability analysis

The variation among the hybrids was further partitioned into genetic components attributed to general combining ability (GCA) variances and specific combining ability (SCA) variances and effects were analyzed by adopting Model-I, Method-2 of Griffin's (1956), since the present study includes parental lines and F₁ hybrids (without reciprocals). The statistical procedure assumes the following mathematical model.

$$X_{ij} = \mu + g_i + g_j + S_{ij} + \frac{1}{bc} \sum_k \sum_l e_{ijkl}$$

$$i, j = 1, 2, \dots, n$$

$$k = 1, 2, \dots, b$$

$$l = 1, 2, \dots, c$$

Where,

μ = population mean

n = number of inbred parent lines

i and j = the male and female parents of ij^{th} hybrid

b = number of replications

c = number of plants per family

g_i and g_j = the general combining ability (gca) effect for the cross between i^{th} and j^{th} parents.

S_{ij} = specific combining ability effect for the cross between i^{th} and j^{th} parents
such that

$$S_{ij} = S_{ji}$$

E_{ijkl} = environmental effect associated with the $ijkl^{\text{th}}$ individual observation.

As only plot mean values were taken for analysis, $Me' = Me / bc$. Restriction imposed on the utility of this model was:

$$\sum_i g_i = 0 \text{ and } \sum_j S_{ij} + S_{ii} = 0 \text{ (for each } i \text{)}$$

3.2.6.1.1 Analysis of variance of combining ability

The variances due to general and specific combining ability were calculated as follows

$$S_g = \frac{1}{n+2} [i (X_{i.} + X_{ij})^2 - \frac{4}{n} X^2 \dots]$$

$$S_s = \sum_i \sum_j \frac{X_{ij}^2}{n+2} - \frac{1}{n+2} [i (X_{i.} + X_{ii})^2 + \frac{2}{(n+1)(n+2)} X^2 \dots]$$

Where

S_g = Sum of squares due to general combining ability

S_s = Sum of squares due to specific combining ability

n = Number of parents

X_i = Total of array of i^{th} parent in diallel table

X_{ii} = Mean of i^{th} parent

X = Grand total of $\frac{n(n+1)}{2}$ values of the diallel table

X_{ij} = Value of each cell of $\frac{n(n+1)}{2}$

The analysis of variance table for combining ability is given below:

Source	df	SS	MSS
General Combining Ability	$n - 1$	S_g	M_g
Specific Combining Ability	$\frac{n(n-1)}{2}$	S_s	M_s
Error	$\frac{(n-1)(n+2)(r-1)}{2}$	S_e	M_e
Total			

The error term in the table was obtained as $Me' = Me / r$

Where,

Me = Error variance of the experiment as determined by the general analysis of variance in the experiment and

r = number of replications

The two combining ability variances were tested for the 'F' ratio against Me' to test the significance or otherwise.

3.2.6.1.2 Estimation of combining ability effects

The general combining ability effects (gca effect = g_i) and specific combining ability effects (sca effects = S_{ij}) were estimated as follows:

$$g_i = \frac{1}{n+2} [i (X_{i.} + X_{ii}) - \frac{2}{n} X \dots]$$

$$S_{ij} = X_{ij} - \frac{1}{n+2} (X_{i.} + X_{.j} + X_{ii} + X_{jj}) + \frac{2X \dots}{(n+1)(n+2)}$$

3.2.6.1.3 Testing the significance of the combining ability

The square root of variance of an estimate is its standard error. The variances of the different estimates were calculated by multiplying the error variance from the combining ability with their respective coefficients as shown below:

Error variance ($\hat{\sigma}_e^2$) = $M_e = \sigma_e^2$ = Error variance from the RCBD analysis.

Variance of ($\hat{g}_i$) = $(n-1)/(n(n+2)) \sigma_e^2$ = Variance of gca effects

Variance of ($\hat{s}_{ij}$) = $(n^2 + (n+2))/(n+1)(n+2)) \sigma_e^2$ = Variance of sca effects

3.2.6.1.4 Testing of significance of differences between estimates

To test the significance of the difference between two estimates, least significant difference was calculated by the product of table value of 't' at appropriate degree of freedom for error and the standard error of the difference of two estimates. The standard error of the difference was taken as the square root of the variance of difference between two estimates. The variance was obtained as follows:

For testing differences between two estimates of gca effects:

$$\text{Variance } (g_i - g_j) = \frac{n}{n+2} \sigma_e^2$$

For testing differences between two estimates of sca effects in the same array:

$$\text{Variance } (S_{ij} - S_{ik}) = \frac{2(n+1)}{n+2} \sigma_e^2$$

For testing differences between two estimates of sca effects in the same array:

$$\text{Variance } (S_{ij} - S_{kl}) = \frac{2n}{n+2} \sigma_e^2$$

3.2.6.2 Analysis of diallel table for genetic components of variance

After construction of diallel table for each trait, the genetic components were computed by methods of Jinks and Hayman (1953), Hayman (1954a, 1954b) and Jinks (1954) and explained through a worked example by Aksel and Johnson (1963).

3.2.6.2.1 Assumptions underlying diallel analysis

The diallel analysis (Hayman's approach) implies following assumptions:

- i) Diploid segregation
- ii) Homozygosity of parents
- iii) No difference between reciprocals
- iv) Independent action of non-allelic genes
- v) Independent or uncorrelated distribution of genes among the parents or no linkage
- vi) Absence of multiple allelism.

3.2.6.2.2 Calculation of various statistics of the diallel table

The following statistics were calculated from diallel table. Each row was considered as an array.

V_0L_0 = Variance of the parents

V_0L_1 = Variance of the array means

V_r = Variance of the rth array

W_r = Co-variance between parents and their offspring in the rth array

V_1L_1 = Mean of the variance of arrays

W_0L_1 = Mean of the co-variance of the array

ML_0 = Mean of the n parents

ML_1 = Mean of the n^2 progeny

E = Environmental variance

The above statistical parameters are made up of different genetic and environmental components of variance as mentioned below:

$$V_0L_0 = D + E$$

$$V_0L_1 = 1/4D - 1/4Fr + 1/4H_1 - 1/4H^2 + [E + 1/2 (n-2) E]/n^2$$

$$V_r = 1/4D - 1/4Fr + 1/4H_1 + [E + 1/2 (n-1) E]/n$$

$$W_r = 1/2D - 1/4Fr + E/n$$

$$V_1L_1 = 1/4D - 1/4Fr + 1/4H_1 + [E + 1/2 (n-1) E]/n$$

$$W_0LO_1 = 1/4D - 1/4Fr + E/n$$

$$(ML_1 - ML_0)^2 = 1/4^N_2 + (n-1) (n-2) E + E/n^3$$

3.2.6.2.3 Estimation of components of variation

With the expectations given below, the six genetic components were estimated by using the following formulae:

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2 V_0L_0 - 4 W_0LO_1 - 2 (n+2) \frac{\hat{E}}{n}$$

$$\hat{H}_1 = 4V_1L_1 - 4 W_0LO_1 + 4 V_1L_1 - (3n-2) \frac{\hat{E}}{n}$$

$$\hat{H}_2 = 4V_1L_1 - 4 W_0LO_1 - 2 \hat{E}$$

$$\hat{h}^2 = 4 (ML_1 - MLO) 4 (n-1) \frac{\hat{E}}{n^2}$$

$$\hat{Fr} = 2 (V_0L_0) - W_0LO_1 + V_1L_1 - W_r - V_r - 2 (n-2) \frac{\hat{E}}{n}$$

Error SS x Block SS

$$\hat{E} = \frac{\text{d. f}}{\text{Number of blocks}}$$

Where,

$\hat{D}$ = the variance due to additive effects of genes

$\hat{F}$ = the mean of Fr value.

$\hat{H}_1$ = the variance due to dominance effects of genes

$\hat{H}_2$ = the proportion of dominance variance due to positive (u) and negative (V) effects of genes

$\hat{h}^2$ = the net dominance effects expressed as the algebraic sum over all loci in heterozygous phase in all crosses

$\hat{Fr}$ = the co-variance of additive and dominance effects in a single array

$\hat{E}$ = the error variance obtained from analyses of variance in the experimental design

3.2.6.2.4 Testing the significance of the components

The variance of $\left(\frac{Wr - Vr}{2}\right)$ was used as S^2 and standard errors of the various genetic parameters were calculated using the terms of the main diagonal of the genetic components given by Hayman (1954b).

The formulae used were as follows:

$$S.E.D. = \sqrt{\frac{s^2(n^5 + n^4)}{n^5}}$$

$$S.E.F. = \sqrt{\frac{s^2(4n^5 + 20n^4 - 16n^3 + 16n^2)}{n^5}}$$

$$S.E.H_1 = \sqrt{\frac{s^2(n^5 + 41n^4 - 12n^3 + 4n^2)}{n^5}}$$

$$S.E.H_2 = \sqrt{\frac{s^2(36n^4)}{n^5}}$$

$$S.E.h^2 = \sqrt{\frac{s^2(16n^4 + 16n^2 + 32n + 16)}{n^5}}$$

$$S.E.Fr = \sqrt{\frac{4s^2(3n^3 + 3n^2 + 4n + 4)}{n^3}}$$

$$S.E.E. = \sqrt{\frac{[(S)^2]}{\frac{n^4}{n^5}}}$$

$$S.E. (D-H) = \sqrt{\frac{4s^2(9n^2 - 2n + 1)}{n^3}}$$

Where, n = number of parents

With the help of these standard errors, the significance of genetic components of variation was tested.

3.2.6.2.5 Proportion of genetic components

With the help of six genetic components, the different types of proportion and differences of genetic components were worked out. The proportions or differences that were worked out and the indications they give about the genetics of the trait are given below:

$$\left[\frac{H1}{D} \right]^{1/2} = \text{mean degree of dominance over all loci.}$$

$H1 - H2 = 0$ showed that the positive (u) and negative (v) alleles at the loci controlling the characters were in equal proportion in the parents.

$$\frac{H2}{4H1} \text{ gave the proportion of genes with positive and negative effect.}$$

$$\frac{K}{D} = \frac{\frac{(4DH1)1}{2} + F}{\frac{(4DH1)1}{2} - F} = \text{This is provided a measure of proportion of dominant and recessive genes in the parents.}$$

$\frac{h^2}{H^2}$ K, gave an estimate of the number of groups of genes controlling the character and exhibiting dominance.

Heritability in narrow sense was calculated by using the following formula of Crumppacker and Allard (1962).

$$\text{Heritability} = \frac{\frac{1}{4D}}{\frac{1}{4D} + \frac{1}{16H} - \frac{1}{8F} + E}$$

When significant dominance effects were observed, the correlation between V_r (parental value) and $W_r + V_r$ (parental order of dominance) was calculated. When correlation coefficient was significantly positive, most of the dominant genes showed a negative effect on the character under consideration. If the correlation coefficient was significantly negative, most of the dominant genes had a positive effect. This correlation was worked out by the usual procedure adopted for calculating the correlation coefficient.

3.2.6.3 Heterosis analysis

3.2.6.3.1 Estimation of heterosis

The magnitude of heterosis was estimated in relation to better parent. They were thus, calculated as percentage increase or decrease of F_1 hybrids over better parent (BP) using the methods of Turner (1953) and Hayes *et al.* (1956).

Heterosis for each trait was computed by using following formula.

$$\text{Per cent heterosis over better parent (BP)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

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

The significance of F_1 heterosis values were tested by comparing them with CD Values obtained separately for BP employing the formula given below.

$$CD = \sqrt{\frac{2MSe}{r}} \times t \text{ value}$$

Where,

MSe = Error mean sum of squares

r = Number of replications

't' = table 't' value at error degrees of freedom

4. EXPERIMENTAL RESULTS

The results of experiment conducted during 2011 to 2014 in the research field and polyhouses of Department of Biotechnology and Crop Improvement are presented in this chapter. Results are presented in the following headings:

- 4.1 Evaluation and screening of tomato genotypes for tolerance to TyLCV
- 4.2 Evaluation and screening of tomato genotypes for tolerance to drought
- 4.3 Selection of parents and hybridization in Diallel design
- 4.4 Evaluation of hybrids for tolerance to TyLCV
- 4.5 Evaluation of hybrids for tolerance to drought

4.1 Evaluation and screening of tomato genotypes for TyLCV

Hundred tomato genotypes collected from different sources were evaluated for their performance against TyLCV stress. This evaluation was conducted during *rabi* of 2011 in research field of Department of Crop Improvement and Biotechnology. The performance of these tomato genotypes was analyzed for different morphological, growth, disease index and yield parameters.

4.1.1 Analysis of variance for morphological, growth, disease index for TyLCV and yield parameters

Analysis of variance was estimated to test the significant differences among 100 genotypes of tomato during *rabi* 2011. Anova results are presented in Table 5.

It was revealed by the statistical analysis that, the evaluations were highly significant for all the morphological characteristics *viz.*, plant height at 45, 60 and 90 DAT (Days After Transplanting), number of branches at 45, 60 and 90 DAT, stem girth at 45, 60 and 90 DAT.

All the hundred genotypes were observed for six growth characters *viz.*, number of leaves at 45, 60 and 90 DAT, leaf area at 45, 60 and 90 DAT. Analysis of variance for all these six characters showed that all these characters are highly significant.

Table 5. Analysis of variance for morphological, growth, disease index for TyLCV and yield parameters

Sl. No.	Characters	MSS			
		Replications	Genotypes	Errors	CD @ 5%
I	Morphological				
1	Plant height at 45 DAT (cm)	3.92	79.60**	10.19	5.14
2	Plant height at 60 DAT (cm)	3.97	781.33**	9.04	4.84
3	Plant height at 90 DAT (cm)	3.22	527.24**	2.01	2.28
4	Number of branches at 45 DAT	1.05	8.97**	1.63	2.05
5	Number of branches at 60 DAT	0.24	8.30**	2.16	2.37
6	Number of branches at 90 DAT	1.02	10.74**	1.25	1.80
7	Stem girth at 45 DAT (cm)	0.14	6.37**	0.71	1.36
8	Stem girth at 60 DAT (cm)	0.40	16.15**	0.64	1.56
9	Stem girth at 90 DAT (cm)	1.34	51.38**	0.69	1.34
II	Growth Parameters				
1	Number of leaves at 45 DAT	0.87	46.91**	4.08	3.25
2	Number of leaves at 60 DAT	7.34	64.58**	2.94	2.76
3	Number of leaves at 90 DAT	4.65	106.95**	2.12	2.34
4	Leaf area at 45 DAT (cm ²)	97.42	1503.88**	72.29	13.69
5	Leaf area at 60 DAT (cm ²)	311.64	4476.79**	75.33	13.98
6	Leaf area at 90 DAT (cm ²)	1.66	2628.95**	25.66	8.16
III	Disease Index for TyLCV				
1	PPS at 30 DAT (%)	20.63	941.38**	11.19	5.39
2	PPS at 45 DAT (%)	23.46	980.03**	70.78	13.54
3	PPS at 60 DAT (%)	3.16	1705.73**	69.57	13.43
4	PPS at 75 DAT (%)	6.90	1734.90**	33.45	9.31
5	PPS at 90 DAT (%)	5.11	1886.15**	20.23	7.24
6	DSI (V) at 30 DAT	0.01	0.60**	0.21	0.74
7	DSI (V) at 45 DAT	0.20	1.38**	0.20	0.71
8	DSI (V) at 60 DAT	0.09	1.94**	0.17	0.66
9	DSI (V) at 75 DAT	0.02	1.85**	0.17	0.67
10	DSI (V) at 90 DAT	0.03	0.54**	0.04	0.31

Contd.....

Sl. No.	Characters	MSS			
		Replications	Genotypes	Errors	CD @ 5%
11	DSI (Flr & Frt) at 30 DAT	0.08	0.75**	0.12	0.57
12	DSI (Flr & Frt) at 45 DAT	0.09	2.49**	0.13	0.57
13	DSI (Flr & Frt) at 60 DAT	0.22	1.91**	0.17	0.66
14	DSI (Flr & Frt) at 75 DAT	0.03	1.35**	0.13	0.59
15	DSI (Flr & Frt) at 90 DAT	15.35	0.91	1.06	1.66
16	Vector Population at 30 DAT	0.05	7.60**	0.68	1.32
17	Vector Population at 45 DAT	1.94	40.75**	2.66	2.62
18	Vector Population at 60 DAT	3.32	75.47**	4.57	3.44
19	Vector Population at 75 DAT	0.23	90.88**	7.44	4.39
20	Vector Population at 90 DAT	5.88	197.84**	1.60	2.04
IV	Yield parameter				
1	Number of fruits per plant	7.60	577.54**	18.18	6.87
2	Average fruit weight (g)	17.32	607.13**	14.90	6.22
3	Yield per plant (Kg)	0.07	0.20**	0.05	0.36

** Significant at 0.01; MSS - Mean sum of squares; DAT- Days after transplanting;
 PPS - Survival percentage of plants; DSI - Disease severity index; V - Vegetative parts;
 Flr & Frt - Flowering and fruiting parts

Disease indexing was done to judge the level of infection of the disease viz., disease survival percentage (PPS) at 30, 45, 60, 75 and 90 DAT, disease severity index on vegetative parts (DSIV) at 30, 45, 60, 75 and 90 DAT, vector population at 30, 45, 60, 75 and 90 DAT were statistically highly significant, disease severity index on flowering and fruiting parts (DSI Flr and Frt) at 30, 45, 60, 75 DAT while it was non-significant at 90 DAT.

Analysis of variance for yield parameters viz., number of fruits per plant, average fruit weight and yield per plant found to be highly significant.

4.1.2 Estimation of genetic variability

Presence of wide genetic variability in collected germplasm is one of the key factors in any breeding program. To reveal the extent of genetic variability, observations on morphological characters were estimated for genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2), genetic advance (GA) and genetic advance over per cent of mean (GAM). This analysis revealed presence of variability among the genotypes.

4.1.2.1 Morphological parameters

Plant height between 45 to 90 DAT revealed that the range varied from 9.73 (90 DAT) to 69.28 (60 DAT). However maximum mean (34.77 cm) was observed during 60 DAT. In all the growth stages PCV was higher than GCV. The difference between GCV and PCV was very little at 60 DAT and 90 DAT, except for 45 DAT. Highest heritability of 98.90 per cent was recorded at 90 DAT with a GA of 27.1 and GAM of 136.03 per cent. Genotype L 06016 (37.22 cm), L 06185 (69.28) and L 06052 (48.67 cm) were found to be tallest genotypes at 45, 60 and 90 DAT, respectively (Table 6).

Considerable amount of variation was found among the genotypes for number of branches. It ranged from 5.10 to 18.74 during 45 to 90 DAT. Highest mean for this trait was observed at 90 DAT (13.97). GCV values were moderate at all the three stages of growth. PCV values were more compared to GCV and the difference between GCV and PCV was more at 45 DAT compared to that at 60 and 90 DAT.

Table 6. Estimates of variability components for morphological parameters

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
1	Plant height at 45 DAT (cm)	25.01 $\pm$ 1.84	17.36 - 37.22	23.13	33.33	19.23	23.08	69.40	8.26	33.00
2	Plant height at 60 DAT (cm)	34.77 $\pm$ 1.74	32.26 - 69.28	257.43	266.47	46.14	46.95	96.60	32.49	93.43
3	Plant height at 90 DAT (cm)	19.92 $\pm$ 0.82	9.73 - 48.66	175.08	177.09	66.41	66.79	98.90	27.10	136.03
4	Number of branches at 45 DAT	8.54 $\pm$ 0.74	5.10 - 11.74	2.45	4.07	18.31	23.63	60.10	2.50	29.24
5	Number of branches at 60 DAT	12.97 $\pm$ 0.85	9.16 - 17.23	2.05	4.21	11.03	15.82	48.60	2.05	15.84
6	Number of branches at 90 DAT	13.97 $\pm$ 0.64	10.49 - 18.71	3.17	4.41	12.74	15.04	71.70	3.11	22.23
7	Stem girth at 45 DAT (cm)	6.31 $\pm$ 0.49	3.56 - 9.46	1.89	2.60	21.78	25.56	72.60	2.41	38.23
8	Stem girth at 60 DAT (cm)	13.72 $\pm$ 0.56	6.70 - 21.93	5.07	6.01	16.41	17.86	84.40	4.26	31.06
9	Stem girth at 90 DAT (cm)	11.52 $\pm$ 0.48	3.90 - 16.63	16.90	17.59	35.68	36.40	96.10	8.30	72.04

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; DAT - Days after transplanting

Heritability was moderate at 60 DAT (48.60%), while it was found high at 45 and 90 DAT (60.10% and 71.70%, respectively). Genetic advance over mean was found to be high at 45 and 90 DAT, while it was moderate at 60 DAT. Genotypes L 06219 (11.74), L 01049 (17.23) and L 02222 (18.71) were found to be genotypes with maximum number of branches at 45, 60 and 90 DAT, respectively (Table 6)

Stem girth varied between 3.56 cm and 21.93 cm during growth period of 45 to 90 DAT. Mean value reached to its maximum at 60 DAT (13.72 cm). GCV was high at 45 and 90 DAT, whereas it was moderate at 60 DAT. PCV values were higher than GCV but the difference between them was found to be less at all stages (Table 6). Highest heritability was observed at 90 DAT (96.10%) with highest GA and GAM (8.30% and 72.04%, respectively). Genotypes Arka Alok (9.47 cm), L 01933 (21.93 cm) and L 06052 (16.33 cm) had highest values for stem girth at 45, 60 and 90 DAT, respectively.

4.1.2.2 Growth characters

Genotypes varied from 18.75 to 47.49 for number of leaves during the growth period of 45 to 90 DAT. Maximum mean value for this trait was observed at 60 DAT (37.71). GCV and PCV were found to be moderate at 45 and 60, while the values were high at 90 DAT. Highest heritability was observed at 90 DAT (94.30%) with highest GA (11.83%) and GAM (42.16%). Genotypes L 02709 (40.88), BL 1188 (47.98) and Nandi (40.37) had highest values for number of leaves at 45, 60 and 90 DAT respectively.

Values for leaf area varied from the lowest of 13.92 cm² to the highest of 203.78 cm² during the growth period of 45 DAT to 90 DAT. Highest mean value for leaf area (116.46 cm²) was noticed at 60 DAT. GCV and PCV were high for this trait at all the three stages of growth and the difference between these two values were less. Heritability was high with high GA and GAM at all stages. Highest heritability for the trait was noticed at 90 DAT. Genotype L 06043 (159.95 cm²), Mukti (203.78 cm²) and CLN 2498 E (132.58 cm²) had highest leaf area at 45, 60 and 90 DAT, respectively.

Variability estimates for number of leaves and leaf area are presented in Table 7.

Table 7. Estimates of variability components for number of leaves, leaf area and plant survival percentage

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
1	Number of leaves at 45 DAT	33.54 $\pm$ 1.17	25.81 - 40.87	14.28	18.36	11.27	12.77	77.80	6.86	20.46
2	Number of leaves at 60 DAT	37.71 $\pm$ 0.99	29.25 - 47.49	20.54	23.49	12.02	12.85	87.50	8.73	23.15
3	Number of leaves at 90 DAT	28.05 $\pm$ 0.84	18.75 - 40.36	34.95	37.06	21.08	21.71	94.30	11.83	42.16
4	Leaf area at 45 DAT (cm ²)	107.77 $\pm$ 4.90	66.47 - 159.95	477.19	549.49	20.27	21.75	86.80	41.94	38.91
5	Leaf area at 60 DAT (cm ²)	116.46 $\pm$ 5.01	64.70 - 203.78	146.72	1542.48	32.87	33.70	95.10	76.95	66.03
6	Leaf area at 90 DAT (cm ²)	37.89 $\pm$ 2.93	13.92 - 132.59	867.76	893.42	77.73	78.87	97.10	59.80	157.81
7	PPS at 30 DAT (%)	82.80 $\pm$ 1.92	18.00 - 100.00	310.06	321.26	21.26	21.64	96.50	35.64	43.04
8	PPS at 45 DAT (%)	58.96 $\pm$ 4.83	14.00 - 97.33	303.08	373.86	29.52	32.79	81.10	32.29	54.76
9	PPS at 60 DAT (%)	52.34 $\pm$ 4.79	6.33 - 88.33	545.39	614.96	44.61	47.38	88.70	45.31	86.56
10	PPS at 75 DAT (%)	34.78 $\pm$ 3.32	2.67 - 84.00	567.15	600.61	68.48	70.47	94.40	47.63	137.08
11	PPS at 90 DAT (%)	21.56 $\pm$ 2.58	0.00 - 78.00	621.97	642.21	115.67	117.54	96.80	50.56	234.51

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation;
 h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; DAT - Days after transplanting; PPS - Per cent Plant Survival

4.1.2.3 Disease Index for TyLCV

Percentage plant survival against TyLCV varied from 100.00 per cent to 0.00 per cent during 30 to 90 DAT. Initially the mean per cent plant survival was 82.80 per cent (30 DAT) and it progressively decreased to 21.56 per cent at 90 DAT. Range at 30 DAT was 18.00 to 100.00 per cent and it decreased to 0.00 to 78.00 per cent at 90 DAT. GCV estimates were high during all growth stages and it was highest at 90 DAT (115.67). PCV estimates were higher than GCV estimates at all stages and highest PCV was observed at 90 DAT (117.54). High heritability was observed for the trait at all stages and highest heritability was observed at 90 DAT (96.80%). Genetic advance estimates were also very high at this stage (234.51%). The genetic variability estimates for per cent plant survival at different stages are given in Table 7. Genotypes LA 3923, L 01933, L 01942, L 02248, L 0 6218, L 06220, Arka Meghali, Nandi and PKM 1 had the highest per cent plant survival (100.00%) at 30 DAT. Genotype PKM 1 had the highest PPS (97.33%) at 45 DAT. Genotypes L 02778 and L 06230 had the highest value of PPS (88.33%) at 60 DAT. Genotype L 06106 had the highest PPS (84.00%) at 75 DAT. Genotype Arka Abha had the highest PPS (78.00%) at 90 DAT.

Range of disease severity index, on vegetative part, at 30 DAT was 0.00 to 1.57 with grand mean of 0.50. Twenty nine genotypes had the lowest severity. Two genotypes viz., L 06223 and Patriot had the highest severity at this stage. There was a large difference between GCV (72.78) and PCV (117.04). At 45 DAT, severity index ranged from 0.00 to 3.03 and the grand mean was 1.40 at this stage. Ten genotypes had the lowest value and L 06190 had the highest severity at this stage. GCV and PCV were 44.78 and 54.84, respectively. Only five genotypes had the lowest severity (0.00) and L 02222 had the highest disease severity (3.63) at 60 DAT. GCV and PCV were 35.62 and 40.42, respectively. BL 1198 had lowest disease severity (0.23) at 75 DAT and L 01696 had highest value (3.93) for this. Grand mean was found to be 3.05 and GCV and PCV were 24.52 and 28.07, respectively. L 01942 had lowest disease severity (2.23) at 90 DAT and 48 genotypes had the highest severity (4.00) at this stage. GCV and PCV were 11.16 and 12.36, respectively (Table 8).

On flowering and fruiting parts, the disease severity ranged from 0.00 to 1.70 at 30 DAT with 0.50 as grand mean. Thirty genotypes showed minimum disease

Table 8. Disease reaction of some genotypes, mean, range, GCV and PCV for disease severity index on vegetative parts

Particulars	Disease Severity Index on vegetative parts						Disease Reaction
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	Average	
Selected Genotypes							
L 01942	0.00	0.00	0.00	0.73	2.23	0.59	Highly Tolerant
BL 1198	0.00	0.00	0.60	0.23	2.50	0.67	Highly Tolerant
L 06052	0.00	0.00	0.00	1.13	2.67	0.76	Highly Tolerant
L 06119	0.00	0.00	0.53	0.87	2.67	0.81	Moderately Tolerant
LA 3923	0.00	0.00	0.60	1.53	2.30	0.89	Moderately Tolerant
L 06185	0.00	0.00	0.00	1.30	4.00	1.06	Moderately Tolerant
L 01933	0.00	0.37	1.67	2.50	4.00	1.71	Tolerant
L 06218	0.00	0.83	1.47	2.27	4.00	1.71	Tolerant
L 06043	0.00	0.50	1.50	2.63	4.00	1.73	Tolerant
BL 1199	0.00	0.47	1.70	3.10	4.00	1.85	Moderately Susceptible
BL 1200	0.60	1.47	1.47	2.80	4.00	2.07	Moderately Susceptible
BL 1188	0.27	1.50	2.20	3.27	4.00	2.25	Moderately Susceptible
S. Harry	0.97	1.67	2.27	3.37	3.33	2.32	Highly Susceptible
W. Cherry	0.47	1.47	2.57	3.47	3.67	2.33	Highly Susceptible
Tommy Toe	0.53	1.70	2.53	3.57	3.47	2.36	Highly Susceptible
Grand mean	0.50 ± 0.26	1.40 ± 0.26	2.16 ± 0.24	3.05 ± 0.24	3.66 ± 0.11		
Range	0.00 - 1.57	0.00 - 3.03	0.00 - 3.63	0.23 - 3.93	2.23 - 4.00		
GCV	72.78	44.78	35.62	24.52	11.16		
PCV	117.04	54.84	40.42	28.07	12.36		

DAT- Days after transplanting; GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation

severity of 0.00 and CLN 2498 E showed highest disease incidence during this period. GCV was high (90.98) with very high PCV (114.86). Disease found to be more severe during 45 DAT and it ranged from 0.00 to 3.73 with a grand mean of 1.66 at this stage. Four genotypes had low disease severity, while genotype L 01869 had the highest value. GCV and PCV were 53.46 and 57.62, respectively. At 60 DAT, it ranged from 0.26 to 3.93, with grand mean of 2.53. Three genotypes had low value and L 02778 had the highest value at this stage. GCV and PCV were 30.14 and 34.24, respectively. This trait ranged from 0.40 to 3.93, with grand mean of 3.09, at 75 DAT. Genotype L 01942 had the lowest value and L 02778 had the highest value at this stage. GCV and PCV were 20.61 and 23.73, respectively. Severity reached to highest *i.e.*, 1.77 to 4.00, with grand mean of 3.33, at 90 DAT. Genotype L 06052 had the lowest severity and 28 genotypes had the highest severity. GCV was low (6.83) but high PCV (30.19) was observed (Table 9).

Vector population, at 30 DAT was ranged from 0.00 to 5.00, with a grand mean of 1.90. The GCV and PCV were, 79.87 and 90.84, respectively. Seventeen genotypes had the lowest vector population and L 01318 had the highest vector population. At 45 DAT, vector population was observed to be ranging from 1.03 to 13.17, were 6.77 was the grand mean. L 06223 had lowest and L 06218 had highest vector population. High GCV (52.66) and PCV (57.91) were estimated at this stage. At 60 DAT, range of vector population was found to be 4.63 to 21.67, with 14.42 as grand mean. PKM 1 found to be genotype with lowest vector population and CLN 2498 E had highest value for this. Estimated GCV and PCV were 33.71 and 36.82, respectively. Range was from 11.23 to 32.10 and grand mean was 22.63, at 75 DAT. BL 1198 had the lowest and L 06122 had highest vectors at this stage. GCV and PCV were 23.31 and 26.24, respectively. Range was reduced to 0.00 to 28.60 with a grand mean of 7.87, at 90 DAT. Vector population was found to be zero on 28 genotypes and L 01023 had the highest vectors at this stage. The GCV and PCV were estimated to be 102.76 and 104.00, respectively (Table 10).

4.1.2.4 Yield parameters

Number of fruits per plant ranged from 16.95 to 65.64 with an average of 39.21 fruits. Genotype Tommy Toe had the lowest and genotype L 06201 had the highest number of fruits per plant. GCV and PCV were found to be 34.83 and 36.49,

Table 9. Disease reaction of some genotypes, mean, range, GCV and PCV for disease severity index on flowering and fruiting parts

Particulars	Disease Severity Index on flowering and fruiting parts						Disease Reaction
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	Average	
Selected Genotypes							
L 06052	0.00	0.00	0.27	0.53	1.77	0.51	Highly Tolerant
L 01942	0.00	0.00	0.27	0.40	2.27	0.59	Highly Tolerant
L 06185	0.00	0.00	0.27	0.87	2.67	0.76	Moderately Tolerant
L 06208	0.00	0.00	0.33	1.03	2.67	0.81	Moderately Tolerant
L 01745	0.00	0.43	1.13	2.23	2.67	1.29	Tolerant
L 01933	0.00	0.30	1.17	2.40	2.67	1.31	Tolerant
BL 1199	0.00	0.37	1.30	2.23	2.67	1.31	Tolerant
L 01023	0.00	0.30	1.17	2.47	2.67	1.32	Tolerant
L 06043	0.00	0.70	1.23	2.07	2.67	1.33	Tolerant
L 06044	0.17	0.77	2.73	3.37	3.07	2.02	Moderately Susceptible
L 06049	0.10	1.20	2.27	3.20	3.53	2.06	Moderately Susceptible
L 02709	0.00	2.03	2.43	3.57	2.67	2.14	Moderately Susceptible
TLB 133	1.47	2.60	2.57	2.73	2.77	2.43	Highly Susceptible
THB 205	0.80	3.17	2.57	3.07	2.67	2.45	Highly Susceptible
TLB 130	1.17	3.07	2.40	3.20	3.53	2.67	Highly Susceptible
Grand mean	0.50 ± 0.20	1.66 ± 0.20	2.53 ± 0.23	3.09 ± 0.21	3.33 ± 0.59		
Range	0.00 - 1.70	0.00 - 3.73	0.26 - 3.93	0.40 - 3.93	1.77 - 4.00		
GCV	90.98	53.46	30.14	20.61	6.83		
PCV	114.86	57.62	34.24	23.73	30.19		

DAT- Days after transplanting; GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation

Table 10. Disease reaction of some genotypes, mean, range, GCV and PCV for vector population

Particulars	Vector population						Disease Reaction
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	Average	
Selected Genotypes							
LA 3922	0.00	1.77	6.40	16.47	6.03	6.13	Highly Tolerant
L 02248	0.00	1.90	7.33	16.53	5.53	6.26	Highly Tolerant
L 01049	0.00	1.50	5.80	16.90	7.73	6.39	Highly Tolerant
L 01869	0.00	1.70	6.43	17.70	6.70	6.51	Moderately Tolerant
BL 1198	0.00	4.70	7.33	11.23	17.40	8.13	Moderately Tolerant
L 01050	0.13	1.53	11.23	24.33	4.73	8.39	Moderately Tolerant
L 06123	0.27	1.67	10.00	26.13	5.17	8.65	Tolerant
L 06119	0.00	4.70	9.90	12.80	16.83	8.85	Tolerant
L 06046	1.00	5.63	9.70	17.47	13.73	9.51	Tolerant
L 06179	1.77	5.80	12.03	17.70	12.77	10.01	Moderately Susceptible
L 1023	2.20	6.47	11.17	19.20	13.83	10.57	Moderately Susceptible
L 06229	0.43	9.80	18.13	23.97	7.80	12.03	Moderately Susceptible
S. Early	4.10	7.90	17.57	17.70	6.10	10.67	Highly Susceptible
Anagha	4.07	9.27	18.83	29.57	0.00	12.35	Highly Susceptible
Nandi	0.50	8.83	14.67	23.37	26.60	14.79	Highly Susceptible
Grand mean	1.90 ± 0.49	6.77 ± 0.94	14.42 ± 1.23	22.63 ± 1.58	7.87 ± 0.73		
Range	0.00 - 5.00	1.03 - 13.17	4.63 - 21.67	11.23 - 32.10	0.00 - 28.60		
GCV	79.87	52.66	33.71	23.31	102.76		
PCV	90.84	57.91	36.82	26.24	104		

DAT- Days after transplanting; GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation

respectively. This trait had 91.10 per cent heritability with 26.85 and 68.48 per cent GA and GAM, respectively (Table 11). Grand mean for all the hundred genotypes for this trait was 31.96 g. Genotype L 06229 had the lowest (13.79 g) and genotype CLN 2585 A (65.47 g) had the highest average fruit weight. This trait recorded 93.00 per cent heritability with 27.91 and 87.34 per cent GA and GAM, respectively. GCV and PCV were found to be 43.97 and 45.60 respectively (Table 11).

In this experiment, yield per plant was ranged from 0.64 to 1.80 kg with a general mean of 1.10 kg per plant. Genotype L 06229 was the lowest yielder and genotype L 06052 was found to be the highest yielder among all the genotypes. GCV and PCV were 19.93 and 28.67, respectively. This trait had 48.30 per cent heritability with GA and GAM of 0.31 and 28.53 per cent, respectively (Table 11).

4.1.2.5 Estimation of genetic divergence in TyLCV trial

Genetic diversity is an important factor for any heritable improvement. Knowledge of genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding program. Mahalanobis's D^2 technique appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity.

Genetic divergence of tomato genotypes was estimated based on 12 characters viz., plant height (60 DAT), number of branches (60 DAT), stem girth (60 DAT), number of leaves (60 DAT), leaf area (60 DAT), per cent plant survival (60 DAT), disease severity index on vegetative parts (60 DAT), disease severity index on flowering and fruiting parts (60 DAT), vector population (60 DAT), number of fruits per plant, average fruit weight and yield per plant.

All hundred genotypes of tomato were grouped into 8 clusters based on 12 characters (Fig. 1). Cluster 3 had maximum number of genotypes (24) which was followed by cluster 6 which had 18 genotypes. Detailed information about clustering and genotypes belonging to each cluster is given in Table 12.

When analyzed for contribution of different characters towards diversity, it was found that plant height contributed most (28.81%) which was followed by average fruit weight (22.34%) and leaf area at 60 DAT (15.37%). Number of branches at 60 DAT (1.02%) contributed least towards diversity (Table 13).

Table 11. Variability analysis for yield parameters

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
1	Number of fruits per plant	39.21 $\pm$ 2.46	16.95 - 65.64	186.45	204.63	34.83	36.49	91.10	26.85	68.48
2	Average fruit weight (g)	31.96 $\pm$ 2.23	13.79 - 65.47	197.41	212.31	43.97	45.60	93.00	27.91	87.34
3	Yield per plant (Kg)	1.10 $\pm$ 0.13	0.64 - 1.80	0.05	0.10	19.93	28.67	48.30	0.31	28.53

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean

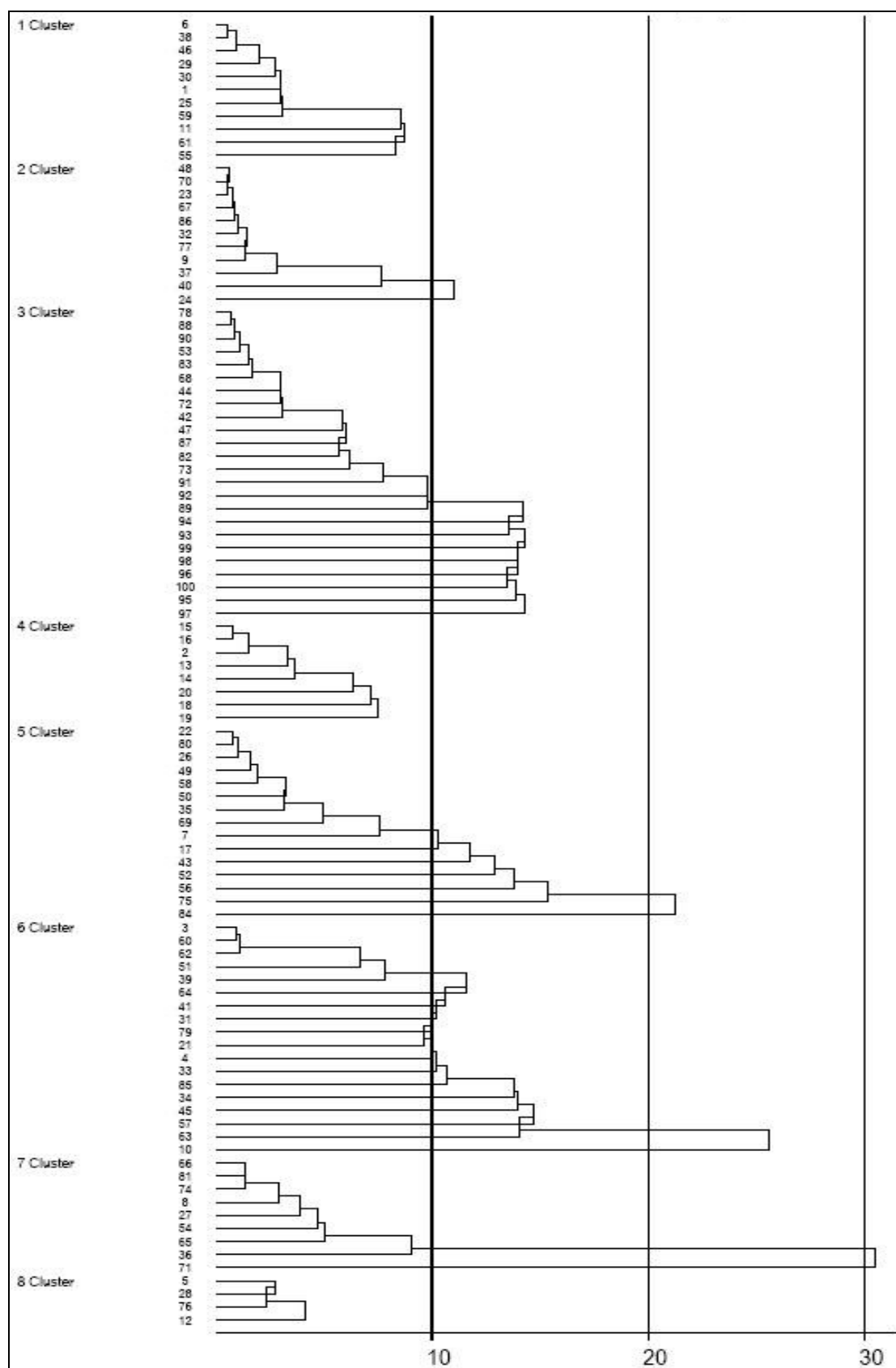


Fig. 1. Dendrogram of clustering pattern of tomato genotypes under TyLCV trial

Table 12. Clustering pattern of tomato genotypes by Mahalanobis's D² analysis for TyLCV

Cluster	No. of Genotypes	Genotypes in the cluster
Cluster 1	11	BL 1187, BL 1201, CLN 2116 B, L 01139, L 01464, L 01696, L 02692, L 06057, L 06181, L 09190 and L 06194
Cluster 2	11	LA 3922, L 01049, L 01050, L 01869, L 02248, L 02778, L 06106, L 06221, L 06230, Araka Abha and PKM-1
Cluster 3	24	L 06044, L 06049, L 06058, L 06123, L 06223, L 06238, L 06240, Arka Alok, Shakti, Mukti, SL-120, DMT-2, GK-2, THB-205, TLB-130, TLB-133, Madanlapalli Tomato, Patriot, Podland Pink, Red Pear, Stuart Early, Stuart Harry, Tommy Toe and W. Cherry
Cluster 4	8	BL1188, CLN 2585 A, CLN 2585 C, CLN 2585 D, CLN 2679 E, CLN 2714 G, CLN 2714 H and CLN 2714 J
Cluster 5	15	LA 3913, CLN 2679 F, L 01033, L 01318, L 02079, L 06046, L 06112, L 06115, L 06122, L 06182, L 06188, L 06229, L 1030, Arka Saurabh and Anagha
Cluster 6	18	BL 1198, BL 1199, LA 3923, L 01023, L 01745, L 01933, L 01942, L 02709, L 06043, L 06052, L 06119, L 06185, L 06193, L 06201, L 06208, L 06218, Arka Meghali and Nandi
Cluster 7	9	LA 3914, L 01462, L 02222, L 06179, L 06219, L 06220, L 06231, L 1023 and Arka Vikas
Cluster 8	4	BL 1200, CLN 2498 E, L 01463 and LA 3923

Table 13. Per cent contribution of different characters towards genetic divergence

Sr. No.	Character	No. of first ranks	% Contribution
1	Plant height (cm) at 60 DAT	1426	28.81
2	Number of branches at 60 DAT	50	1.02
3	Stem girth (cm) at 60 DAT	154	3.11
4	Number of leaves at 60 DAT	124	2.51
5	Leaf area at 60 DAT (cm ²)	761	15.37
6	Per cent plant survival at 60 DAT	363	7.33
7	Disease Severity Index (Vegetative) 60 DAT	71	1.43
8	Disease Severity Index (Flr & Fruiting) 60 DAT	85	1.72
9	Vector Population at 60 DAT	200	4.04
10	Number of fruits	536	10.83
11	Average fruit weight (g)	1106	22.34
12	Yield per plant (kg)	74	1.49
	Total	4950	100.00

DAT- Days after transplanting; Flr & Fruiting - Flowering and fruiting

Cluster 8 had the least intra cluster distance followed by cluster 3 (2.09 and 2.17 respectively). Cluster 6 had the maximum intra cluster distance followed by cluster 7 (3.78 and 3.52 respectively). Least inter cluster distance was found between clusters 2 and 7 which was followed by distance between clusters 1 and 8 (4.78 and 5.07 respectively). Highest inter cluster distance was found between clusters 4 and 6 which was followed by distance between clusters 1 and 6 (14.85 and 13.11 respectively). Table 14 shows inter and intra cluster distances.

Cluster 5 had the lowest mean for plant height at 60 DAT (14.68 cm) and Cluster 6 had the highest value for the trait (60.58 cm). Lowest value of cluster mean for number of branches at 60 DAT was found in cluster 3 (11.84) and cluster 2 had the highest value (14.82). For stem girth, least value was 8.80 cm (Cluster 1) and highest value was 15.51cm (Cluster 6). Cluster 2 had the lowest value for number of leaves (31.79) and the highest value was found in cluster 8 (46.74). Lowest mean value of 683.07 cm² was found in cluster 1 for leaf area and highest value (1908.56 cm²) was found in cluster 6. Cluster 8 had the lowest disease survival percentage (14.33%) and cluster 2 had the highest value (86.73%) for this trait. Disease severity index on vegetative parts was least in cluster 6 (0.85) and it was found highest in cluster 5 (2.75). Disease severity index on flowering and fruiting parts was least in cluster 6 (1.61) and it was found highest in cluster 2 (3.45). Mean value for vector population was found least in cluster 2 (6.71) whereas it was maximum in cluster 8 (20.39). Cluster mean for number of fruits was found least in cluster 4 (20.76) while it was highest in cluster 6 (58.48). Lowest value for average fruit weight was found in cluster 5 (21.71 g) whereas the highest value was found in cluster 4 (62.52 g). Lowest mean value for yield per plant was found in cluster 7 (0.93 kg) and the highest was in cluster 6 (1.33 kg). Cluster mean values are presented in Table 15.

4.2 Evaluation of tomato genotypes for drought stress

The genotypes which were used for screening for TyLCV resistance were used for screening for drought tolerance. This experiment was conducted in *Summer* 2012. Genotypes were exposed for two types of irrigation treatments, one with normal irrigation (IR1) and the other with restricted irrigation *i.e.*, once in a week (IR2). Results pertaining to this experiment are presented below.

Table 15. Cluster means for different characters

Clusters	Plant height (cm) at 60 DAT	Number of branches at 60 DAT	Stem girth (cm) at 60 DAT	Number of leaves at 60 DAT	Leaf area at 60 DAT (cm ²)	Per cent plant survival at 60 DAT	Disease Severity Index (Vegetative) 60 DAT	Disease Severity Index (Flr & Fruiting) 60 DAT	Vector Population at 60 DAT	Number of fruits	Average fruit weight (g)	Yield per plant (kg)
Cluster 1	20.07	12.89	8.80	39.25	683.07	35.58	2.72	2.53	20.02	40.26	25.78	1.04
Cluster 2	35.57	14.82	14.68	31.79	905.94	86.73	2.26	3.45	6.71	46.32	22.06	1.02
Cluster 3	38.18	11.84	15.34	35.03	1143.07	73.93	2.51	2.26	12.20	22.77	47.17	1.09
Cluster 4	19.35	12.69	12.38	43.14	976.70	34.38	1.93	2.82	20.13	20.76	62.52	1.30
Cluster 5	14.68	12.20	12.84	36.05	1119.30	22.89	2.75	2.66	17.60	43.33	21.71	0.94
Cluster 6	60.58	13.75	15.51	43.93	1908.56	55.78	0.85	1.61	13.70	58.48	22.68	1.33
Cluster 7	46.18	14.23	13.19	33.10	972.63	48.30	2.42	3.18	11.36	42.28	22.34	0.93
Cluster 8	16.91	11.97	14.06	46.74	980.59	14.33	1.77	3.19	20.39	43.16	25.25	1.11

DAT - Days after transplanting; Flr & Fruiting - Flowering and fruiting

4.2.1 Analysis of variance for morphological, growth and yield parameters

The data on analysis of variance was revealed that there was significant difference among the genotypes for all the morphological characteristics viz., plant height at 45, 60 and 90 DAT, number of branches at 45, 60 and 90 DAT, stem girth at 45 and 60 DAT. While, stem girth at 90 DAT, was found to be significant only in IR 1. Root characters viz., root length and volumes were highly significant at both irrigation levels (Table 16).

Analysis of variance revealed that there was a significant difference for all the growth parameters viz., number of leaves at 45, 60 and 90 DAT, leaf area at 45, 60 and 90 DAT, absolute growth rate from 45 to 60 DAT, 45 to 90 DAT and 60 to 90 DAT, relative growth rate from 45 to 60 DAT, 45 to 90 DAT and 60 to 90 DAT and crop growth rate from 45 to 60 DAT, 45 to 90 DAT and 60 to 90 DAT for both IR1 and IR 2 (Table 17).

It was revealed by the statistical analysis that the evaluation was significant for all the yield parameters viz., number of fruits per plant, average fruit weight and yield per plant (Table 18).

4.2.2 Estimation of genetic variability for morphological, growth and yield parameters

To reveal the extent of genetic variability, observations on morphological characters were statistically analyzed to estimate genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2), genetic advance (GA) and genetic advance over per cent of mean (GAM).

4.2.2.1 Morphological parameters

Plant height between 45 to 90 DAT was ranged from 17.36 cm (45 DAT) to 102.07 cm (90 DAT) in IR 1. While, it ranged from 13.46 cm (45 DAT) to 83.86 cm (90 DAT) in IR 2. Highest mean value for this trait was observed at 90 DAT, which was 82.03 cm for IR 1 and 62.48 cm for IR 2. Moderate GCV was observed in normal

Table 16. Anova for morphological characters of tomato genotypes under two irrigation regimes

Sl. No.	Characters	IR 1				IR 2			
		MSS				MSS			
		Replications	Genotypes	Errors	CD @ 5%	Replications	Genotypes	Errors	CD @ 5%
1	Plant height at 45 DAT (cm)	7.74	39.60**	7.16	4.31	5.83	80.45**	4.63	3.47
2	Plant height at 60 DAT (cm)	68.00	272.39**	58.44	12.31	2.49	196.33**	20.07	7.21
3	Plant height at 90 DAT (cm)	2.97	532.57**	1.27	1.81	2784.88	522.63**	203.64	22.98
4	Number of branches at 45 DAT	0.84	6.02**	0.43	1.06	1.08	4.00**	0.74	1.38
5	Number of branches at 60 DAT	0.98	13.56**	0.77	1.41	16.57	5.22**	2.80	2.69
6	Number of branches at 90 DAT	1.27	35.72**	0.84	1.48	71.14	15.47**	10.92	5.32
7	Stem girth at 45 DAT (cm)	0.05	0.65**	0.06	0.39	4.91	0.72**	0.27	0.83
8	Stem girth at 60 DAT (cm)	0.02	1.08**	0.05	0.37	1.96	0.80**	0.36	0.96
9	Stem girth at 90 DAT (cm)	0.13	0.57**	0.06	0.40	45.54	1.37	1.21	1.77
10	Root length (cm)	3.90	25.21**	4.07	3.25	5.93	46.86**	5.79	3.87
11	Root volume (cc)	1.10	32.12**	10.30	5.17	3.28	29.46**	11.47	5.45

** Significant at 0.01; DAT - Days after transplanting; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 17. Anova for growth characters of tomato genotypes under two irrigation regimes

Sl. No.	Characters	IR 1				IR 2			
		MSS				MSS			
		Replications	Genotypes	Errors	CD @ 5%	Replications	Genotypes	Errors	CD @ 5%
1	Number of leaves at 45 DAT	0.73	59.59**	1.38	1.89	47.21	72.12**	10.21	5.15
2	Number of leaves at 60 DAT	0.76	164.14**	1.73	2.12	973.62	382.91**	79.28	14.34
3	Number of leaves at 90 DAT	1.00	232.39**	1.40	1.91	575.77	313.37**	95.85	15.76
4	Leaf area at 45 DAT (cm ²)	70.27	10829.79**	100.46	16.13	57.75	6860.43**	97.21	15.87
5	Leaf area at 60 DAT (cm ²)	172.57	50486.75**	337.96	29.60	161.12	29570.64**	225.40	24.17
6	Leaf area at 90 DAT (cm ²)	35483.92	175111.69**	1356.10	59.52	321.34	86450.00**	455.26	34.36
7	AGR 45 - 60 DAT	0.007	0.045**	0.006	0.127	0.014	0.047**	0.003	0.099
8	AGR 45 - 90 DAT	0.014	0.047**	0.003	0.099	0.002	0.002**	0.001	0.055
9	AGR 60 - 90 DAT	0.023	0.146**	0.010	0.162	0.014	0.123**	0.010	0.163
10	RGR 45 - 60 DAT	0.059	0.733**	0.020	0.228	0.005	0.380**	0.009	0.159
11	RGR 45 - 90 DAT	0.001	0.144**	0.001	0.045	0.007	0.118**	0.002	0.080
12	RGR 60 - 90 DAT	0.001	0.202**	0.000	0.027	0.000	0.149**	0.000	0.031
13	CGR 45 - 60 DAT	0.001	0.360**	0.022	0.241	0.037	0.462**	0.015	0.197
14	CGR 45 - 90 DAT	0.016	0.013**	0.005	0.116	0.007	0.007**	0.004	0.102
15	CGR 60 - 90 DAT	0.176	4.301**	0.240	0.789	0.136	0.909**	0.038	0.315

** Significant at 0.01; DAT - Days after transplanting; AGR - Absolute growth rate; RGR - Relative growth rate; CGR - Crop growth rate;
IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 18. Anova for yield parameters of tomato genotypes under two irrigation regimes

Sl. No.	Characters	IR 1				IR 2			
		MSS				MSS			
		Replications	Genotypes	Errors	CD @ 5%	Replications	Genotypes	Errors	CD @ 5%
1	Number of fruits per plant	99.83	4102.71**	77.70	14.19	303.03	4178.31**	122.17	17.80
2	Average fruit weight (g)	12.51	1204.63**	17.73	6.78	0.31	1154.70**	0.73	1.37
3	Yield per plant (Kg)	0.14	5.56**	0.07	0.42	0.21	3.90**	0.09	0.49

** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

irrigation treatment (IR 1) during these stages and it was moderate to high in stressed condition (IR 2). PCV was higher than GCV in all the growth stages in both IR 1 and IR 2. Heritability was found ranging from moderate to high in both the conditions during all growth stages. Highest heritability in IR 2 was noticed for plant height at 45 DAT and the lowest was for that at 90 DAT. GA values ranged from low to high in IR 1, while the range was from low to moderate in IR 2. GAM was found to be moderate to high in both the conditions. Heritability, GA and GAM values, for 45 and 60 DAT, were more in stressed (IR 2) condition than in non-stressed (IR 1) condition. It was found to be vice-versa at 90 DAT (Table 19). Genotype L 01023 and L 01049 had the highest plant height, whereas genotype CLN 2679 F and CLN 2679 E had the least, respectively in IR 1 and IR 2 at 45 DAT. Genotype Patriot and L 06223 had the highest plant height, whereas genotype BL 1199 and CLN 2116 B had the least, respectively in IR 1 and IR 2 at 60 DAT. Genotype Patriot and L 06223 had the highest plant height, whereas genotype BL 1199 and CLN 2116 B had the least, respectively in IR 1 and IR 2 at 60 DAT.

Range of number of branches from 45 to 90 DAT was from 4.33 to 36.06 in IR 1 and it was from 6.00 to 25.80 in IR 2. At 45 DAT, number of branches in stressed condition (6.00 to 11.13) was found to be more than that in non-stressed condition (4.33 to 10.73). In the later stages of growth the values were more in non-stressed condition than in stressed condition. Highest mean value for this trait, 17.26 in IR 2, was observed at 90 DAT, which was far less than that in IR 1 (28.38 at 90 DAT). GCV was found to be low to moderate in IR 2 and it was moderate in IR 1. Moderate PCV was noticed in all the growth stages, in both the treatments. Heritability values were moderate to high in IR 2 and high in IR 1. Highest heritability in IR 1 was observed for number of branches at 45 DAT, whereas it was for number of branches at 90 DAT in IR 1. GAM values were low to moderate in IR 2 and they were high in IR 1 (Table 19). Genotypes L 1023, BL 1198 and BL 1200 had maximum number of branches at 45, 60 and 90 DAT, respectively in IR 2. Genotypes L 06057, CLN 2714 J and Tommy Toe had maximum number of branches at 45, 60 and 90 DAT, respectively in IR 1.

Values for stem girth were ranged from the lowest of 1.25 cm to the highest of 5.36 cm from 45 to 90 DAT in IR 2, while, it ranged from 2.78 cm to 8.40 cm in the

Table 19. Genetic variability estimates of tomato genotypes for morphological characters under two irrigation regimes

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
I	IR 1									
1	Plant height at 45 DAT (cm)	27.10 $\pm$ 1.54	17.36 - 33.81	10.81	17.98	12.13	15.65	60.20	5.25	19.39
2	Plant height at 60 DAT (cm)	56.19 $\pm$ 4.41	32.26 - 69.28	71.32	129.76	15.03	20.27	55.00	12.90	22.95
3	Plant height at 90 DAT (cm)	82.03 $\pm$ 0.65	57.60 - 102.07	177.10	178.37	16.22	16.28	99.30	27.32	33.30
4	Number of branches at 45 DAT	8.05 $\pm$ 0.38	4.33 - 10.73	1.86	2.29	16.95	18.83	81.10	2.53	31.46
5	Number of branches at 60 DAT	18.72 $\pm$ 0.51	14.13 - 22.26	4.26	5.03	11.03	11.98	84.70	3.92	20.91
6	Number of branches at 90 DAT	28.38 $\pm$ 0.53	21.73 - 36.06	11.63	12.47	12.02	12.44	93.20	6.78	23.90
7	Stem girth at 45 DAT (cm)	3.45 $\pm$ 0.14	2.78 - 4.32	0.20	0.25	12.07	14.43	76.80	0.80	22.84
8	Stem girth at 60 DAT (cm)	5.20 $\pm$ 0.13	4.35 - 6.38	0.34	0.39	11.23	12.06	86.70	1.12	21.53
9	Stem girth at 90 DAT (cm)	7.43 $\pm$ 0.14	6.75 - 8.40	0.17	0.23	5.56	6.48	73.50	0.73	9.81
10	Root length (cm)	27.07 $\pm$ 1.17	20.40 - 32.76	7.05	11.12	9.81	12.32	63.40	4.35	10.08
11	Root volume (cc)	21.13 $\pm$ 1.85	12.89 - 27.32	7.27	17.57	12.76	19.84	41.40	3.57	16.91
II	IR 2									
1	Plant height at 45 DAT (cm)	22.39 $\pm$ 1.24	13.46 - 34.80	25.27	29.90	22.45	24.43	84.50	9.52	42.52
2	Plant height at 60 DAT (cm)	38.68 $\pm$ 2.59	22.51 - 62.32	58.75	78.83	19.82	22.96	74.50	13.63	35.25
3	Plant height at 90 DAT (cm)	62.48 $\pm$ 8.24	29.20 - 83.86	106.33	309.97	16.50	28.18	34.30	12.44	19.91
4	Number of branches at 45 DAT	3.37 $\pm$ 0.50	6.00 - 11.13	1.09	1.83	12.47	16.14	59.60	1.66	19.83
5	Number of branches at 60 DAT	10.58 $\pm$ 0.97	6.68 - 12.80	0.81	3.61	8.49	17.95	22.40	0.88	8.27
6	Number of branches at 90 DAT	17.26 $\pm$ 1.91	11.22 - 25.80	1.52	12.44	7.14	20.43	12.20	0.89	5.14
7	Stem girth at 45 DAT (cm)	2.40 $\pm$ 0.30	1.25 - 3.22	0.15	0.42	16.14	26.95	35.90	0.48	19.91
8	Stem girth at 60 DAT (cm)	3.44 $\pm$ 0.34	1.96 - 4.24	0.15	0.50	11.20	20.65	29.40	0.43	12.52
9	Stem girth at 90 DAT (cm)	4.45 $\pm$ 0.64	3.08 - 5.36	0.05	1.26	5.16	25.24	4.20	0.10	2.17
10	Root length (cm)	44.94 $\pm$ 1.39	38.93 - 52.83	13.69	19.48	8.23	9.82	70.30	6.39	14.22
11	Root volume (cc)	28.71 $\pm$ 1.96	20.52 - 34.82	6.00	17.47	8.53	14.56	34.30	2.96	10.30

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; DAT - Days after transplanting; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

same duration in IR 1. Low to moderate GCV was observed in both irrigation treatments. GCV values were higher in IR 2 than in IR 1. Heritability was found to be low to moderate in stressed condition, whereas it was high in non-stressed condition. Highest heritability for stem girth in IR 2 was observed at 45 DAT, while it was highest at 60 DAT in IR 1. Genetic advance over mean was found to be low to moderate in IR 2 and it was low and high in IR 1 (Table 19). Genotypes BL 1198, L 06223 and L 01139 had the highest values for stem girth in IR 2. Genotypes L 06183, L 06043 and DMT-2 had the highest values for stem girth in IR 1.

Considerable range of variability was found with respect to root length in both irrigation conditions among the tomato genotypes. Mean root length was found to be 44.94 cm in IR 2, which ranged from 38.93 cm (THB 205) to 52.83 (L 0 6231). GCV and PCV were 8.23 per cent and 9.82 per cent respectively. Heritability was found to be 70.30 per cent with GA and GAM of 6.39 and 14.22 per cent respectively in IR 2. In IR 1 it ranged from 20.40 cm (L 06240) to 32.76 cm (CLN 2679 E) with grand mean of 27.07 cm. GCV and PCV were found to be 9.81 per cent and 12.32 per cent respectively. It was 63.40 per cent heritable with 10.08 per cent GAM (Table 19).

In IR 2, grand mean for root volume was found to be 28.71 cc which ranged from 20.52 cc (Madanpalli Tomato) to 34.82 cc (L 06231). It had a low GCV (8.53%) and moderate PCV (14.56%). This trait was 34.30 per cent heritable with GA and GAM of 2.96 and 10.30 per cent respectively. Root volume ranged from 12.89 cc (L 0 6112) to 27.32 cc (L 01745) in IR 1 with a grand mean of 21.13 cc. This trait had a moderate GCV (12.76%) and PCV (19.84%). Heritability and genetic advance over mean were found to be moderate (41.40% and 16.91% respectively). Genetic variability estimates for root volume are presented in Table 19.

4.2.2.2 Growth parameters

Number of leaves was ranged from 20.66 to 93.00 during 45 to 90 DAT in IR 2. Whereas, range was found to be higher (26.00 to 108.00) in normal irrigation treatment. Moderate GCV was observed in IR 2 and it was low to moderate in IR 1. Highest GCV was observed at 60 DAT in both irrigation treatments. PCV was moderate to high in IR 2 and low to moderate in IR 1. Heritability estimates were found to be low in IR 2, when compared with the estimates of IR 1. These were

moderate to high in IR 2, but high in IR 1. Highest heritability in IR 2 was observed at 45 DAT for this trait. Genetic advance estimates were moderate to high in both the treatments (Table 20). Genotypes having highest values for this trait in IR 2 are L 01696 and L 06219 (at 45 DAT), L 06057 (at 60 DAT) and L 06057 (at 90 DAT). Arka Alok, L 06122 and LA 3914 had the highest values at 45, 60 and 90 DAT, respectively in IR 1.

Leaf area per plant was ranged from 41.58 cm² to 813.48 cm² during 45 to 90 DAT in IR 2. The range was little higher (70.83 cm² to 1154.92 cm²) in IR 1. High GCV was observed in both the treatments. Among the three stages, leaf area at 45 DAT (30.95) had the highest GCV in IR 2 and that at 60 DAT (28.50) in IR 1. PCV estimates were more than GCV estimates and the difference between GCV and PCV was more in all stages of IR 2 than in IR 1. High heritability was observed in both the treatments for this trait (Table 20). Highest heritability in IR 2 was observed at 90 DAT (98.40%) but the genetic advance over mean was highest at 60 DAT (60.96%). Highest leaf area per plant was observed in genotype Arka Saurabh (230.31 cm², 478.57 cm² and 813.48 cm² at 45, 60 and 90 DAT, respectively) in IR 2. Highest leaf area per plant in IR 1 was found in Arka Alok (319.81 cm²), Patriot (669.24 cm²) and Stuart Harry (1154.93 cm²) at 45, 60 and 90 DAT, respectively.

Grand mean of absolute growth rate from 45 to 60 DAT was found to be 0.41 which ranged from 0.21 (Arka Vikas and Stuart Harry) to 0.72 (L 06185) in IR 1. GCV (27.99%) and PCV (49.71%) were found to be high. Heritability was found to be high (67.50%) with high GAM of 47.38 per cent in IR 1. Genotype Tommy Toe had the lowest value (0.08) while genotype L 06185 had the highest value (0.64) for this trait in IR 2. Grand mean was found to be 0.27. This trait had a high GCV (44.24%) and PCV (49.71%). High heritability was found (79.20%) with high GAM of 81.09 per cent for this trait (Table 21).

Grand mean of absolute growth rate from 45 to 90 DAT was found to be 0.27 which ranged from 0.08 (CLN 2498 E) to 0.64 (BL 1187) in IR 1. GCV (44.24%) and PCV (46.80%) were found to be high. Heritability was found to be high (79.20%) with high GAM of 81.09 per cent in IR 1. Genotype Podland Pink had the lowest value (0.14) while genotype BL 1187 had the highest value (0.32) for this trait in IR 2. Grand mean was found to be 0.21. This trait had moderate GCV (10.04%) and PCV

Table 20. Genetic variability estimates of tomato genotypes for number of leaves and leaf area under two irrigation regimes

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
I	IR 1									
1	Number of leaves at 45 DAT	37.12 $\pm$ 0.67	26.00 - 45.33	19.40	20.78	11.87	12.28	93.40	8.77	23.62
2	Number of leaves at 60 DAT	60.34 $\pm$ 0.76	47.00 - 74.00	54.14	55.86	12.19	12.39	96.90	14.92	24.73
3	Number of leaves at 90 DAT	92.20 $\pm$ 0.68	80.33 - 108.00	77.00	78.40	9.52	9.60	98.20	17.91	19.43
4	Leaf area at 45 DAT (cm ²)	227.17 $\pm$ 5.79	70.83 - 319.81	3576.44	3676.90	26.33	26.69	97.30	121.50	53.48
5	Leaf area at 60 DAT (cm ²)	453.56 $\pm$ 10.61	157.58 - 669.24	16716.26	17054.22	28.50	28.79	98.00	263.68	58.14
6	Leaf area at 90 DAT (cm ²)	846.08 $\pm$ 21.26	306.47 - 1154.92	57918.53	59274.63	28.45	28.78	97.70	490.06	57.92
II	IR 2									
1	Number of leaves at 45 DAT	32.02 $\pm$ 1.84	20.66 - 41.00	20.64	30.85	14.19	17.34	66.90	7.65	23.90
2	Number of leaves at 60 DAT	51.85 $\pm$ 5.14	27.80 - 68.66	101.21	180.49	19.40	25.91	56.10	15.52	29.93
3	Number of leaves at 90 DAT	77.02 $\pm$ 5.65	49.00 - 93.00	72.50	168.36	11.06	16.85	43.10	11.51	14.95
4	Leaf area at 45 DAT (cm ²)	153.41 $\pm$ 5.69	41.58 - 230.31	2254.41	2351.62	30.95	31.61	95.90	95.77	62.42
5	Leaf area at 60 DAT (cm ²)	330.46 $\pm$ 8.67	147.58 - 478.58	9781.75	10007.14	29.93	30.27	97.70	201.43	60.96
6	Leaf area at 90 DAT (cm ²)	569.14 $\pm$ 12.32	229.56 - 813.48	28664.91	29120.18	29.75	29.98	98.40	346.04	60.80

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation; h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; DAT - Days after transplanting; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 21. Genetic variability estimates of tomato genotypes for different growth rates under two irrigation regimes

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
I	IR 1									
1	AGR 45 - 60 DAT	0.41 ± 0.05	0.21 - 0.72	0.01	0.02	27.99	49.71	67.50	0.19	47.38
2	AGR 45 - 90 DAT	0.27 ± 0.04	0.08 - 0.64	0.01	0.02	44.24	46.80	79.20	0.22	81.09
3	AGR 60 - 90 DAT	0.50 ± 0.06	0.09 - 0.92	0.05	0.06	42.28	46.80	81.60	0.40	78.68
4	RGR 45 - 60 DAT	0.60 ± 0.08	0.02 - 1.52	0.24	0.26	81.29	84.67	92.20	0.97	160.77
5	RGR 45 - 90 DAT	0.23 ± 0.02	0.32 - 0.63	0.05	0.05	97.32	98.13	98.40	0.45	198.82
6	RGR 60 - 90 DAT	0.10 ± 0.01	0.00 - 1.21	0.07	0.07	267.95	268.51	99.60	0.53	550.81
7	CGR 45 - 60 DAT	0.81 ± 0.09	0.04 - 1.83	0.11	0.14	41.64	45.58	83.40	0.63	78.34
8	CGR 45 - 90 DAT	0.57 ± 0.04	0.39 - 0.72	0.00	0.01	9.10	15.41	34.90	0.06	11.08
9	CGR 60 - 90 DAT	2.22 ± 0.28	0.15 - 3.67	1.35	1.59	52.47	56.94	84.90	2.21	99.61
II	IR 2									
1	AGR 45 - 60 DAT	0.27 ± 0.03	0.08 - 0.64	0.01	0.02	44.24	49.71	79.20	0.22	81.09
2	AGR 45 - 90 DAT	0.21 ± 0.02	0.14 - 0.32	0.00	0.00	10.04	19.33	27.00	0.02	10.73
3	AGR 60 - 90 DAT	0.54 ± 0.059	0.08 - 0.84	0.04	0.05	45.97	51.88	78.50	0.35	83.91
4	RGR 45 - 60 DAT	0.44 ± 0.06	0.02 - 1.08	0.12	0.13	80.07	83.17	92.70	0.70	158.77
5	RGR 45 - 90 DAT	0.18 ± 0.03	0.02 - 0.63	0.04	0.04	112.57	116.16	93.90	0.94	224.73
6	RGR 60 - 90 DAT	0.09 ± 0.01	0.00 - 1.05	0.05	0.05	237.82	238.73	99.20	0.46	488.04
7	CGR 45 - 60 DAT	0.54 ± 0.07	0.14 - 1.59	0.15	0.16	72.02	75.56	90.80	0.76	141.38
8	CGR 45 - 90 DAT	0.39 ± 0.04	0.26 - 0.50	0.00	0.01	8.35	18.58	20.20	0.03	7.74
9	CGR 60 - 90 DAT	1.17 ± 0.11	0.27 - 2.68	0.29	0.33	46.21	49.17	88.30	1.04	89.46

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation;
 h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; DAT - Days after transplanting; AGR - Absolute growth rate;
RGR - Relative growth rate; CGR - Crop growth rate; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

(19.33%). Low heritability was found (27.00%) with moderate GAM of 10.73 per cent for this trait (Table 21).

Grand mean of absolute growth rate from 60 to 90 DAT was found to be 0.50 which ranged from 0.09 (L 06201) to 0.92 (L 01696) in IR 1. GCV (42.28%) and PCV (46.80%) were found to be high. Heritability was found to be high (81.60%) with high GAM of 78.68 per cent in IR 1. Genotype LA 3922 had the lowest value (0.08) while genotype L 01696 had the highest value (0.84) for this trait in IR 2. Grand mean was found to be 0.54. This trait had high GCV (45.97%) and PCV (51.88%). High heritability was found (78.50%) with moderate GAM of 83.91 per cent for this trait (Table 21).

Genotypes Arka Vikas and CLN 2498 E had the least relative growth rate (0.02) and genotype L 01933 had the highest value (1.52) from 45 to 60 DAT in IR 1. Grand mean was found to be 0.60 for the character. This trait had a high GCV (81.29%) and PCV (84.67%). Heritability was found to be high (92.20%) with high GAM (160.77%). Mean relative growth rate from 45 to 60 DAT for IR 2 was found to be 0.44 which ranged from 0.02 (BL 1199) to 1.08 (L 02222). GCV was found to be high (80.07%) with high PCV (83.17%). High heritability (92.70%) was found for the character with high GAM of 158.77 per cent in IR 2 (Table 21).

Genotype CLN 2498 E had the least relative growth rate (0.32) and genotype L 06188 had the highest value (0.63) from 45 to 90 DAT in IR 1. Grand mean was found to be 0.23 for the character. This trait had a high GCV (97.32%) and PCV (98.13%). Heritability was found to be high (98.40%) with high GAM (198.82%). Mean relative growth rate from 45 to 90 DAT for IR 2 was found to be 0.18 which ranged from 0.02 (L 01745) to 0.63 (L 01696). GCV was found to be high (112.57%) with high PCV (116.16%). High heritability (93.90%) was found for the character with high GAM of 224.73 per cent in IR 2 (Table 21).

Genotype L 06231 had the least relative growth rate (0.00) and genotype L 01696 had the highest value (1.21) from 60 to 90 DAT in IR 1. Grand mean was found to be 0.10 for the character. This trait had a high GCV (267.95%) and PCV (268.51%). Heritability was found to be high (99.60%) with high GAM (550.81%). Mean relative growth rate from 60 to 90 DAT for IR 2 was found to be 0.09 which

ranged from 0.00 (CLN 2714 J) to 1.05 (SL 120). GCV was found to be high (237.82%) with high PCV (238.73%). High heritability (99.20%) was found for the character with high GAM of 488.04 per cent in IR 2 (Table 21).

Grand mean of crop growth rate from 45 to 60 DAT was found to be 0.81 which ranged from 0.04 (Arka Vikas and Stuart Harry) to 1.83 (L 01696) in IR 1. GCV (41.64%) and PCV (45.58%) were found to be high. Heritability was found to be high (83.40%) with high GAM of 78.34 per cent in IR 1. Genotype Podland Pink had the lowest value (0.14) while genotype THB 205 had the highest value (1.59) for this trait in IR 2. Grand mean was found to be 0.54. This trait had high GCV (72.02%) and PCV (75.56%). High heritability was found (90.80%) with high GAM of 141.38 per cent for this trait (Table 21).

Grand mean of crop growth rate from 45 to 90 DAT was found to be 0.57 which ranged from 0.39 (CLN 2498 E) to 0.72 (L 06230) in IR 1. GCV was low (9.10%) and PCV was found to be moderate (15.41%). Heritability was found to be moderate (34.90%) with moderate GAM of 11.08 per cent in IR 1. Genotype CLN 2585 D had the lowest value (0.26) while genotype L 01696 had the highest value (0.50) for this trait in IR 2. Grand mean was found to be 0.39. This trait had low GCV (8.35%) and moderate PCV (18.58%). Low heritability was found (20.20%) with low GAM of 7.74 per cent for this trait (Table 21).

Grand mean of crop growth rate from 60 to 90 DAT was found to be 2.22 which ranged from 0.15 (Tommy Toe) to 3.67 (L 01696) in IR 1. GCV was high (52.47%) and PCV was found to be high (56.94%). Heritability was found to be high (84.90%) with high GAM of 99.61 per cent in IR 1. Genotype CLN 2585 C had the lowest value (0.27) while genotype L 01869 had the highest value (2.68) for this trait in IR 2. Grand mean was found to be 1.17. This trait had high GCV (46.21%) and PCV (49.17%). High heritability was found (88.30%) with high GAM of 89.46 per cent for this trait (Table 21).

4.2.2.3 Yield parameters

Genotype CLN 2585 C had the lowest number of fruits per plant (16.35) and genotype L 1030 had the highest value (166.06) in IR 1. Grand mean was found to be 108.41 for the character. This trait had a high GCV (33.79%) and PCV (34.75%).

Heritability was found to be high (94.50%) with high GAM (67.67%). Mean number of fruits per plant for IR 2 was found to be 95.22 which ranged from 11.06 (L 02692) to 156.00 (L 06188). GCV was found to be high (38.61%) with high PCV (40.32%). High heritability (91.70%) was found for the character with high GAM of 76.18 per cent in IR 2 (Table 22).

Genotype SL 120 had the lowest average fruit weight (10.85 g) and genotype L 06194 had the highest value (63.15 g) in IR 1. Grand mean was found to be 28.32 g for the character. This trait had a high GCV (70.23%) and PCV (71.78%). Heritability was found to be high (95.70%) with high GAM (141.53%). Mean average fruit weight for IR 2 was found to be 27.82 g which ranged from 10.75 g (L 01049) to 61.81 g (L 06122). GCV was found to be high (70.50%) with high PCV (70.57%). High heritability (99.80%) was found for the character with high GAM of 145.09 per cent in IR 2 (Table 22).

Genotype L 01049 had the lowest yield per plant (1.08 kg) and genotype L 06194 had the highest value (5.37 kg) in IR 1. Grand mean was found to be 2.49 kg/plant for the character. This trait had a high GCV (54.43%) and PCV (55.41%). Heritability was found to be high (96.50%) with high GAM (110.13%). Mean yield per plant for IR 2 was found to be 2.12 kg which ranged from 0.71 kg/plant (L 01049) to 4.47 kg/plant (L 06122). GCV was found to be high (53.20%) with high PCV (55.15%). High heritability (93.10%) was found for the character with high GAM of 105.73 per cent in IR 2 (Table 22).

4.2.2.4 Estimation of genetic divergence in drought trial

Genetic divergence in tomato in drought trial was estimated based on 13 characters viz., plant height (60 DAT), number of branches (60 DAT), stem girth (60 DAT), root length, root volume, number of leaves (60 DAT), leaf area (60 DAT), absolute growth rate (45 to 60 DAT), relative growth rate (45 to 60 DAT), crop growth rate (45 to 60 DAT), number of fruits per plant, average fruit weight and yield per plant.

All hundred genotypes of tomato were grouped into 7 clusters based on 13 characters in IR 1 (Fig. 2). Cluster 2 had the maximum number of genotypes (32) which was followed by cluster 3 which had 19 genotypes. Detailed information about clustering and genotypes belonging to each cluster is given in Table 23.

Table 22. Genetic variability estimates of tomato genotypes for yield attributing parameters under two irrigation regimes

Sl. No.	Characters	Mean $\pm$ S. Em	Range	GV	PV	GCV	PCV	h^2 (%)	GA	GAM (%)
I	IR 1									
1	Number of fruits per plant	108.41 $\pm$ 5.09	16.35 - 166.06	1341.67	1419.37	33.79	34.75	94.50	73.36	67.67
2	Average fruit weight (g)	28.32 $\pm$ 2.43	10.85 - 63.15	395.63	413.37	70.23	71.78	95.70	40.09	141.53
3	Yield per plant (Kg)	2.49 $\pm$ 0.15	1.08 - 5.37	1.83	1.90	54.43	55.41	96.50	2.74	110.13
II	IR 2									
1	Number of fruits per plant	95.22 $\pm$ 6.38	11.06 - 156.00	1352.05	1474.22	38.61	40.32	91.70	72.54	76.18
2	Average fruit weight (g)	27.82 $\pm$ 0.49	10.75 - 61.81	384.66	385.38	70.50	70.57	99.80	40.36	145.09
3	Yield per plant (Kg)	2.12 $\pm$ 0.18	0.71 - 4.47	1.27	1.36	53.20	55.15	93.10	2.24	105.73

GV- Genotypic variation; PV - Phenotypic variation; GCV - Genotypic coefficient of variation; PCV - Phenotypic coefficient of variation;
 h^2 - Heritability; GA - Genetic advance; GAM - Genetic advance over percentage of mean; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

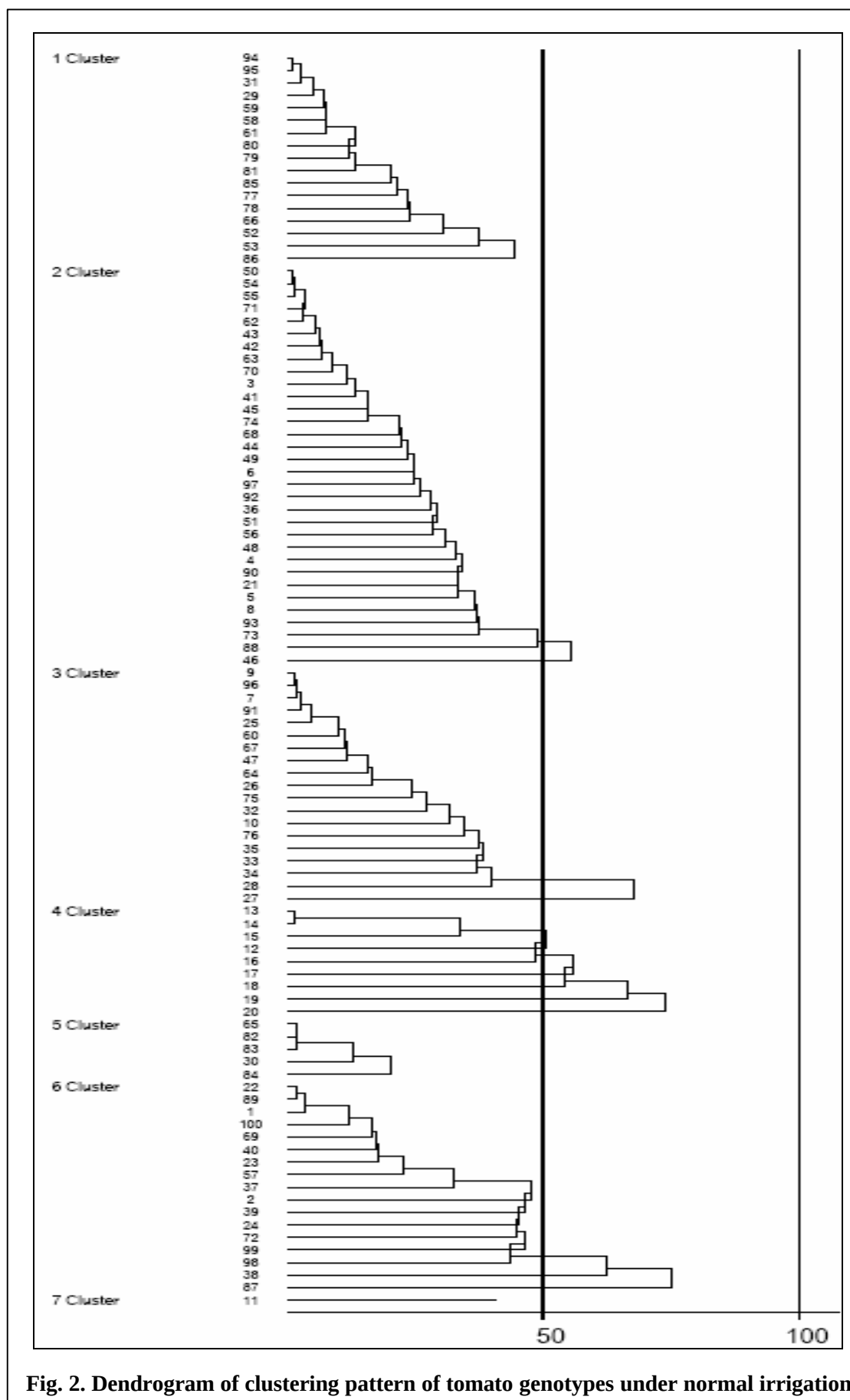


Table 23. Clustering patter of tomato genotypes in normal irrigation

Cluster	No. of Genotypes	Genotypes in the cluster
Cluster 1	17	L 01464, L 01745, L 06122, L 06123, L 06188, L 06190, L 06194, L 06220, Araka Abha, Arka Alok, Arka Meghali, Arka Saurabh, Arka Vikas, Nandi, PKM-1, Patriot and Podland Pink
Cluster 2	32	BL 1198, BL 1199, BL 1200, BL 1201, LA 3914, L 01023, L 02222, L 06043, L 06044, L 06046, L 06049, L 06052, L 06057, L 06106, L 06112, L 06115, L 06119, L 06179, L 06181, L 06182, L 06201, L 06208, L 06223, L 06230, L 6231, L 06240, L 1023, DMT-2, THB-205, TLB-133, Madanpalli Tomato and Stuart Early
Cluster 3	19	LA 3913, LA 3922, LA 3923, L 01139, L 01318, L 01462, L 01463, L 01869, L 01933, L 01942, L 02079, L 06058, L 06193, L 06218, L 06221, L 1030, LA 3924, TLB-130 and Red Pear
Cluster 4	9	CLN 2498 E, CLN 2585 A, CLN 2585 C, CLN 2585 D, CLN 2679 E, CLN 2679 F, CLN 2714 G, CLN 2714 H and CLN 2714 J
Cluster 5	5	L 01696, L 06219, Shakti, Mukti and Anagha
Cluster 6	17	BL 1187, BL 1188, L 01033, L 01049, L 1050, L 02248, L 02692, L 02709, L 02778, L 06185, L 06229, L 06238, SL-120, GK-2, Stuart Harry, Tommy Toe and W. Cherry
Cluster 7	1	CLN 2116 B

Tomato genotypes were grouped into 10 clusters in IR 2 (Fig. 3). Cluster 1 had the maximum number of genotypes (33) which was followed by cluster 2 and cluster 3 which had 15 genotypes. Detailed information about clustering and genotypes belonging to each cluster is given in Table 24.

When analyzed for contribution of different characters towards diversity in IR 1, it was found that yield per plant contributed most (27.49%) which was followed by leaf area at 60 DAT (24.02%). Plant height (0.10%) contributed least towards diversity (Table 25).

Analysis for contribution of different characters towards diversity in IR 2 revealed that average fruit weight contributed most (68.81%) which was followed by relative growth rate (12.26%). Stem girth at 60 DAT and number of leaves at 60 DAT (0.12%) contributed least towards diversity (Table 26).

Cluster 7 had the least intra cluster distance followed by cluster 5 (0.00 and 3.98 respectively). Cluster 4 had the maximum intra cluster distance followed by cluster 6 (8.26 and 6.93 respectively). Least inter cluster distance was found between clusters 1 and 5 which was followed by distance between clusters 2 and 3 (7.56 and 9.08 respectively). Highest inter cluster distance was found between clusters 1 and 6 which was followed by distance between clusters 6 and 7 (19.04 and 17.06 respectively). Table 27 shows inter and intra cluster distances in IR 1.

Cluster 5, cluster 9 and cluster 10 had the least intra cluster distance followed by cluster 7 (0.00 and 4.31 respectively). Cluster 6 had the maximum intra cluster distance followed by cluster 8 (6.59 and 5.67 respectively). Least inter cluster distance was found between clusters 9 and 10 which was followed by distance between clusters 1 and 5 (5.04 and 5.79 respectively). Highest inter cluster distance was found between clusters 8 and 9 which was followed by distance between clusters 2 and 8 (35.79 and 35.24 respectively). Table 28 shows inter and intra cluster distances in IR 2.

In IR 1, cluster 4 had the lowest mean for plant height at 60 DAT (38.34 cm) and Cluster 1 had the highest value for the trait (61.84 cm). Lowest value of cluster mean for number of branches at 60 DAT was found in cluster 6 (17.37) and cluster 7 had the highest value (21.00). For stem girth, least value was 4.48 cm (Cluster 5) and

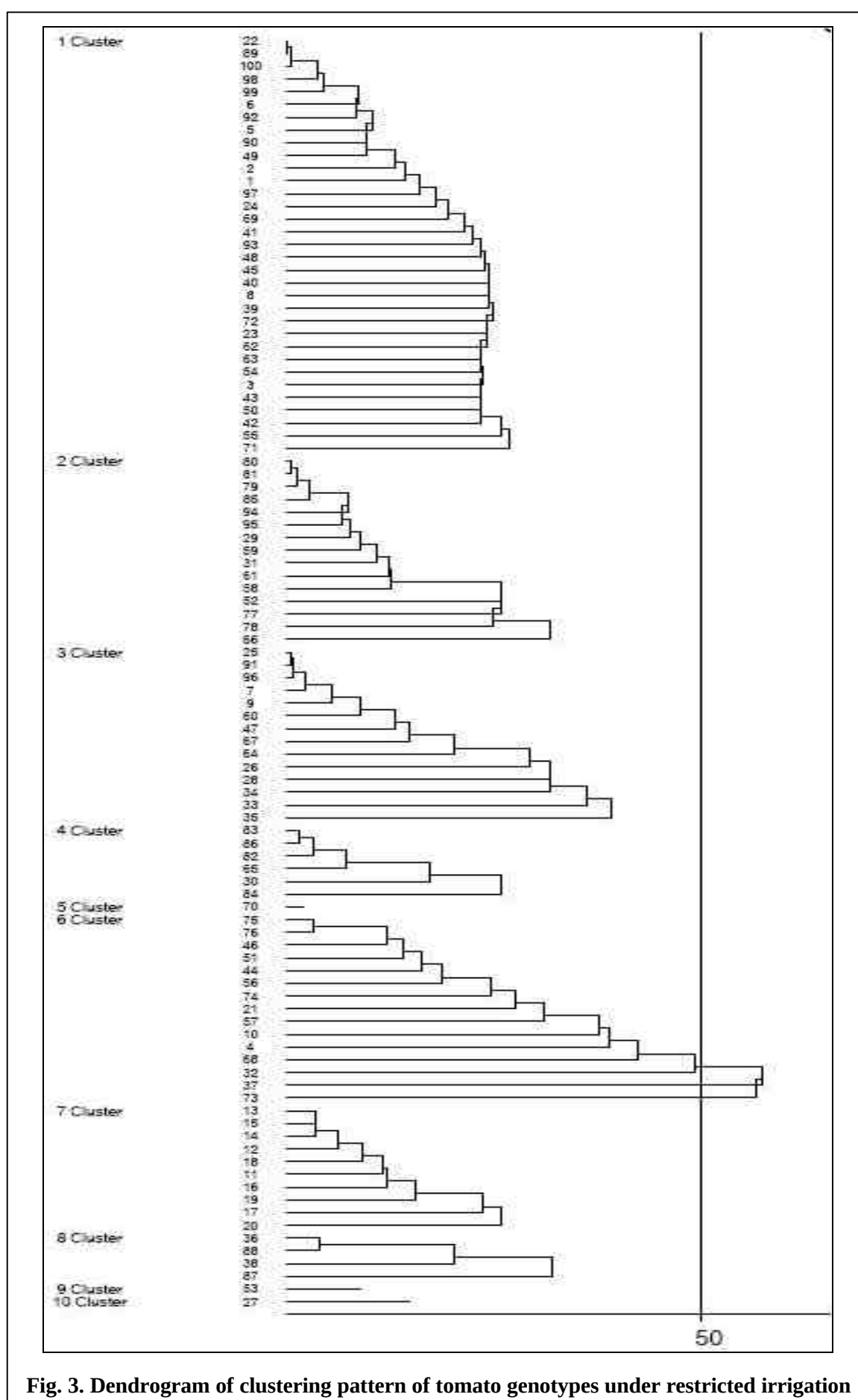


Fig. 3. Dendrogram of clustering pattern of tomato genotypes under restricted irrigation

Table 24. Clustering pattern of tomato genotypes in restricted irrigation

Cluster	No. of Genotypes	Genotypes in the cluster
Cluster 1	33	BL 1187, BL 1188, BL 1198, BL 1200, BL 1201, LA 3914, L 01033, L 01049, L 01050, L 02709, L 02778, L 06043, L 06044, L 06046, L 06052, L 06106, L 06112, L 06115, L 06179, L 06181, L 06201, L 06208, L 06229, L06231, L 06238, GK-8, THB-205, TLB-133, Madanpalli Tomato, Stuart Early, Staurt Harry, Tommy Toe and W. Cherry
Cluster 2	15	L 01464, L 01745, L 06122, L 06188, L 06190, L 60194, L 06220, Arka Abha, Arka Alok, Arka Meghali, Arka Saurabh, Arka Vikas, Nandi, Patriot and Podland Pink
Cluster 3	14	LA 3913, LA 3922, L 01139, L 01318, L 01463, L 01933, L 01942, L 02079, L 06058, L 06193, L 06218, L 06221, TLB-130 and Red Pear
Cluster 4	6	L 01696, L 06219, Shakti, Mukti, Anagha and PKM-1
Cluster 5	1	L 06230
Cluster 6	15	BL 1199, LA 3923, L 01023, L 01869, L 02248, L 06049, L 06057, L 06119, L 06182, L 06185, L 06223, L 06240, L 1023, L 1030 and LA 3924
Cluster 7	10	CLN 2116 B, CLN 2498 E, CLN 2585 A, CLN 2585 C, CLN 2585 D, CLN 2679 E, CLN 2679 F, CLN 2714 G, CLN 2714 H and CLN 2714 J
Cluster 8	4	L 02222, L 02692, SL-120 and DMT-2
Cluster 9	1	L 01462
Cluster 10	1	L 06123

Table 25. Per cent contribution of different characters towards genetic divergence in normal irrigation

Sr. No.	Character	No. of first ranks	% Contribution
1	Plant height (cm) at 60 DAT	5	0.10
2	Number of branches at 60 DAT	88	1.78
3	Stem girth (cm) at 60 DAT	65	1.31
4	Root length (cm)	35	0.71
5	Root volume (cc)	7	0.14
6	Number of leaves at 60 DAT	873	17.64
7	Leaf area at 60 DAT (cm ²)	1189	24.02
8	Absolute Growth Rate 45 - 60 DAT	41	0.83
9	Relative Growth Rate 45 - 60 DAT	471	9.52
10	Crop Growth Rate 45 - 60 DAT	270	5.45
11	Number of fruits	464	9.37
12	Average fruit weight (g)	81	1.64
13	Yield per plant (kg)	1361	27.49
	Total	4950	100.00

DAT - Days after transplanting

Table 26. Per cent contribution of different characters towards genetic divergence in restricted irrigation

Sr. No.	Character	No. of first ranks	% Contribution
1	Plant height (cm) at 60 DAT	67	1.35
2	Number of branches at 60 DAT	7	0.14
3	Stem girth (cm) at 60 DAT	5	0.12
4	Root length (cm)	58	1.17
5	Root volume (cc)	7	0.14
6	Number of leaves at 60 DAT	6	0.12
7	Leaf area at 60 DAT (cm ²)	51	1.03
8	Absolute Growth Rate 45 - 60 DAT	202	4.08
9	Relative Growth Rate 45 - 60 DAT	607	12.26
10	Crop Growth Rate 45 - 60 DAT	440	8.89
11	Number of fruits	72	1.45
12	Average fruit weight (g)	3406	68.81
13	Yield per plant (kg)	22	0.44
	Total	4950	100.00

DAT - Days after transplanting

Table 27. Intra and inter cluster distances for normal irrigation

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	5.03	15.59	11.47	14.82	7.56	19.04	10.23
Cluster 2		5.63	9.08	11.80	13.99	10.32	12.49
Cluster 3			5.86	11.77	10.31	11.93	9.44
Cluster 4				8.26	13.56	13.24	10.75
Cluster 5					3.98	16.54	11.15
Cluster 6						6.93	17.06
Cluster 7							0.00

Table 28. Intra and inter cluster distances for restricted irrigation

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	4.79	33.78	10.28	32.96	5.79	6.12	22.14	8.41	34.11	33.74
Cluster 2		4.43	25.32	8.06	34.71	32.36	14.42	35.24	6.05	6.03
Cluster 3			5.27	24.62	11.38	9.32	14.37	12.86	25.82	25.37
Cluster 4				4.34	34.08	31.46	14.72	33.15	9.30	7.72
Cluster 5					0.00	6.69	22.94	10.55	34.51	34.38
Cluster 6						6.59	20.93	9.33	32.65	32.28
Cluster 7							4.31	24.07	14.73	13.69
Cluster 8								5.67	35.79	35.16
Cluster 9									0.00	5.04
Cluster 10										0.00

highest value was 6.00 cm (Cluster 6). The lowest value for root length was found in cluster 7 (25.70 cm) whereas the highest value was in cluster 6 (29.44 cm). For root volume, cluster 6 had the lowest value (18.28 cc) whereas cluster 5 had the highest value (23.12 cc). Cluster 2 had the lowest value for number of leaves (54.13) and the highest value was found in cluster 5 (69.00). Lowest mean value of 2288.83 cm² was found in cluster 6 for leaf area and highest value (6587.14 cm²) was found in cluster 5. Cluster 6 had the lowest absolute growth rate (0.36) and cluster 1 had the highest value (0.47) for this trait. Relative growth rate was least in cluster 1 (0.04) and it was found highest in cluster 7 (0.88). Crop growth rate was least in cluster 5 (0.63) and it was found highest in cluster 2 (1.68). Cluster mean for number of fruits was found least in cluster 1 (24.28) while it was highest in cluster 4 (139.94). Lowest value for average fruit weight was found in cluster 7 (11.88 g) whereas the highest value was found in cluster 1 (59.88 g). Lowest mean value for yield per plant was found in cluster 1 (1.33 kg) and the highest was in cluster 7 (5.14 kg). Cluster mean values are presented in Table 29.

In IR 2, cluster 7 had the lowest mean for plant height at 60 DAT (27.58 cm) and cluster 9 had the highest value for the trait (48.41 cm). Lowest value of cluster mean for number of branches at 60 DAT was found in cluster 6 (9.82) and cluster 8 had the highest value (12.13). For stem girth, least value was 2.92 cm (Cluster 5) and highest value was 4.07 cm (Cluster 10). The lowest value for root length was found in cluster 9 (42.13 cm) whereas the highest value was in cluster 8 (50.60 cm). For root volume, cluster 2 had the lowest value (24.69 cc) whereas cluster 4 had the highest value (31.88 cc). Cluster 1 had the lowest value for number of leaves (36.10) and the highest value was found in cluster 9 (67.10). Lowest mean value of 2330.53 cm² was found in cluster 4 for leaf area and highest value (4625.84 cm²) was found in cluster 7. Cluster 2 had the lowest absolute growth rate (0.16) and cluster 5 had the highest value (0.54) for this trait. Relative growth rate was least in cluster 3 (0.20) and it was found highest in cluster 10 (0.94). Crop growth rate was least in cluster 4 (0.25) and it was found highest in cluster 1 (1.47). Cluster mean for number of fruits was found least in cluster 2 (19.63) while it was highest in cluster 3 (135.13). Lowest value for average fruit weight was found in cluster 4 (10.94 g) whereas the highest value was found in cluster 7 (61.13 g). Lowest mean value for yield per plant was found in cluster 6 (0.86 kg) and the highest was in cluster 3 (4.33 kg). Cluster mean values are presented in Table 30.

Table 29. Cluster means for different characters in normal irrigation

Clusters	Plant height (cm) at 60 DAT	Number of branches at 60 DAT	Stem girth (cm) at 60 DAT	Root length (cm)	Root volume (cc)	Number of leaves at 60 DAT	Leaf area at 60 DAT (cm ²)	Absolute Growth Rate 45 - 60 DAT	Relative Growth Rate 45 - 60 DAT	Crop Growth Rate 45 - 60 DAT	Number of fruits	Average fruit weight (g)	Yield per plant (kg)
Cluster 1	61.84	20.05	4.74	25.83	22.47	68.80	6175.73	0.36	0.50	0.75	85.89	59.88	5.14
Cluster 2	57.00	17.77	5.27	26.77	20.38	54.13	4368.22	0.47	0.70	0.83	129.82	13.25	1.72
Cluster 3	59.84	20.69	4.77	26.39	21.92	66.89	5088.27	0.40	0.64	0.69	113.75	21.35	2.31
Cluster 4	38.34	18.40	5.60	27.44	20.10	56.41	3924.77	0.39	0.28	0.63	24.28	52.39	1.34
Cluster 5	51.52	17.57	4.48	27.39	23.21	66.93	5579.00	0.36	0.88	1.68	87.42	52.55	4.19
Cluster 6	56.58	17.37	6.00	29.44	20.45	55.88	2488.83	0.37	0.58	0.80	139.94	11.88	1.64
Cluster 7	43.00	21.00	5.34	25.70	18.28	69.00	6587.14	0.44	0.04	0.63	31.03	48.63	1.33

DAT - Days after transplanting

Table 30. Cluster means for different characters in restricted irrigation

Clusters	Plant height (cm) at 60 DAT	Number of branches at 60 DAT	Stem girth (cm) at 60 DAT	Root length (cm)	Root volume (cc)	Number of leaves at 60 DAT	Leaf area at 60 DAT (cm ²)	Absolute Growth Rate 45 - 60 DAT	Relative Growth Rate 45 - 60 DAT	Crop Growth Rate 45 - 60 DAT	Number of fruits	Average fruit weight (g)	Yield per plant (kg)
Cluster 1	40.82	10.70	3.24	47.31	28.14	44.76	2452.02	0.26	0.44	0.40	123.04	11.83	1.43
Cluster 2	42.80	10.45	3.40	42.36	29.11	58.09	3897.99	0.20	0.28	0.41	69.44	59.91	4.16
Cluster 3	40.50	10.28	3.92	42.13	29.48	67.10	4181.84	0.30	0.45	0.47	86.77	24.07	2.14
Cluster 4	32.78	9.82	3.54	43.11	30.15	64.28	4625.84	0.21	0.68	1.47	70.54	58.24	3.88
Cluster 5	43.85	12.13	4.07	50.60	31.88	45.33	2857.06	0.54	0.84	0.32	135.13	11.35	1.53
Cluster 6	37.42	10.65	3.46	43.20	28.37	47.07	3288.92	0.36	0.51	0.57	123.04	14.20	1.74
Cluster 7	27.58	11.13	3.51	46.75	28.67	47.18	2726.54	0.30	0.20	0.34	19.63	41.69	0.86
Cluster 8	39.10	10.35	2.92	48.58	29.22	43.36	2330.53	0.16	0.65	1.46	115.68	10.94	1.36
Cluster 9	48.41	10.87	3.50	44.43	24.69	36.10	3659.61	0.35	0.94	0.25	70.87	61.13	4.33
Cluster 10	28.91	9.93	3.49	44.57	26.10	63.33	4619.00	0.16	0.63	0.28	72.20	60.33	2.74

DAT - Days after transplanting

4.3 Selection of parents and hybridization

A successful approach of crop breeding program depends on proper choice of best parents for hybridization. But selection of parents for hybridization is relatively tough process. Ideal selection can be done when *per se* performances of breeding lines are considered for selection. In a population, it is also important to consider genetic divergence while selecting lines for breeding program. Tomato is a self pollinated crop and genetic divergence in self pollinated crops is very important because crosses involving genetically diverse parents are likely to produce high heterozygous as well as heterotic effect.

Based on the *per se* performances and genetic divergence, four lines were selected from each trial for the further study on drought and TyLCV tolerance.

4.3.1 Selection for TyLCV tolerance

Lines for TyLCV tolerance were selected based on 12 characters viz., plant height (60 DAT), number of branches (60 DAT), stem girth (60 DAT), number of leaves (60 DAT), leaf area (60 DAT), per cent plant survival (60 DAT), disease severity index on vegetative parts (60 DAT), disease severity index on flowering and fruiting parts (60 DAT), vector population (60 DAT), number of fruits per plant, average fruit weight and yield per plant. Results of genetic divergence study were also considered while selecting the parents.

Genotypes L 01942 (cluster 6) and L 06052 (cluster 7) were selected as tolerant parents and genotype L 02079 (cluster 2) and LA 3913 (cluster 5) were selected as susceptible parents for the further study (Plate 1 to 4).

4.3.2 Selection for drought tolerance

Lines for drought tolerance were selected based on based on 13 characters viz., plant height (60 DAT), number of branches (60 DAT), stem girth (60 DAT), root length, root volume, number of leaves (60 DAT), leaf area (60 DAT), absolute growth rate (45 to 60 DAT), relative growth rate (45 to 60 DAT), crop growth rate (45 to 60 DAT), number of fruits per plant, average fruit weight and yield per plant. Results of genetic divergence study were also considered while selecting the parents.



Plate 1. L 01942



Plate 2. L 06052



Plate 3. L 2079



Plate 4. LA 3913

Genotype TLB 133 (cluster 3 in IR 1 and IR 2) and L 06231 (cluster 2 in IR 1 and cluster 1 in IR 2) were selected as tolerant parents. Genotype L 02692 (cluster 6 in IR 1 and cluster 8 in IR 2) and BL 1188 (cluster 4 in IR 1 and cluster 2 in IR 2) were selected as susceptible parents (Plate 5 to 8).

4.3.3 Hybridization

Selected eight parents are used for hybridization. Crossing was done in 8 x 8 diallel fashion to produce 28 hybrids. These hybrids are further evaluated for drought and TyLCV tolerance along with their parents.

4.4 Evaluation of hybrids and parents in diallel approach for drought tolerance

Diallel cross analysis provides the estimates of genetic parameters regarding combining ability as well as a rapid overall picture of the dominance relationship of the parents studied using the first filial generations (F1) with or without reciprocals. Diallel analysis involving parents give the additional information as presence or absence of epistasis, average degree of dominance, distribution of dominant and recessive genes in the parents.

4.4.1 Analysis of variance

Analysis of variance in treatments for morphological characters viz., plant height, number of branches and stem girth at 45, 60 and 90 days showed highly significant differences in both IR 1 and IR 2. Highly significant difference was also found for parents and hybrids for all the above mentioned characters in both IR 1 and IR 2. For parents vs. hybrids, highly significant difference was observed in plant height in all the stages for both IR 1 and IR 2. Differences were non-significant in both IR 1 and IR 2 for number of branches at all stages and for stem girth at 45 and 60 DAT. Differences were found to be significant, at 0.05 per cent level, for stem girth at 90 DAT in IR 1 and IR 2 (Table 31).

Highly significant differences were observed for treatments, parents, hybrids and parents vs. hybrids, in both IR 1 and IR 2, for root length, root volume and stomata count. Difference was highly significant for number of pubescence for treatment,



Plate 5. TLB 133



Plate 6. L 06231



Plate 7. L 02692



Plate 8. BL 1188

Table 31. Anova for diallel analysis for drought for plant height, number of branches and stem girth under two irrigation regimes

Source of Variation	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1									
Replication	27.98	1.46	113.80	6.00	108.63	111.33	3.51	13.85	0.90
Treatments	60.77**	293.06**	619.24**	12.40**	55.85**	70.20**	1.19**	2.87**	4.53**
Parents	103.04**	456.33**	1165.05**	20.53**	62.43**	112.29**	2.14**	5.14**	9.00**
Hybrids	48.22**	209.76**	439.87**	10.75**	55.94**	60.81**	0.98**	2.37**	3.45**
Parents Vs. Hybrids	100.20**	1399.39**	1641.66**	0.09	7.43	29.09	0.02	0.52	2.43*
Error	3.88	9.68	12.03	1.41	3.06	9.03	0.09	0.53	0.24
IR 2									
Replication	26.07	122.08	99.84	1.29	59.14	1.28	69.30	2.39	6.43
Treatments	97.13**	198.78**	569.75**	9.14**	18.24**	40.49**	1.19**	1.99**	2.30**
Parents	214.89**	312.97**	1382.51**	10.12**	15.90**	31.78*	2.41**	1.44**	4.46**
Hybrids	61.71**	164.59**	332.14**	9.15**	19.44**	44.14**	0.91**	2.17**	1.78**
Parents Vs. Hybrids	229.19**	322.71**	1295.94**	1.76	2.08	2.82	0.03	1.04*	1.33*
Error	6.22	4.92	4.40	0.65	1.85	13.90	0.20	0.21	0.22

* Significant at 0.05; ** Significant at 0.01; DAT - Days after transplanting; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

parents, hybrids and parents vs. hybrids in IR 1. In IR 2, differences were found to non significant for all the sources of variation (Table 32).

All the growth parameters viz., number of leaves, leaf area, absolute growth rate (45-60, 45-90 and 60-90), relative growth rate (45-60, 45-90 and 60-90) and crop growth rate (45-60, 45-90 and 60-90) showed highly significant differences for treatments, parents, hybrids and parent vs. hybrids. This result was observed both in IR 1 and IR 2 (Table 33 and 34).

All the biochemical parameters viz., proline content, chlorophyll (a, b and total) content were found to have highly significant differences for treatments, parents, hybrids and parents vs. hybrids in both IR 1 and IR 2. Only chlorophyll b content was found to have a non significant difference for parents vs. hybrids in IR 1 (Table 35).

All the yield parameters viz., number of fruits, average fruit weight and yield per plant had highly significant differences for treatments, parents, hybrids, parents vs. hybrids in both IR 1 and IR 2 (Table 35).

4.4.2 Analysis of variance for combining ability and genetic components of various characters

Analysis of variance for general (GCA) and specific (SCA) combining ability showed highly significant differences for all the morphological, growth, biochemical and yield parameters in both IR 1 and IR 2. GCA and SCA variance for number of pubescence (abaxial) and SCA variance for number of pubescence (adaxial) was found to be non-significant. This indicates importance of both additivity and non-additivity in the inheritance of these characters (Table 36, 37 and 38).

Variance due to SCA (V_s) was found to higher for all the growth parameters viz., plant height (45, 60 and 90 DAT), number of branches (45, 60 and 90 DAT), stem girth (45, 60 and 90 DAT), root length, root volume, stomata count and number of pubescence on abaxial layer in both IR 1 and IR 2. Number of pubescence on adaxial layer had high variation due to GCA (V_g). The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for all the morphological characters. In IR 1, dominance variation was high for plant height, stem girth, root length, root volume,

Table 32. Anova for diallel analysis for drought for root length, volume, stomata count and number of pubescence under two irrigation regimes

Source of Variation	Root length (cm)	Root volume (cc)	Stomata count	Number of pubescence	
				AB	AD
IR 1					
Replication	15.01	106.47	18.12	91.29	2657.86
Treatments	103.99**	152.80**	8.86**	527098.08**	200466.20**
Parents	116.82**	171.71**	11.48**	45869.45**	158063.70**
Hybrids	100.38**	151.49**	8.45**	55942.23**	241972.40**
Parents Vs. Hybrids	111.85*	55.76	1.34	13291.56**	105616.10**
Error	21.15	33.03	0.88	200.12	295.62
IR 2					
Replication	168.79	1.53	1.96	19112460.00	8065764.00
Treatments	365.10**	189.02**	6.98**	1254775.00	1224378.00
Parents	407.58**	178.35**	10.08**	1401296.00	712367.30
Hybrids	360.42**	197.33**	6.38**	1225153.00	1360312.00
Parents Vs. Hybrids	193.96**	39.15	1.41**	92392.90	1138240.00
Error	22.41	15.77	0.19	881193.10	880772.80

** Significant at 0.01; AB - Abaxial; AD - Adaxial; IR 1 - Normal Irrigation;
IR 2 - Restricted Irrigation

Table 33. Anova for diallel analysis for drought for number of leaves and leaf area under two irrigation regimes

Source of Variation	Number of leaves			Leaf area (cm ²)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1						
Replication	37.74	6.06	17.51	99.10	344.84	4868.70
Treatments	79.27**	366.81**	541.33**	4740.64**	21629.03**	90828.45**
Parents	32.83*	235.29**	254.41**	2435.45**	12138.09**	60621.87**
Hybrids	82.04**	358.45**	502.08**	5141.24**	22866.13**	92585.23**
Parents Vs. Hybrids	329.91**	1513.14**	3609.55**	10060.76**	54663.97**	254841.52**
Error	13.81	6.58	4.50	130.27	278.52	696.63
IR 2						
Replication	197.54	4.16	98.48	3834.64	644.27	1067.27
Treatments	98.44**	588.41**	593.94**	4477.09**	28412.27**	56383.33**
Parents	76.14**	317.94**	518.46**	3636.06**	19651.15**	57917.17**
Hybrids	78.34**	655.45**	524.04**	4596.69**	30615.71**	55311.75**
Parents Vs. Hybrids	727.10**	671.35**	3009.39**	7135.10**	30247.16**	74578.95**
Error	7.96	7.73	5.21	165.10	187.25	128.29

* Significant at 0.05; ** Significant at 0.01; DAT - Days after transplanting;
IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 34. Anova for diallel analysis for drought for AGR, CGR and RGR under two irrigation regimes

Source of Variation	Absolute growth rate			Relative growth rate			Crop growth rate		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
IR 1									
Replication	0.019	0.020	0.431	0.133	0.004	0.004	0.013	0.073	0.018
Treatments	0.065**	0.019**	0.075**	0.570**	0.095**	0.264**	0.233**	0.067**	2.605**
Parents	0.037**	0.017**	0.146**	0.716**	0.055**	0.123**	0.233**	0.047**	2.421**
Hybrids	0.073**	0.020**	0.057**	0.467**	0.094**	0.303**	0.212**	0.072**	2.198**
Parents Vs. Hybrids	0.038**	0.009*	0.059*	2.335**	0.420**	0.200**	0.792**	0.066**	14.878**
Error	0.002	0.001	0.012	0.005	0.001	0.000	0.016	0.002	0.005
IR 2									
Replication	0.003	0.002	0.003	0.013	0.005	0.288	0.361	0.153	0.241
Treatments	0.040**	0.012**	0.090**	0.342**	0.070**	0.250**	0.295**	0.048**	0.584**
Parents	0.021**	0.008**	0.117**	0.395**	0.011**	0.264**	0.366**	0.044**	0.635**
Hybrids	0.047**	0.013**	0.086**	0.287**	0.076**	0.231**	0.254**	0.050**	0.048**
Parents Vs. Hybrids	0.000	0.003	0.016*	1.455**	0.330**	0.652**	0.900**	0.014	2.938**
Error	0.003	0.001	0.002	0.009	0.000	0.016	0.007	0.007	0.023

* Significant at 0.05; ** Significant at 0.01; DAT - Days after transplanting; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 35. Anova for diallel analysis for drought for biochemical and yield parameters under two irrigation regimes

Source of Variation	Proline content ($\mu\text{g g}^{-1}$)	Chlorophyll content (mg/100g)			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
		A	B	Total			
IR 1							
Replication	162.39	0.315	0.150	0.210	3192.36	741.67	25.41
Treatments	8880.55**	0.830**	0.140**	1.480**	1677.18**	574.38**	15.92**
Parents	8226.39**	0.486**	0.115**	0.737**	2254.13**	1160.78**	25.03**
Hybrids	9039.82**	0.910**	0.150**	1.680**	1542.54**	400.93**	13.54**
Parents Vs. Hybrids	9159.51**	1.080**	0.004	1.220**	1274.19*	1152.27**	16.24**
Error	24.91	0.012	0.004	0.010	305.56	33.61	0.74
IR 2							
Replication	375.55	0.004	0.005	0.002	865.53	418.94	12.72
Treatments	31041.92**	0.684**	0.043**	0.945**	3418.78**	568.83**	19.89**
Parents	18802.13**	0.492**	0.065**	0.771**	2515.34**	1167.83**	33.43**
Hybrids	34285.22**	0.743**	0.037**	1.000**	3735.53**	408.83**	16.38**
Parents Vs. Hybrids	29151.36**	0.443**	0.023**	0.668**	1190.85*	695.69**	19.84**
Error	47.81	0.001	0.001	0.001	195.01	63.92	0.89

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 36. Anova for GCA and SCA for morphological parameters in drought evaluation under two irrigation regimes

Sl. No.	Characters	IR 1			IR 2		
		GCA	SCA	Error	GCA	SCA	Error
1	Plant height (cm) at 45 DAT	26.93**	18.55**	1.29	35.77**	31.53**	2.07
2	Plant height (cm) at 60 DAT	97.82**	97.66**	3.23	90.96**	60.09**	1.64
3	Plant height (cm) at 90 DAT	182.84**	212.31**	4.01	266.39**	170.80**	1.47
4	Number of branches at 45 DAT	12.68**	2.00**	0.47	3.36**	1.72**	0.22
5	Number of branches at 60 DAT	55.97**	9.28**	1.02	10.98**	4.86*	0.62
6	Number of branches at 90 DAT	66.29**	12.68**	3.01	36.94**	7.64**	4.63
7	Stem girth (cm) at 45 DAT	0.64**	0.34**	0.03	0.77**	0.30**	0.07
8	Stem girth (cm) at 60 DAT	1.42**	0.84**	0.18	1.18**	0.54**	0.07
9	Stem girth (cm) at 90 DAT	2.11**	1.36**	0.08	1.16**	0.67**	0.07
10	Root length (cm)	68.04**	26.36**	7.05	263.89**	86.15**	7.47
11	Root volume (cc)	92.10**	40.64**	11.01	113.31**	50.43**	5.26
12	Stomata count	1.24**	3.38**	0.29	0.91**	2.68**	0.06
13	Number of pubescence (AB)	14633.01**	18303.87**	66.71	440200.30	411522.80	293731.00
14	Number of pubescence (AD)	55009.98**	69775.07**	98.54	1079475.00**	240288.90	293590.90

* Significant at 0.05; ** Significant at 0.01; DAT - Days after transplanting; GCA - General Combining Ability; SCA - Specific Combining Ability; AB - Abaxial; AD - Adaxial; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 37. Anova for GCA and SCA for growth parameters in drought evaluation

Sl. No.	Characters	IR 1			IR 2		
		GCA	SCA	Error	GCA	SCA	Error
1	Number of leaves at 45 DAT	30.83**	25.33**	4.60	29.82**	32.73**	2.65
2	Number of leaves at 60 DAT	104.69**	126.67**	2.19	312.04**	167.16**	2.58
3	Number of leaves at 90 DAT	222.55**	169.92**	1.50	171.22***	204.67**	1.74
4	Leaf area at 45 DAT (cm ²)	2029.68**	1467.85**	43.42	2164.01**	1324.45**	55.03
5	Leaf area at 60 DAT (cm ²)	12561.51**	5871.71**	92.84	14309.52**	8261.07**	62.42
6	Leaf area at 90 DAT (cm ²)	55725.59**	23913.79**	232.21	23512.48**	17614.93**	42.76
7	AGR 45 - 60 DAT	0.033**	0.019**	0.001	0.015**	0.013**	0.001
8	AGR 45 - 90 DAT	0.015**	0.004**	0.000	0.005**	0.004**	0.000
9	AGR 60 - 90 DAT	0.027**	0.024**	0.004	0.016**	0.033**	0.001
10	RGR 45 - 60 DAT	0.257**	0.173**	0.002	0.151**	0.105**	0.003
11	RGR 45 - 90 DAT	0.031**	0.032**	0.000	0.019**	0.024**	0.000
12	RGR 60 - 90 DAT	0.255**	0.046**	0.000	0.105**	0.078**	0.005
13	CGR 45 - 60 DAT	0.093**	0.074**	0.005	0.080**	0.103**	0.002
14	CGR 45 - 90 DAT	0.045**	0.017**	0.001	0.025**	0.014**	0.002
15	CGR 60 - 90 DAT	1.210**	0.783**	0.002	0.372**	0.150**	0.008

** Significant at 0.01; DAT - Days after transplanting; GCA - General Combining Ability; SCA - Specific Combining Ability; AGR - Absolute Growth Rate; RGR - Relative Growth Rate; CGR - Crop Growth Rate; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 38. Anova for GCA and SCA for biochemical and yield parameters in drought evaluation

Sl. No.	Characters	IR 1			IR 2		
		GCA	SCA	Error	GCA	SCA	Error
	Biochemical Parameters						
1	Proline content ($\mu\text{g g}^{-1}$)	4461.57**	2584.84**	8.30	12262.82**	9868.43**	15.94
2	Chlorophyll a ($\text{mg } 100\text{g}^{-1}$)	0.310**	0.268**	0.004	0.203**	0.234**	0.000
3	Chlorophyll b ($\text{mg } 100\text{g}^{-1}$)	0.060**	0.044**	0.001	0.014**	0.014**	0.000
4	Chlorophyll total ($\text{mg } 100\text{g}^{-1}$)	0.528**	0.485**	0.003	0.314**	0.345**	0.000
	Yield parameter						
1	Number of fruits per plant	1337.49**	364.45**	101.86	1877.30**	955.17**	65.01
2	Average fruit weight (g)	264.34**	173.24**	11.21	197.10**	187.74**	21.31
3	Yield per plant (Kg)	7.34**	4.80**	0.25	7.44**	6.43**	0.30

** Significant at 0.01 GCA - General Combining Ability; SCA - Specific Combining Ability; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

stomata count and number of pubescence (abaxial). Additive variance was found to be higher for number of branches and number of pubescence (adaxial). In IR 2, dominance variation was found higher for plant height, number of branches (60 DAT), stem girth, root length, root volume, stomata count and number of pubescence (abaxial). Additive variance was found higher for number of branches (45 and 90 DAT) and number of pubescence (adaxial). Ratio of additive to dominant variation was found to be less than unity in plant height, stem girth, root length, root volume, stomata count and number pubescence (abaxial). It was more than unity for number of branches and number of pubescence (adaxial) in IR 1. The ratio of additive to dominant variance was less than unity for plant height, number of branches (60 DAT), stem girth, root length, root volume, stomata count and number of pubescence (abaxial). This was more than unity for number of branches (45 and 90 DAT) and number of pubescence (adaxial). Broad sense heritability was found to be high for all characters in IR 1 and IR 2 except for number of pubescence on abaxial layer (medium) and low for number of pubescence on adaxial layer (Table 39 and 40).

Variance due to SCA was higher for all the growth characters viz., number of leaves, leaf area (60 DAT), absolute growth rate, crop growth rate and relative growth rate in IR 1 and IR 2 except for leaf area (45 and 90 DAT) which had higher variance due to GCA effects. The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for all the growth characters in both IR 1 and IR 2. Additive variance was found to high for number of leaves in IR 1 and for leaf area (45 DAT) in both IR 1 and IR 2. Dominant variance was found to higher for other growth parameters in both IR 1 and IR 2. Ratio of additive to dominant variance was found to less than unity for all the growth parameters in IR 1 and IR 2 except for RGR (60-90) in IR 1. Heritability (broad sense) was found to be higher for all the growth parameters in IR 1 and IR 2 (Table 41 and 42).

Variance due to SCA was higher for all the biochemical parameters viz., proline content and chlorophyll (a, b and total) content. The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for all the biochemical parameters in both IR 1 and IR 2. Dominant variance was high for all the biochemical parameters in both IR 1 and IR 2. Ratio of additive to dominant variance was found to less than unity for all the biochemical parameters. Broad sense heritability was found to be high (Table 43).

Table 39. Genetic components of variation for plant height, number of branches and stem girth

Source of Variation	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1									
V_g	2.56	9.46	17.88	1.22	5.50	6.33	0.06	0.12	0.20
V_s	17.26	94.43	208.30	1.53	8.26	9.67	0.31	0.67	1.28
V_g/V_s	0.15	0.10	0.09	0.80	0.67	0.65	0.20	0.19	0.16
V_A	5.13	18.92	35.77	2.44	10.99	12.66	0.12	0.25	0.41
V_D	17.26	94.43	208.30	1.53	8.26	9.67	0.31	0.67	1.28
V_A/V_D	0.30	0.20	0.17	1.60	1.33	1.31	0.40	0.37	0.32
h^2 NS	0.22	0.16	0.14	0.55	0.54	0.40	0.27	0.23	0.23
h^2 BS	0.95	0.97	0.98	0.89	0.95	0.88	0.94	0.84	0.95
IR 2									
V_g	3.37	8.93	26.49	0.81	1.04	3.23	0.07	0.11	0.11
V_s	29.46	58.45	169.34	1.50	4.24	3.00	0.24	0.47	0.59
V_g/V_s	0.14	0.15	0.16	0.54	0.24	1.08	0.30	0.24	0.18
V_A	6.74	17.86	52.99	1.63	2.07	6.46	0.14	0.22	0.22
V_D	29.46	58.45	169.34	1.50	4.24	3.00	0.24	0.47	0.59
V_A/V_D	0.29	0.31	0.31	1.09	0.49	2.15	0.60	0.48	0.37
h^2 NS	0.18	0.23	0.24	0.49	0.30	0.46	0.32	0.29	0.25
h^2 BS	0.95	0.98	0.99	0.94	0.91	0.67	0.85	0.91	0.92

DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h^2 -heritability; NS- narrow sense; BS- broad sense; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 40. Genetic components of variation for root length, root volume, stomata count and number of pubescence

Source of Variation	Root length (cm)	Root volume (cc)	Stomata count	Number of pubescence	
				AB	AD
IR 1					
V_g	6.10	8.11	0.10	1456.63	5491.14
V_s	19.27	29.63	3.09	18237.16	6967.53
V_g/V_s	0.32	0.27	0.03	0.08	0.79
V_A	12.20	16.22	0.19	2913.26	10982.29
V_D	19.27	29.63	3.09	18237.16	6967.53
V_A/V_D	0.63	0.55	0.06	0.16	1.58
h^2 NS	0.32	0.29	0.05	0.14	0.14
h^2 BS	0.82	0.81	0.92	1.00	1.00
IR 2					
V_g	25.64	10.80	0.09	14646.93	78588.38
V_s	78.68	45.17	2.61	117791.80	-53301.98
V_g/V_s	0.33	0.24	0.03	0.12	-1.47
V_A	51.84	21.64	0.17	29293.86	157176.80
V_D	78.68	45.17	2.62	117791.80	-53301.98
V_A/V_D	0.66	0.48	0.06	0.25	-2.95
h^2 NS	0.37	0.3	0.06	0.06	0.39
h^2 BS	0.94	0.92	0.98	0.33	0.26

AB - Abaxial; AD - adaxial; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h^2 -heritability; NS- narrow sense; BS- broad sense;
 IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 41. Genetic components of variation for number of leaves and leaf area

Source of Variation	Number of leaves			Leaf area (cm ²)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1						
V _g	2.62	10.25	22.11	198.63	1246.87	5549.37
V _s	20.72	124.47	168.42	1424.43	5778.88	23681.58
V _g /V _s	0.13	0.08	0.13	0.14	0.22	0.23
V _A	5.25	20.50	44.21	397.25	2493.74	11098.67
V _D	20.72	124.47	168.42	1424.43	5778.88	23681.58
V _A /V _D	0.25	0.16	0.26	0.28	0.43	0.47
h ² NS	0.17	0.14	0.21	0.21	0.30	0.32
h ² BS	0.85	0.99	0.99	0.98	0.99	0.99
IR 2						
V _g	2.72	30.95	16.95	210.90	1424.71	2346.97
V _s	30.08	164.58	202.93	1269.42	8198.65	17572.17
V _g /V _s	0.09	0.19	0.08	0.17	0.17	0.13
V _A	5.43	61.89	33.90	1269.42	8198.65	17572.17
V _D	30.08	164.58	202.93	421.80	2849.42	4693.94
V _A /V _D	0.18	0.38	0.17	3.01	2.88	3.74
h ² NS	0.14	0.27	0.14	0.24	0.26	0.21
h ² BS	0.93	0.99	0.99	0.97	0.99	1.00

DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h² -heritability; NS- narrow sense; BS- broad sense;
 IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 42. Genetic components of variation for AGR, CGR and RGR

Source of Variation	Absolute growth rate			Relative growth rate			Crop growth rate		
	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
IR 1									
V _g	0.003	0.001	0.002	0.026	0.003	0.026	0.009	0.004	0.121
V _s	0.018	0.004	0.020	0.172	0.031	0.046	0.068	0.016	0.782
V _g /V _s	0.167	0.250	0.100	0.151	0.097	0.565	0.132	0.250	0.155
V _A	0.006	0.002	0.005	0.055	0.006	0.051	0.017	0.009	0.242
V _D	0.018	0.004	0.020	0.172	0.031	0.046	0.068	0.016	0.782
V _A /V _D	0.333	0.500	0.250	0.320	0.194	1.109	0.250	0.563	0.309
h ² NS	0.253	0.399	0.159	0.228	0.163	0.524	0.191	0.344	0.236
h ² BS	0.978	0.939	0.859	0.993	0.991	0.999	0.942	0.973	0.998
IR 2									
V _g	0.001	0.001	0.002	0.015	0.002	0.010	0.008	0.002	0.036
V _s	0.012	0.003	0.033	0.101	0.024	0.072	0.100	0.011	0.143
V _g /V _s	0.083	0.333	0.061	0.149	0.083	0.139	0.080	0.182	0.252
V _A	0.003	0.001	0.003	0.030	0.004	0.020	0.016	0.005	0.073
V _D	0.012	0.003	0.033	0.101	0.024	0.072	0.100	0.011	0.143
V _A /V _D	0.250	0.333	0.091	0.297	0.167	0.278	0.160	0.455	0.510
h ² NS	0.178	0.219	0.083	0.221	0.134	0.203	0.132	0.253	0.326
h ² BS	0.946	0.924	0.978	0.977	0.997	0.944	0.920	0.873	0.965

V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h² -heritability; NS- narrow sense; BS- broad sense;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 43. Genetic components of variation for biochemical and yield parameters

Source of Variation	Proline content ($\mu\text{g g}^{-1}$)	Chlorophyll content (mg/100g)			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
		A	B	Total			
IR 1							
V_g	445.33	0.031	0.006	0.052	123.56	25.31	0.71
V_s	2576.54	0.264	0.042	0.481	262.60	162.03	4.55
V_g/V_s	0.17	0.117	0.143	0.108	0.47	0.16	0.16
V_A	890.65	0.061	0.012	0.105	247.13	50.63	1.42
V_D	2576.54	0.264	0.042	0.481	262.60	162.03	4.55
V_A/V_D	0.35	0.231	0.286	0.218	0.94	0.31	0.31
h^2 NS	0.26	0.186	0.211	0.178	0.40	0.23	0.23
h^2 BS	1.00	0.988	0.973	0.994	0.83	0.95	0.96
IR 2							
V_g	1224.68	0.020	0.001	0.031	181.22	17.57	0.71
V_s	9852.49	0.234	0.014	0.315	890.16	166.43	6.12
V_g/V_s	0.12	0.085	0.071	0.098	0.20	0.11	0.12
V_A	2449.37	0.041	0.003	0.063	362.45	35.15	1.42
V_D	9852.49	0.234	0.014	0.315	890.16	166.43	6.12
V_A/V_D	0.25	0.175	0.214	0.200	0.41	0.21	0.23
h^2 NS	0.19	0.148	0.164	0.166	0.27	0.15	0.18
h^2 BS	0.99	0.999	0.985	0.999	0.95	0.90	0.96

V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h^2 -heritability; NS- narrow sense; BS- broad sense;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

SCA variance was high compared to GCA variance for all the yield parameters viz., number of fruits per plant, average fruit weight and yield per plant in both stressed and non-stressed condition. Genetic component ratio (V_g/V_s) was less than unity in both IR 1 and IR 2. Dominant variance was found to be high and ratio of additive to dominant variance was less than unity for the yield parameters in both the conditions. Broad sense heritability was found to be high in both conditions (Table 43).

4.4.3 Combining Ability analysis for drought tolerance

General combining ability for eight parents and specific combining ability for 28 hybrids are estimated separately for the two irrigation regimes. Detailed results of this are presented as follows.

4.4.3.1 Morphological parameters

Out of eight parents, L 02079 and TLB 133 showed highly significant positive GCA effects in all the three stages (45, 60 and 90 DAT) for plant height. L 06052 and LA 3913 showed highly significant negative GCA effects in all the three stages. These four genotypes showed similar responses in both IR 1 and IR 2. L 02079 and TLB 133 found to be good general combiner for plant height in both IR 1 and IR 2 (Table 44). Out of 28 hybrids, P4 x P8, P1 x P5, P1 x P6, P2 x P8, P1 x P4 and P6 x P7 had significant positive combining ability for this trait in all the stages, consistently for IR 1 and IR 2. These may be considered as good specific combiners for plant height (Table 45).

Highest significant positive GCA effects was seen in L 01942 in all the stages (45, 60 and 90 DAT) for number of branches in IR 1. The same for negative side was observed in BL 1188 in IR 1 for all the three stages. The result was something different in IR 2 where L 01942 showed highest significant positive effect in 45 and 60 DAT but had a negative effect for 90 DAT. BL 1188 also had highest negative GCA effect for 45 and 60 DAT but had a positive effect for 90 DAT. L 2079 had significant positive GCA at 45 and 60 DAT both in IR 1 and IR 2. L 01942 and L 2079 were found to be good general combiners for this trait at 45 and 60 DAT (Table 44). Hybrids P1 x P2, P2 x P8 and P3 x P5 had consistent positive combining

Table 44. GCA estimates of parents for plant height, number of branches and stem girth in IR 1 and IR 2

Parents	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1									
L 01942	1.50**	-0.32	1.08	1.71**	4.49**	5.06**	-0.13*	-0.28*	0.13
L 06052	-3.02**	-3.88**	-2.11**	0.71**	0.05	-0.29	0.10	0.03	-0.01
L 02079	1.73**	5.05**	8.63**	1.22**	2.33**	0.73	0.00	0.00	-0.02
LA 3913	-1.14**	-3.69**	-5.94**	-0.02	-0.25	1.25*	0.38**	0.63**	0.81**
TLB 133	1.42**	3.42**	2.50**	-0.48*	-0.98**	0.60	0.19**	0.41**	0.33**
L 06231	-0.40	-1.35*	-1.64**	-0.49*	-0.95**	-2.12**	0.02	-0.13	-0.12
L 02692	0.67*	0.80	-0.72	-1.31**	-1.72**	-2.73**	-0.49**	-0.58**	-0.73**
BL 1188	-0.77*	-0.04	-1.80**	-1.34**	-2.96**	-2.52**	-0.36	-0.08	-0.39**
SE	0.51	0.80	0.90	0.31	0.45	0.78	0.08	0.19	0.13
CD @ 5%	1.20	1.90	2.12	0.73	1.07	1.84	0.18	0.44	0.30
CD @ 1%	1.78	2.81	3.14	1.08	1.58	2.72	0.27	0.66	0.45
IR 2									
L 01942	1.10*	-0.96*	1.01**	1.45**	1.26**	-0.97	0.43**	0.49**	-0.25**
L 06052	-3.08**	-6.42**	-5.23**	-0.02	-0.72**	-3.49**	0.17*	-0.23**	0.47**
L 02079	2.50**	3.20**	10.60**	1.20**	8.67**	0.70	0.14	0.11	0.30**
LA 3913	-1.69**	-0.05	-3.45**	0.01	1.31**	-0.89	-0.03	0.31**	0.24**
TLB 133	1.97**	1.81**	0.17	-0.48**	0.09	0.01	0.09	0.18*	0.22**
L 06231	-0.90*	0.1	-1.01**	-0.37**	-0.47*	2.79**	-0.20*	-0.32**	-0.20*
L 02692	0.55	2.78**	2.86**	-0.50**	-0.92**	-0.05	-0.11	-0.01	-0.40**
BL 1188	-0.46	-0.44	-4.96**	-1.30**	-1.42**	1.90**	-0.49**	-0.53**	-0.36**
SE	0.64	0.57	0.54	0.21	0.35	0.96	0.12	0.11	0.12
CD @ 5%	1.52	1.35	1.28	0.49	0.83	2.28	0.27	0.27	0.28
CD @ 1%	2.25	2.00	1.90	0.73	1.23	3.37	0.40	0.41	0.42

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 45. SCA estimates of hybrids for plant height under two irrigation regimes

Hybrids	Plant height (cm)					
	IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-3.40**	-11.69**	-20.00**	-1.85	-4.53**	-9.90**
P1xP3	-10.23**	-24.90**	-38.36**	-10.79**	-15.85**	-32.62**
P1xP4	3.21**	-0.03	0.57	0.27	5.03**	4.56**
P1xP5	5.23**	9.84**	11.77**	6.82**	12.35**	21.77**
P1xP6	4.02**	7.80**	6.67**	5.96**	8.47**	4.58**
P1xP7	4.27**	5.23**	3.14	1.53	4.57**	-0.70
P1xP8	-3.35**	1.13	11.59**	-0.31	-9.27**	5.95**
P2xP3	-3.01**	-11.42**	-15.43**	-5.21**	-4.99**	-16.63**
P2xP4	-3.29**	-1.92	-1.33	0.52	-7.52**	-4.66**
P2xP5	-3.45**	-3.10	0.00	-1.61	-6.61**	-6.86**
P2xP6	2.03	8.19**	4.56*	1.63	1.94	-6.20**
P2xP7	2.26*	6.27**	12.34**	2.42	2.77*	13.64**
P2xP8	2.84*	-2.20	0.53	3.50*	4.11**	13.00**
P3xP4	-1.46	-0.78	2.57	4.08**	-7.11**	-0.99
P3xP5	-2.12*	-3.95*	-5.54**	-0.74	-6.16**	-6.83**
P3xP6	-0.77	-2.37	-3.72	-7.16**	2.03	-3.42**
P3xP7	-2.96**	-2.96	-4.44*	-6.60**	-1.98	-6.08**
P3xP8	-2.21*	-3.70*	-5.52**	-6.54**	-0.09	-4.12**
P4xP5	-3.14**	-12.88**	-15.09**	-4.36**	-2.62*	-4.58**
P4xP6	-1.76	-9.00**	-12.24**	-2.06	-1.76	-8.22**
P4xP7	-0.28	-5.10**	-8.97**	-3.11*	-0.85	-11.08**
P4xP8	1.60	5.98**	5.20**	7.95**	5.44**	8.44**
P5xP6	0.02	2.98	-4.75*	2.03	4.08**	-9.76**
P5xP7	6.27**	1.15	6.73**	2.28	2.07	8.66**
P5xP8	-2.77*	2.57	19.70**	-3.53*	-12.64**	3.49**
P6xP7	1.03	7.92**	13.95**	-5.25**	4.06**	9.89**
P6xP8	-0.07	-12.07**	-13.67**	-4.09**	1.73	-1.49
P7xP8	-3.06**	-4.85**	-8.61**	2.41	-2.55*	-11.70**
SE	1.52	2.41	2.69	1.93	1.72	1.62
CD @ 5%	3.13	4.95	5.51	3.96	3.53	3.33
CD @ 1%	4.23	6.68	7.45	5.35	4.76	4.50

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

ability for number of branches in both IR 1 and IR 2. These may be considered as good specific combiners for this trait (Table 46).

Parent LA 3913 had highest significant positive GCA effect in all the three stages (45, 60 and 90 DAT) for stem girth in IR 1. L 02692 had highest significant negative effect for the same. In IR 2, although L 01942 had highest significant positive effect for 45 and 60 DAT, it showed a significant negative effect in 90 DAT. L 6052 had highest significant positive effect at 90 DAT. BL 1188 had highest significant negative. LA 3913 and TLB 133 were found to be good general combiners in IR 1 but only TLB 133 was found to be good general combiner in IR 2 (Table 44). Hybrids P4 x P8, P4 x P5 and P1 x P3 were found to be consistent good specific combiners for this trait (Table 47).

Highest significant positive GCA effects was seen in LA 3913 in all the stages (45, 60 and 90 DAT) for root length and root volume in both IR 1 and IR 2. Parent L 02692 had the highest negative GCA for root length in IR 1 and L 06231 had the same in IR 2. BL 1188 had the highest negative GCA for root volume in IR 1 as well as in IR 2. L 06052, L 02079 and LA 3913 found to be good general combiners for root characters. BL 1188 had highest significant positive GCA effects for stomata count in both IR 1 and 2. BL 1188 and L 06231 found to be good general combiners for stomatal count. All eight parents had highly significant GCA effects for number of pubescence (both abaxial and adaxial) in IR 1. Highest significant GCA effect in positive direction was observed in LA 3913 and that in negative direction was in BL 1188 (both abaxial and adaxial). Only one parent (L 06231) showed significant GCA effect for number of pubescence (abaxial) in IR 2 and it was in negative direction. L 01942 was the only parent to have highest significant GCA effect for number of pubescence (adaxial) in IR 2 and it was in positive direction. BL 1188 showed significant GCA effect for the same trait and it was in negative direction. L 01942, L 06052, LA 3913 and TLB 133 were found to be good general combiners for number of pubescence in IR 1 and L 01942 was found to be good general combiner for the same in IR 2 (Table 48). Hybrids P2 x P8, P3 x P7 and P1 x P8 were found to be good specific combiners for root length in both IR 1 and IR 2. The crosses P4 x P5, P2 x P8, P3 x P6, P3 x P7 and P1 x P4 were found to be good specific combiners for root volume. Good specific combiners for stomata count were P5 x P6, P7 x P8, P3 x P5, P3 x P4, P2 x P5, P1 x P6, P3 x P8, P1 x P2, P2 x P7 and P1 x P7 (Table 49).

Table 46. SCA estimates of hybrids for number of branches under two irrigation regimes

Hybrids	Number of branches					
	IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	2.45**	7.15**	3.81	2.81**	3.71**	-1.02
P1xP3	-0.98	0.88	0.53	0.58	-861.00	-1.35
P1xP4	-1.10	-1.53	-2.74	-0.97*	0.27	1.51
P1xP5	-1.35*	-1.96*	-4.26	-0.37	0.00	1.60
P1xP6	-1.46*	-0.51	1.98	0.00	-0.77	-1.00
P1xP7	-0.99	-0.24	2.41	-0.97*	0.35	-2.09
P1xP8	2.20**	0.11	-4.97	0.31	-0.98	-2.56
P2xP3	-1.20	-4.83**	-0.05	-2.50**	0.42	-3.41
P2xP4	-0.35	-2.82**	-1.79	-8.31	-1.08	1.54
P2xP5	-0.45	-1.15	1.59	-0.15	-2.02**	-5.29*
P2xP6	-0.72	-1.50	4.58	-1.42**	-0.53	0.34
P2xP7	2.69**	6.26**	1.08	2.88**	1.35	2.63
P2xP8	1.65*	3.12**	-1.07	1.23**	3.73**	-0.66
P3xP4	1.77**	3.69**	1.53	1.46**	-0.58	0.02
P3xP5	2.28**	4.83**	3.75	1.15*	1.99**	1.17
P3xP6	-1.03	-1.71	-0.57	-0.55	-0.11	-2.27
P3xP7	-0.74	-1.79	-1.62	-0.31	-0.87	-0.49
P3xP8	-1.07	0.37	0.67	0.82	-1.98**	2.35
P4xP5	0.33	-1.36	-2.13	-0.10	2.39**	-3.16
P4xP6	0.34	-1.40	0.59	-0.21	2.94**	-3.98
P4xP7	0.17	-0.09	4.24	-1.21**	1.94*	1.19
P4xP8	0.68	1.48	2.24	1.60**	4.50*	3.42
P5xP6	-0.26	1.91*	8.59	0.79	0.43	3.55
P5xP7	-0.43	1.88*	-2.20	-0.06	-1.69*	2.97
P5xP8	0.22	-3.28**	-5.84	-1.49**	-4.62**	4.03*
P6xP7	-0.33	0.36**	-0.33	0.68	-3.55**	-0.13
P6xP8	-1.15	-3.72	-4.04	-1.72**	1.64*	2.75
P7xP8	-0.73	-0.25	2.73	0.37	-1.45	-4.07*
SE	0.92	1.36	2.33	0.62	1.05	2.89
CD @ 5%	1.89	2.78	4.78	1.28	2.16	5.93
CD @ 1%	2.56	3.76	6.45	1.73	2.92	8.00

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 47. SCA estimates of hybrids for stem girth under two irrigation regimes

Hybrids	Stem girth (cm)					
	IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-0.07	-0.35	-0.62*	-0.14	0.51*	-0.64*
P1xP3	0.12	0.21	0.85**	0.90**	0.28	0.26
P1xP4	-0.35*	-0.68	0.26	-0.09	0.32	-0.53*
P1xP5	-0.98**	-1.25**	-1.35**	-0.31	0.22	-0.73**
P1xP6	0.24	0.58	0.59*	0.32	0.06	-0.07
P1xP7	0.40*	0.59	0.51	-0.48	0.18	-0.70**
P1xP8	0.25	0.10	-0.62*	0.03	-0.63*	1.23**
P2xP3	0.35*	0.46	1.44**	-0.23	0.12	0.17
P2xP4	-0.63**	-0.61	-1.04**	0.07	0.00	0.36
P2xP5	-0.03	-0.03	-0.25	-0.21	-1.08**	-0.17
P2xP6	0.82**	1.56**	1.23**	-0.14	0.54*	0.32
P2xP7	0.11	-0.29	-0.66*	0.13	-0.29	0.08
P2xP8	-2.99	-0.86*	-0.61*	-0.36	0.53*	-0.54*
P3xP4	-0.31	-0.76	-1.79**	-0.52*	-1.60**	-0.96**
P3xP5	0.08	-0.17	-1.12**	-1.27**	-0.45	-1.47**
P3xP6	-5.00	0.00	1.31**	0.25	0.35	0.23
P3xP7	-0.12	-0.08	-0.13	0.43	0.31	0.79**
P3xP8	0.24	0.41	0.62*	0.77**	-0.64*	0.29
P4xP5	-0.42*	-0.54	0.17	0.06	1.02**	0.63*
P4xP6	-0.03	-0.06	0.33	-0.16	-0.51*	-0.23
P4xP7	1.16**	1.47**	2.02**	-0.59*	0.51*	-0.06
P4xP8	0.52**	1.10**	1.65**	1.55***	0.98**	1.67**
P5xP6	0.91**	1.49**	1.04**	-0.19	-0.43	-0.11
P5xP7	-0.74**	-1.37**	-0.49	0.37	0.52*	-1.49**
P5xP8	-0.98**	-1.53**	-1.73**	-0.12	-1.16**	-0.13
P6xP7	-0.49**	-0.63	-0.46	0.80**	-0.72**	0.43
P6xP8	-0.47**	-0.72	0.89**	-0.32	0.78**	-0.31
P7xP8	0.56**	0.79*	0.57*	0.10	-1.17**	0.03
SE	0.23	0.56	0.38	0.35	0.35	0.36
CD @ 5%	0.47	1.16	0.79	0.71	0.72	0.75
CD @ 1%	0.64	1.56	1.07	0.96	0.98	1.01

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 48. GCA estimates of parents for root length, volume and stomata count in IR 1 and IR 2

Parents	Root length (cm)	Root volume (cc)	Stomata count
IR 1			
L 01942	-0.05	-1.44	-0.04
L 06052	2.49**	2.77**	-0.37*
L 02079	2.69**	3.50**	-0.21
LA 3913	3.32**	4.06**	-0.18
TLB 133	-0.31	-2.39*	-0.11
L 06231	-2.56**	-0.31	0.47**
L 02692	-3.47**	-2.37*	-0.19
BL 1188	-2.11**	-3.82**	0.62**
SE	1.19	1.48	0.24
CD @ 5%	2.81	3.51	0.57
CD @ 1%	4.16	5.19	0.85
IR 2			
L 01942	-0.47	-0.29	0.05
L 06052	6.29**	2.55**	-0.24**
L 02079	5.21**	3.36**	-0.03
LA 3913	5.79**	4.98**	-0.36**
TLB 133	-1.07	0.37	-2.05**
L 06231	-5.74**	-2.41**	0.45**
L 02692	-5.29**	-3.51**	-0.22**
BL 1188	-4.72**	-4.62**	0.46**
SE	1.22	1.03	0.11
CD @ 5%	2.89	2.43	0.26
CD @ 1%	4.28	3.59	0.39

AB - Abaxial; AD - Adaxial * Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 49. SCA estimates of parents for root length, volume, stomata count and number of pubescence in IR 1 and IR 2

Hybrids	IR 1			IR 2		
	Root length (cm)	Root volume (cc)	Stomata count	Root length (cm)	Root volume (cc)	Stomata count
P1xP2	-2.90	-3.12	0.95	-10.78**	-3.87	1.04**
P1xP3	-3.22	-2.19	0.07	-3.42	-8.22**	0.02
P1xP4	0.95	6.73*	-0.74	4.09	6.77**	-0.69**
P1xP5	1.98	6.15	-1.43**	3.88**	9.59**	-1.11**
P1xP6	4.79	-2.90	1.37**	2.36	-0.34	0.92**
P1xP7	5.74*	-0.60	0.90	5.68*	-1.34	0.82**
P1xP8	6.15*	0.64	-0.43	11.74**	1.30	-0.18
P2xP3	-0.94	1.24	-1.26*	2.34	4.83*	-1.38**
P2xP4	-2.15	-7.86*	-1.14*	1.42	-0.58	-1.11**
P2xP5	2.06	-8.72**	1.64**	-1.86	-9.53**	1.27**
P2xP6	-0.54	-3.93	0.72	-0.78	-0.71	0.43
P2xP7	6.38*	1.91	0.43	8.48**	-3.41	0.86**
P2xP8	8.77**	9.20**	-1.92**	14.07**	10.02**	-1.33**
P3xP4	-5.35*	-11.95**	1.28*	-17.81**	-12.61**	1.35**
P3xP5	-1.49	-2.12	1.57**	-7.75**	-6.38**	1.73**
P3xP6	2.38	12.47**	-0.95	10.19**	9.29**	-0.95**
P3xP7	5.47*	8.17*	-0.04	14.42**	9.75**	-0.11
P3xP8	4.39	3.04	1.04*	3.68	-1.52	0.82**
P4xP5	3.49	9.97**	-3.16**	12.42**	13.22**	-2.75**
P4xP6	5.15*	2.96	-0.73	5.32*	5.57*	-0.97**
P4xP7	-2.59	5.12	-0.30	-4.90	4.30*	-0.38
P4xP8	3.87	-1.86	-0.76	6.60*	4.63*	-0.93**
P5xP6	-0.01	-1.90	3.60**	-4.75	-3.32	2.85**
P5xP7	-6.48*	-4.84	-0.05	-12.75**	-6.66**	0.25
P5xP8	-11.51**	-6.50*	-1.53**	-12.65**	-7.63**	-1.18**
P6xP7	-5.56*	5.16	-0.07	-4.75	-2.52	0.21
P6xP8	-1.92	1.81	-4.08**	3.01	2.30	-3.75**
P7xP8	-1.67	-5.40	3.31**	-10.44**	-3.97	2.54**
SE	3.56	4.45	0.72	3.67	3.08	0.33
CD @ 5%	7.31	9.13	1.49	7.52	6.31	0.68
CD @ 1%	9.87	12.33	2.01	10.16	8.52	0.92

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

4.4.3.2 Growth parameters

Out of 8 parents, only one parent showed significant GCA effect (negative) in IR2 for number of pubescence (abaxial) and two parents showed significant GCA effect for number of pubescence (adaxial), one each in positive and negative direction. But in non-stressed condition, all eight parents showed highly significant GCA effects for this trait both on abaxial and adaxial layers. Five parents had positive and three had negative GCA effect on both abaxial and adaxial layer (Table 50). Under non-stressed condition, 14 hybrids had highly significant SCA effects for number of pubescence on abaxial layer and 13 on adaxial layer. Only two hybrids had significant positive SCA effect for number of pubescence, one each on abaxial (P2 x P4) and adaxial (P5 x P7) layer in stressed as well as non stressed condition (Table 51).

Three parents showed highly significant GCA effects for number of leaves at 45 DAT, one was in positive direction (L 02079) and other two in negative direction (L 06231 and BL 1188) in IR 1. At 60 DAT, six parents showed highly significant GCA effects, three each in positive and negative direction. At 90 DAT, seven parents showed highly significant GCA effects, three in positive direction and four in negative direction. L 02079 had the highest positive GCA effect and BL 1188 had that in negative direction at all the stages in IR 1 for this trait. Four parents showed highly significant GCA effects for number of leaves at 45 DAT in IR 2, two each in positive and negative direction. At 60 DAT, seven parents showed highly significant GCA effects (four in positive direction and three in negative direction) and five at 90 DAT (two in positive and three in negative direction). L 02079 had highest GCA effect in positive and BL 1188 had that in negative direction in all the three stages for this trait in IR 2 (Table 50). Hybrids P3 x P7, P2 x P7, P3 x P4, P1 x P8, P2 x P8, P3 x P6 and P1 x P6 had consistent significant positive SCA effects for number of leaves in both IR 1 and IR 2. These may be considered as good specific combiners for number of leaves (Table 52).

Six parents had significant GCA effects (2 in positive and 4 in negative direction) for leaf area in IR 2 at 45 DAT. Seven parents had the same (3 positive and 4 negative) at 60 DAT. Eight parents had that (4 each in positive and negative direction) at 90 DAT. All the eight parents had significant GCA effects in IR 1. Genotypes L 02079, L 02692 and L 06052 found to be good general combiners for

Table 50. GCA estimates for number of pubescence, number of leaves and leaf area in IR 1 and IR 2

Parents	Number of pubescence		Number of leaves			Leaf area (cm ²)		
	AB	AD	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1								
L 01942	18.94**	50.05**	0.08	2.23**	2.64**	-6.91**	26.05**	72.22**
L 06052	28.15**	26.77**	1.04	1.74**	3.71**	23.48**	33.10**	79.21**
L 02079	7.85**	10.09**	2.65**	5.60**	7.66**	14.22**	53.68**	91.35**
LA 3913	47.63**	103.12**	0.74	-0.24	0.38	4.12*	-13.17**	-24.70**
TLB 133	24.32**	50.26**	0.72	-2.29**	-1.98**	5.49**	-26.10**	47.08**
L 06231	-40.46**	-65.35**	-1.89**	0.20	-1.62**	-15.68**	-10.20**	-35.01**
L 02692	-23.23**	-52.47**	-0.39	-2.50**	-2.97**	-9.08**	-7.45*	-13.80**
BL 1188	-63.20**	-122.47**	-2.95**	-4.73**	-7.84**	-15.63**	-55.89**	-122.19**
SE	3.65	4.44	0.96	0.66	0.55	2.95	4.31	6.81
CD @ 5%	8.64	10.50	2.27	1.57	1.29	6.97	10.19	16.11
CD @ 1%	12.78	15.54	3.36	2.32	1.92	10.31	15.08	23.85
IR 2								
L 01942	-31.98	717.60**	0.35	4.29**	4.19**	-7.88**	55.59**	59.07**
L 06052	279.50	-104.58	1.44**	1.83**	0.39	23.49**	-0.04	19.52**
L 02079	-17.40	-134.17	2.73**	8.85**	6.03**	21.48**	44.95**	61.27**
LA 3913	76.94	-30.56	0.42	-2.12**	0.32	-0.48	-14.61**	-14.13**
TLB 133	272.61	152.59	0.16	-5.41**	0.67	-11.18**	-24.29**	-21.10**
L 06231	-345.87*	-205.81	-0.62	-0.45	-1.04**	-3.52	-6.33**	-20.65**
L 02692	-39.49	-14.34	-1.70**	1.97**	-3.26**	-5.39*	7.96**	3.87*
BL 1188	-144.32	-380.74*	-2.79**	-8.97**	-7.31**	-16.52**	-63.23**	-87.95**
SE	242.38	242.32	0.73	0.72	0.59	3.32	3.53	2.92
CD @ 5%	573.13	573.00	1.72	1.70	1.39	7.84	8.35	6.92
CD @ 1%	848.20	848.00	2.55	2.21	2.06	11.61	12.36	10.23

AB - Abaxial; AD - Adaxial; DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231; P7 - L 02692; P8 - BL 1188

Table 51. SCA estimates for number of pubescence of tomato hybrids under two irrigation regimes

Hybrids	Number of pubescence			
	IR 1		IR 2	
	AB	AD	AB	AD
P1xP2	-66.51**	-59.62**	-685.82	169.19
P1xP3	-57.78**	-136.03**	-399.14	80.73
P1xP4	61.39**	155.31**	-305.20	407.74
P1xP5	165.06**	320.93**	585.60	760.55
P1xP6	-32.67**	-34.51**	-87.26	469.28
P1xP7	-87.27**	-142.97**	-396.03	-25.85
P1xP8	42.53**	36.11**	588.43	-626.01
P2xP3	213.58**	433.87**	541.02	460.83
P2xP4	133.41**	201.52**	1338.31*	288.72
P2xP5	-113.43**	-224.63**	-247.74	-437.00
P2xP6	-45.66**	-117.05**	423.97	-97.84
P2xP7	-99.17**	-174.49**	-734.11	-395.49
P2xP8	46.38**	162.96**	-556.91	239.95
P3xP4	-199.00**	-341.76**	-654.22	-346.10
P3xP5	-182.31**	-316.66**	-859.01	-571.12
P3xP6	103.24**	173.17**	19.96	133.84
P3xP7	22.05**	-12.07	276.45	-189.78
P3xP8	-78.66**	-168.45**	-416.27	-67.41
P4xP5	266.30**	524.47**	671.60	330.31
P4xP6	74.95**	186.53**	-0.56	163.74
P4xP7	52.80**	153.65**	-317.20	-56.44
P4xP8	78.37**	137.01**	794.01	315.49
P5xP6	-195.62**	-363.39**	-594.20	-616.46
P5xP7	-7.97	32.74**	-593.41	1439.33**
P5xP8	36.61**	-17.52	662.66	-112.24
P6xP7	-42.43**	-167.33**	-119.89	-401.57
P6xP8	206.06**	430.72**	177.52	500.96
P7xP8	-128.21**	-207.48**	-441.70	-280.67
SE	10.96	13.32	727.13	726.96
CD @ 5%	22.48	27.33	1491.94	1491.58
CD @ 1%	30.36	36.90	2014.65	2014.17

AB - Abaxial; AD - Adaxial; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 52. SCA estimates for number of leaves of tomato hybrids under two irrigation regimes

Hybrids	Number of leaves					
	IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-5.56**	-3.47*	-10.61**	-4.19**	2.27	1.59
P1xP3	-0.14	4.95**	5.60**	-1.05	11.78**	-7.54**
P1xP4	-0.93	-0.46	1.81	1.92	2.79	8.65**
P1xP5	3.98	-1.18	3.14**	1.68	8.57**	7.40**
P1xP6	7.33**	10.97**	16.16**	8.82**	0.26	17.03**
P1xP7	0.57	5.94**	1.03	-3.96*	-7.93**	-6.90**
P1xP8	4.86*	7.38**	12.15**	5.98**	9.34**	10.90**
P2xP3	0.29	-6.57**	-1.43	2.47	-14.43**	3.30*
P2xP4	-0.39	-13.64**	-11.67**	-2.31	-9.77**	-6.57**
P2xP5	1.57	2.92*	5.09**	4.60**	-8.05**	2.36
P2xP6	5.12*	3.43*	2.76*	-3.57*	-12.97**	-12.07**
P2xP7	5.07*	22.59**	23.90**	6.71**	30.74**	17.87**
P2xP8	3.93	11.86**	15.07**	7.49**	20.20**	30.39**
P3xP4	4.94*	16.11**	16.76**	9.62**	5.09**	25.12**
P3xP5	3.39	16.97**	10.67**	-2.37	5.94**	2.18
P3xP6	3.36	4.41**	11.84**	3.91*	10.24**	2.64*
P3xP7	11.50**	8.66**	20.00**	7.62**	15.18**	10.92**
P3xP8	0.11	4.69**	6.06**	1.95	7.51**	-4.66**
P4xP5	-1.73	-10.51**	-7.52**	-0.35	0.85	2.97*
P4xP6	-1.32	-4.86*	-2.96*	3.18*	-9.82**	5.96**
P4xP7	-2.27	-0.02	-3.96**	-3.73*	-12.46**	-6.29**
P4xP8	3.97	-2.80*	1.61	4.65**	0.46	10.68**
P5xP6	1.20	4.94**	0.31	-2.86	-10.96**	-9.92**
P5xP7	-4.34*	3.89**	1.38	-1.55	9.66**	5.90**
P5xP8	-5.45**	-11.88**	-11.11**	-3.79*	-7.06**	-17.05**
P6xP7	-5.73**	-3.26*	-5.65**	-5.44**	10.03**	-23.06**
P6xP8	-4.17*	-13.03**	-9.80**	-0.34	-5.02**	3.32**
P7xP8	-3.01	-2.00	-4.12**	3.74*	-15.11**	3.88**
SE	2.88	1.99	1.64	2.19	2.15	1.77
CD @ 5%	5.91	4.08	3.37	4.49	4.42	3.63
CD @ 1%	7.98	5.51	4.55	6.06	5.97	4.90

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

this trait (Table 50). Hybrids P2 x P8, P2 x P7, P1 x P5, P1 x P4, P1 x P8, P3 x P6 and P4 x P5 were found to be good specific combiners for leaf area per plant (Table 53).

Four parents had highly significant positive GCA effect for AGR (45-60) and two had highly significant negative effect in IR 1 and IR 2. All the eight parents had significant GCA effects for AGR (45-90), RGR (60-90) and CGR (45-90 and 60-90) in IR 1. L 06052 had highly significant positive GCA effect for AGR (45-60, 45-90 and 60-90 DAT), RGR (45-60 and 45-90 DAT) and CGR (45-60, 45-90 and 60-90 DAT). It had negative GCA effect only for RGR (60-90 DAT) in IR 1. LA 3913 and L 02079 had highly significant positive GCA effect for AGR, RGR and CGR in almost all time intervals. L 06052 had highly significant positive GCA effect for AGR (45-60 and 60-90), RGR (45-60) and CGR (60-90). So, LA 3913, L 02079 and L 06052 may be considered as good general combiners for these traits in IR 2 (Table 54). Hybrids P1 x P8 (for AGR); P2 x P3, P1 x P4, P2 x P8 and P6 x P8 (for RGR); P2 x P3, P4 x P6, P1 x P6, P4 x P7, P1 x P8 and P4 x P5 (for CGR) were found to be good specific combiners for the above mentioned traits (Table 55, 56 and 57).

4.4.3.3 Biochemical parameters

All the eight parents had highly significant GCA effects for proline content in IR 1. Among them, five had positive and three had negative effects. In IR 2, seven parents had highly significant GCA effects, out of which four had positive and three had negative effects. L 06052, L 02079, LA 3913 and TLB 133 had highly significant positive GCA effects in both IR 1 and IR 2. So, these four parents may be considered as good general combiners for this trait (Table 58). Hybrids P4 x P5, P2 x P3, P1 x P5, P6 x P8, P4 x P6, P3 x P6, P4 x P7, P4 x P8, P2 x P4, P2 x P8 and P1 x P6 were good specific combiners for proline content (Table 59).

For chlorophyll content (a, b and total), LA 3913 and TLB 133 had highly significant positive GCA effects in both IR 1 and IR 2. These two parents may be considered as good general combiners for this trait (Table 58). Good specific combiner for chlorophyll a content were P4 x P5, P3 x P6, P6 x P8, P2 x P3, P1 x P5, P3 x P7, P1 x P4, P2 x P4, P4 x P8, P4 x P6 and P4 x P7. The hybrids P3 x P4, P3 x P6, P2 x P6, P2 x P3, P1 x P5, P4 x P8, P2 x P4, P4 x P6 and P4 x P7 were good specific combiners for chlorophyll b. The crosses P4 x P5, P3 x P6, P2 x P3, P1 x P5,

Table 53. SCA estimates for leaf area of tomato hybrids under two irrigation regimes

Hybrids	Leaf Area (cm ²)					
	IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-60.65**	-29.03**	-89.55**	-36.68**	64.73**	37.99**
P1xP3	-24.41**	3.02**	57.44**	0.25	16.71*	-23.80**
P1xP4	1.86	17.85	102.74**	14.47*	71.67**	111.45**
P1xP5	29.11**	42.82**	126.79**	22.45**	82.36**	139.86**
P1xP6	15.58*	13.37	-22.06	-17.36*	-16.65*	-23.12**
P1xP7	-17.29**	-37.17**	-126.75**	-43.66**	-45.88**	-122.27**
P1xP8	72.09**	114.79**	224.83**	70.94**	46.18**	121.03**
P2xP3	41.86**	-41.64**	31.69*	19.14**	-42.78**	15.02*
P2xP4	30.91**	-42.46**	-15.91	6.14	-44.47**	5.32
P2xP5	7.09	-28.96**	-89.55**	-6.82	-97.20**	-115.18**
P2xP6	33.46**	-36.30**	-98.13**	-29.46**	-102.61**	-154.66**
P2xP7	4.63	175.90**	248.48**	45.27**	159.50**	161.16**
P2xP8	20.98**	125.64**	260.87**	43.75**	216.90**	298.50**
P3xP4	7.82	60.67**	16.20	-4.72	38.03**	37.27**
P3xP5	-1.10	59.21**	5.36	-16.64*	50.19**	-15.25*
P3xP6	31.41**	61.96**	188.68**	46.69**	40.50**	78.65**
P3xP7	84.20**	112.92**	250.28**	60.98**	57.87**	132.55**
P3xP8	-30.11**	8.18	-32.37*	-7.30	-40.09**	-88.42**
P4xP5	21.29**	-0.74	98.74**	36.70**	58.31**	140.35**
P4xP6	-2.80	-54.62**	-75.37**	-6.65	-43.67**	-23.53**
P4xP7	-6.24	-52.38**	-97.32**	-18.38*	-48.24**	-83.54**
P4xP8	20.50**	-2.70	-0.60	0.87	8.10	53.19**
P5xP6	-24.55**	-69.87**	-234.57**	-52.81**	-116.10**	-214.09**
P5xP7	-51.43**	40.72**	124.87**	-29.13**	132.10**	113.87**
P5xP8	19.85**	-10.67	64.70**	31.96**	-70.43**	-41.07**
P6xP7	-43.97**	8.86	-3.71	11.56	-45.32**	-101.07**
P6xP8	7.05	-35.98**	73.60**	25.89**	47.03**	126.51**
P7xP8	-42.69**	-100.69**	-262.36**	-45.82**	-126.26**	-173.42**
SE	8.84	12.93	20.44	9.95	10.60	8.77
CD @ 5%	18.14	26.52	41.95	20.42	21.75	18.00
CD @ 1%	24.50	35.82	56.65	27.58	29.37	24.31

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 54. GCA estimates of parents for AGR, CGR and RGR in IR 1 and IR 2

Parents	Absolute growth rate			Relative growth rate			Crop growth rate		
	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
IR 1									
L 01942	0.042**	0.025**	0.025	0.275**	-0.003	0.368**	-0.017	0.040**	0.502**
L 06052	0.061**	0.030**	0.076**	0.060**	0.040**	-0.079**	0.008	0.037**	0.172**
L 02079	0.025**	0.013*	0.036	-0.025*	0.002	-0.076**	0.057*	0.024**	-0.137**
LA 3913	0.040**	0.028**	0.005	-0.035**	0.049**	-0.075**	0.108**	0.071**	0.072**
TLB 133	0.003	0.037**	0.026	0.014	-0.012*	0.044**	0.067**	0.060**	0.120**
L 06231	-0.010	-0.039**	-0.036	0.069**	0.056**	-0.064**	0.045*	-0.052**	0.151**
L 02692	-0.114**	-0.059**	-0.073**	-0.278**	-121.000**	0.022**	-0.195**	-0.089**	-0.679**
BL 1188	-0.044**	-0.037**	-0.050*	-0.011**	-0.012*	-0.139**	-0.071**	-0.091**	-0.205**
SE	0.010	0.009	0.028	0.018	0.008	0.003	0.032	0.011	0.017
CD @ 5%	0.025	0.022	0.068	0.043	0.020	0.008	0.077	0.028	0.043
CD @ 1%	0.037	0.032	0.100	0.064	0.029	0.012	0.114	0.041	0.063
IR 2									
L 01942	0.024**	-0.003	0.031**	0.231**	-0.031**	-0.054*	0.010	0.011	0.320**
L 06052	0.032**	0.003	0.055**	0.010	0.008**	-0.020	-0.067**	0.017	0.141**
L 02079	0.030**	0.023**	0.020*	-0.024	-0.004	0.085**	0.073**	0.045**	-0.068*
LA 3913	0.037**	0.036**	-0.021*	-0.024	0.068**	0.131**	0.089**	0.058**	0.017
TLB 133	-0.001	0.013*	0.033**	0.024	-0.031**	0.088**	0.057**	0.033*	0.063*
L 06231	-0.013	-0.021**	-0.029**	0.069**	0.047**	0.260	0.043**	-0.047**	0.008
L 02692	-0.071**	-0.020**	-0.062**	-0.193**	-0.073**	-0.176**	-0.153**	-0.028*	-0.321**
BL 1188	-0.037**	-0.032**	-0.027**	-0.092**	-0.002	-0.081**	-0.081**	-0.088**	-0.160**
SE	0.013	0.008	0.013	0.024	0.003	0.033	0.021	0.021	0.039
CD @ 5%	0.031	0.020	0.030	0.059	0.009	0.078	0.051	0.051	0.093
CD @ 1%	0.046	0.030	0.040	0.087	0.014	0.116	0.076	0.075	0.138

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 55. SCA estimates for absolute growth rate of tomato hybrids under two irrigation regimes

Hybrids	Absolute growth rate					
	IR 1			IR 2		
	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
P1xP2	0.02	-0.06**	-0.18**	0.04	-0.02	-0.13**
P1xP3	-0.20**	-0.10**	0.07	-0.14**	-0.04*	0.09**
P1xP4	0.11**	0.10	-0.12	0.06*	0.04*	-0.18**
P1xP5	0.08**	0.10**	0.02	0.10**	0.11**	-0.34
P1xP6	-0.09**	0.04*	0.18**	-0.10**	0.00	0.21**
P1xP7	0.02	-0.02	-0.05	0.04	-0.03	-0.02
P1xP8	0.18**	0.07**	0.08	0.13**	0.01	0.05*
P2xP3	0.20**	0.11**	-0.15	0.10**	0.06**	-0.10**
P2xP4	-0.04	0.06*	-0.05	-0.03	0.02	-0.04
P2xP5	-0.14**	-0.05*	0.08	-0.16**	-0.08**	0.13**
P2xP6	0.00	0.04	0.03	0.03	-0.02	0.06*
P2xP7	0.01	-0.06**	0.03	0.04	-0.02	0.05
P2xP8	0.23**	0.03	-0.22**	0.19**	0.08**	-0.30**
P3xP4	-0.07**	-0.07**	0.01	-0.10**	-0.11**	0.12**
P3xP5	0.11**	-0.07**	-0.14*	0.15**	-0.06**	-0.08*
P3xP6	0.04	0.02	0.06	0.02	0.07**	-0.04
P3xP7	-0.02	0.06**	0.14*	0.00	0.07*	0.09**
P3xP8	-0.23**	-0.06**	0.25**	-0.20**	-0.04*	0.29**
P4xP5	0.16**	0.07**	-0.17**	0.13**	0.11**	-0.28**
P4xP6	0.06**	0.06**	0.08	-0.01	0.04*	0.04
P4xP7	0.24**	0.05*	-0.08	0.19**	0.04*	-0.14**
P4xP8	-0.09**	0.07**	0.12*	-0.08**	0.04*	0.13**
P5xP6	-0.06**	0.00	0.18**	-0.03	-0.02	0.24**
P5xP7	0.03	-0.03	-0.06	0.01	-0.05**	-0.03
P5xP8	0.00	-0.02	0.02	-0.05	-0.07**	0.01
P6xP7	-0.21**	-0.10**	0.15*	-0.14**	-0.04*	0.15**
P6xP8	0.04	-0.03	-0.32**	0.01	0.04*	-0.40**
P7xP8	0.11**	0.01	0.24**	-0.17**	-0.05*	0.30**
SE	0.03	0.03	0.09	0.04	0.03	0.04
CD @ 5%	0.07	0.06	0.18	0.08	0.05	0.08
CD @ 1%	0.09	0.08	0.24	0.11	0.07	0.11

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 56. SCA estimates for relative growth rate of tomato hybrids under two irrigation regimes

Hybrids	Relative growth rate					
	IR 1			IR 2		
	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
P1xP2	0.36**	0.02	0.15**	0.31**	-0.04**	0.17*
P1xP3	-0.39**	-0.18**	0.13**	-0.27**	-0.10**	-0.35**
P1xP4	0.43**	0.23**	0.16**	0.33**	0.22**	0.13
P1xP5	-0.17**	-0.10**	0.22**	-0.09	-0.06**	0.11
P1xP6	0.22**	-0.02	0.27**	0.24**	-0.01	0.24**
P1xP7	-0.04	-0.07**	0.08**	-0.05	-0.03**	-0.12
P1xP8	0.21**	0.14**	-0.38**	0.07	0.02*	0.16*
P2xP3	0.49**	0.35**	0.00	0.33**	0.33**	0.24**
P2xP4	-0.37**	-0.16**	0.00	-0.28**	-0.15**	-0.12
P2xP5	0.20**	0.09**	-0.12**	0.15**	0.07**	0.14
P2xP6	-0.43**	-0.16**	-0.01	-0.35**	-0.12**	-0.24**
P2xP7	0.16**	0.01	-0.09**	0.11*	-0.04**	0.14*
P2xP8	0.34**	0.12**	0.07**	0.27**	0.09**	0.08
P3xP4	0.59**	0.08**	0.01	0.46**	-0.04**	0.17*
P3xP5	0.01	-0.03	-0.10**	-0.03	-0.09**	-0.14
P3xP6	-0.12**	0.10**	-0.02*	-0.10	0.17**	-0.03
P3xP7	-0.49**	-0.14**	-1.40**	-0.37**	-0.08**	-0.02
P3xP8	-0.05	-0.07**	0.06**	0.00	-0.02*	0.07
P4xP5	-0.01	0.15**	-0.12**	-0.03	0.17**	0.17*
P4xP6	0.55**	0.29**	-0.01	0.44**	0.26**	0.47**
P4xP7	0.31**	0.26**	-0.10**	0.20**	0.23**	0.16*
P4xP8	-0.10*	-0.11**	0.06**	-0.03	-0.10**	0.22**
P5xP6	-0.20**	-0.08**	-0.13**	-0.13*	-0.05**	0.08
P5xP7	0.63**	0.02	0.79**	0.53**	-0.03**	-0.26**
P5xP8	0.01	0.03	-0.07**	-0.08	-0.02	-0.38**
P6xP7	-0.64**	-0.23**	-0.13**	-0.50**	-0.14**	-0.44**
P6xP8	0.08*	0.18**	0.04**	0.06	0.23**	-0.09
P7xP8	0.64**	0.21**	-0.04**	0.53**	0.14**	0.61**
SE	0.05	0.02	0.01	0.07	0.01	0.10
CD @ 5%	0.11	0.05	0.02	0.15	0.02	0.20
CD @ 1%	0.15	0.07	0.03	0.21	0.03	0.27

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 57. SCA estimates for crop growth rate of tomato hybrids under two irrigation regimes

Hybrids	Crop growth rate					
	IR 1			IR 2		
	45 – 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
P1xP2	0.15*	-0.06*	0.17**	0.35**	-0.05	-0.03
P1xP3	-0.34**	-0.17**	-0.79**	-0.31**	-0.07	-0.36**
P1xP4	0.12	0.04	0.84**	0.17**	0.04	0.41**
P1xP5	0.00	0.17**	-0.43**	0.04	0.20**	-0.07
P1xP6	0.27**	0.08**	0.83**	0.32**	0.02	0.31**
P1xP7	-0.01	-0.03	-0.11**	-0.15**	-0.09	-0.08
P1xP8	0.23**	0.12**	0.40**	0.13**	0.07	0.25**
P2xP3	0.31**	0.24**	1.62**	0.16**	0.12*	0.85**
P2xP4	-0.17*	0.10**	-0.74**	-0.23**	0.11*	-0.19*
P2xP5	0.15*	-0.07**	0.69**	0.12**	-0.11*	0.20*
P2xP6	-0.19**	0.11**	-0.50**	-0.41**	0.01	-0.13
P2xP7	0.12	-0.08**	-0.11**	0.23**	-0.02	-0.05
P2xP8	0.04	-0.11**	0.06	0.24**	-0.04	-0.05
P3xP4	0.19**	-0.17**	0.83**	0.33**	-0.22**	0.20*
P3xP5	-0.12	-0.12**	0.39**	-0.13**	-0.17**	-0.25**
P3xP6	-0.02	0.07*	0.09*	-0.07	0.11*	0.12
P3xP7	-0.07	0.11**	-0.80**	-0.14**	0.16**	-0.27**
P3xP8	0.05	-0.09**	0.11**	0.09*	-0.04	-0.05
P4xP5	0.15*	0.18**	0.03	0.15**	0.22**	0.12
P4xP6	0.45**	0.12**	1.48**	0.47**	0.06	0.60**
P4xP7	0.23**	0.14**	0.95**	0.13**	0.02	0.44**
P4xP8	0.19**	0.12**	-0.09*	0.25**	0.14**	-0.05
P5xP6	0.06	-0.05*	-0.13**	0.01	-0.11*	-0.22**
P5xP7	-0.18**	-0.07**	0.95**	-0.07	-0.09*	0.57**
P5xP8	-0.31**	-0.05	0.06	-0.48**	-0.05	0.23**
P6xP7	-0.43**	-0.20**	-1.34**	-0.46**	-0.05	-0.58**
P6xP8	0.06	0.01	0.21**	-0.02	0.07	0.17*
P7xP8	0.58**	0.03	1.67**	0.65**	-0.07	0.52**
SE	0.10	0.04	0.05	0.06	0.06	0.12
CD @ 5%	0.20	0.08	0.11	0.13	0.13	0.24
CD @ 1%	0.27	0.10	0.15	0.18	0.18	0.33

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 58. GCA estimates of parents for biochemical and yield characters

Parents	Proline content ($\mu\text{g g}^{-1}$)	Chlorophyll content (mg/100g)			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
		A	B	Total			
IR 1							
L 01942	12.05**	0.105**	-0.067**	0.037*	-1.21	-5.37**	-0.89**
L 06052	10.70**	-0.007	-0.081**	-0.088**	15.29**	-3.45**	-0.19
L 02079	4.53**	0.111**	0.014	-0.125**	14.67**	3.05**	0.92**
LA 3913	25.51**	0.249**	0.156**	0.405**	9.80**	4.62**	4.01**
TLB 133	19.05**	0.077**	0.059**	0.136**	-6.49*	4.32**	0.50**
L 06231	-18.06**	-0.121**	-0.037**	-0.158**	-11.73**	-6.16**	-1.15**
L 02692	-21.51**	-0.096**	-0.006	-0.102**	-11.49**	6.61**	0.55**
BL 1188	-32.26**	0.319**	0.037**	-0.357**	-8.84**	-3.65**	-0.77**
SE	1.29	0.028	0.017	0.026	4.51	1.50	0.22
CD @ 5%	3.05	0.067	0.041	0.062	10.67	3.54	0.53
CD @ 1%	4.51	0.100	0.061	0.092	15.80	5.24	0.78
IR 2							
L 01942	1.93	0.040**	-0.016**	0.024**	-11.35**	-3.25*	-0.86**
L 06052	9.89**	0.002	0.024**	0.026**	19.70**	-1.79	0.19
L 02079	5.51**	0.076**	0.021**	0.096**	16.51**	20.94*	1.00**
LA 3913	60.44**	0.216**	0.057**	0.272**	11.21**	3.43*	0.75**
TLB 133	28.15**	0.074**	0.029**	0.103**	-5.70*	4.22**	0.32
L 06231	-25.77**	-1.440**	-0.041**	-0.185**	-16.40**	-6.16**	-1.25**
L 02692	-32.00**	-0.015**	-0.024**	-0.039**	-6.68**	5.21**	0.71**
BL 1188	-48.15**	-0.249**	-0.048**	-0.298**	-7.28**	-4.58**	-0.86**
SE	1.79	0.007	0.007	0.008	3.61	2.06	0.24
CD @ 5%	4.22	0.017	0.017	0.021	8.56	4.88	0.58
CD @ 1%	6.25	0.025	0.025	0.031	12.62	7.22	0.85

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Table 59. SCA estimates for biochemical parameters of tomato hybrids under two irrigation regimes

Hybrids	IR 1				IR 2			
	Proline content ($\mu\text{g g}^{-1}$)	Chlorophyll content (mg/100g)			Proline content (mg/100g)	Chlorophyll content (mg/100g)		
		a	b	total		a	B	total
P1xP2	-2.265	-0.21**	-0.05	-0.26**	-22.52**	-0.39**	-0.18**	-0.57**
P1xP3	-34.305**	-0.22**	-140.00**	-0.36**	-54.31**	-0.06**	0.04*	-0.03
P1xP4	-0.616	0.52**	0.13**	0.65**	19.12**	0.38**	-0.02	0.36**
P1xP5	80.62**	0.71**	0.25**	0.95**	140.60**	0.64**	0.10**	0.74**
P1xP6	20.577**	0.04	0.00	0.03	12.90**	0.00	0.09**	0.09**
P1xP7	-34.91**	-0.31**	0.06	-0.25**	-44.61**	-0.29**	-0.03	-0.31**
P1xP8	14.255**	-0.03	-0.14**	-0.18*	1.71	-0.12**	-0.02	-0.13**
P2xP3	86.29**	0.77**	0.26**	1.03**	186.37**	0.65**	0.11**	0.76**
P2xP4	42.455**	0.26**	0.09*	0.35**	58.00**	0.36**	0.05**	0.41**
P2xP5	-27.162**	-0.40**	-0.17**	-0.56**	-64.70**	-0.33**	0.01	-0.32**
P2xP6	-23.719**	-0.15*	0.16**	0.01	-29.16**	-0.03*	0.12**	0.09**
P2xP7	-34.062**	-0.23**	-0.18**	-0.41**	30.92**	-0.35**	-0.07**	-0.41**
P2xP8	7.783**	0.08	0.03	0.11*	30.92**	-0.08**	-0.22**	-0.30**
P3xP4	-56.751**	-0.91**	-0.39**	-1.31**	-146.20**	-0.97**	-0.22**	-1.19**
P3xP5	77.155**	-0.71**	-0.07	-0.78**	-123.72**	-0.77**	-0.15**	-0.93**
P3xP6	32.948**	0.72**	0.19**	0.90**	88.24**	0.71**	0.16**	0.86**
P3xP7	0.085	0.46**	0.14**	0.60**	4.15	0.54**	0.18**	0.72**
P3xP8	3.893	-0.23**	-0.19**	-0.42**	-16.36**	-0.13**	0.10**	-0.03
P4xP5	101.098**	1.02**	0.35**	1.36**	210.68**	0.89**	0.06**	0.95**
P4xP6	46.24**	0.37**	0.09*	0.46**	90.50**	0.26**	0.04*	0.30**
P4xP7	19.914**	0.32**	0.26**	0.58**	78.96**	0.16**	0.04*	0.20**
P4xP8	55.649**	0.28**	0.06	0.34**	65.52**	0.28**	0.08**	0.36**
P5xP6	-58.654**	-0.55**	0.02	-0.53**	-95.23**	-0.46**	0.06**	-0.40**
P5xP7	-8.29**	-0.03	-0.22**	-0.25**	-40.50**	-0.14**	-0.13**	-0.27**
P5xP8	-28.238**	-0.17**	-0.28**	-0.45**	-63.70**	-0.02**	-0.02	-0.04*
P6xP7	-30.51**	-0.32**	-0.25**	-0.57**	-59.20**	-0.08**	0.06**	-0.02
P6xP8	48.765**	0.71**	0.24**	0.96**	133.76**	0.67**	-0.05**	0.61**
P7xP8	-7.108*	-0.29**	-0.14**	-0.43**	-42.82**	-0.36**	0.04**	0.32**
SE	3.866	0.09	0.05	0.08	5.36	0.02	0.02	0.03
CD @ 5%	7.933	0.18	0.11	0.16	10.99	0.04	0.04	0.06
CD @ 1%	10.712	0.24	0.14	0.22	14.84	0.06	0.06	0.07

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

P3 x P7, P6 x P8, P2 x P4, P1 x P4, P4 x P8, P4 x P6 and P4 x P7 were good specific combiners for total chlorophyll content (Table 59).

4.4.3.4 Yield parameters

Three parents (L 06052, L 02079 and LA 3913) had highly significant positive GCA effects for number of fruits per plant in IR 1 and IR 2. These parents may be considered as good general combiners for number of fruits per plant. Good specific combiners for number of fruits per plant were P3 x P7, P3 x P6, P4 x P7, P2 x P4, P1 x P8, P2 x P8, P2 x P6, P1 x P5 and P6 x P8. Four parents (L 02079, LA 3913, TLB 133 and L 02692) had highly significant positive GCA effects for average fruit weight in IR 1 and IR 2. These parents may be considered as good general combiners for this trait. The same four genotypes had highly significant positive GCA effects for yield per plant in IR 1. But in IR 2, only three parents (L 02079, LA 3913 and L 02692) had highly significant positive GCA effects for this trait. So, these parents may be considered as good general combiners for yield per plant. In general L 02079 and LA 3913 had highly significant positive GCA effects for all the yield parameters in both IR 1 and IR 2. So, these two may be considered as good general combiners for yield parameters (Table 58). Good specific combiners for average fruit weight were P2 x P4, P1 x P5, P4 x P5, P4 x P8, P3 x P7 and P6 x P8. The crosses P2 x P4, P1 x P5, P4 x P5, P3 x P7, P4 x P8 and P6 x P8 were good specific combiners for yield per plant (Table 60).

4.4.4 Gene action for drought tolerance traits using diallel analysis

The genetic components of variation like D (variation due to additive effect), F (mean of the covariance of additive and dominant effect over arrays), H_1 and H_2 (dominance genetic effects), h^2 (sum of dominance effect over all loci), E (Environmental component of variation) with their respective standard errors and their ratios and differences viz. $(H_1/D)^{1/2}$ (mean degree of dominance), $H_2/4H_1$ (the proportion of genes with positive and negative effects on the parents), KD/KH (number of dominance and recessive genes in parents) h^2/H_2 (number of genes groups controlling that character and exhibiting dominance) and heritability in narrow sense are estimated separately for stressed and non-stressed conditions. The results of this analysis is presented here under.

Table 60. SCA estimates for yield parameters of tomato hybrids under two irrigation regimes

Hybrids	IR 1			IR 2		
	Number of fruits	Average fruit weight (g)	Yield per plant (Kg)	Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
P1xP2	-32.42**	-4.44	-1.29**	-41.17**	-3.72	-1.33*
P1xP3	-4.95	-1.93	-0.57	-26.03**	-4.77	-1.48**
P1xP4	-5.19	-7.43*	-1.39**	-10.55	-3.56	-0.81
P1xP5	10.95	20.59**	3.42**	24.73**	20.53**	3.44**
P1xP6	21.96*	2.62	0.79	-8.83	0.55	0.01
P1xP7	13.74	-5.97	-0.40	12.59	-9.71*	-1.30*
P1xP8	4.02	-1.45	-0.17	30.27**	2.50	1.01
P2xP3	-2.21	-1.87	-0.48	8.68	2.54	0.35
P2xP4	5.99	18.91**	3.63**	43.32**	20.58**	5.19**
P2xP5	14.01	-10.13**	-1.43**	-11.02	-10.99*	-1.82**
P2xP6	0.92	5.86	0.81	27.98**	1.46	0.57
P2xP7	9.54	-11.07**	-1.43**	-12.81	-10.76*	-2.11**
P2xP8	24.08*	-0.44	0.28	22.43**	4.48	0.98
P3xP4	-33.89**	-18.43**	-3.81**	-60.84**	-16.38**	-3.82**
P3xP5	-10.21	-14.52**	-2.66**	3.16	-16.26**	-2.55**
P3xP6	28.81**	3.47	1.04*	24.00**	3.33	0.67
P3xP7	28.65**	12.27**	3.18**	42.69**	10.19*	2.79**
P3xP8	5.34	-4.21	-0.64	-41.54**	-8.23	-2.18**
P4xP5	-12.73	16.12**	1.74**	11.50	19.96**	3.28**
P4xP6	22.22*	-2.97	-0.18	-3.73	-0.98	-0.41
P4xP7	19.02*	-9.95**	-0.96*	30.78**	-10.28*	-1.06*
P4xP8	17.92	19.11**	3.68**	0.70	18.99**	2.45**
P5xP6	-15.47	-2.40	-0.85	-20.81**	-9.93*	-1.49**
P5xP7	-23.63*	-22.48**	-3.52**	-46.63**	-16.53**	-3.40**
P5xP8	-5.74	-12.63**	-2.00**	17.76*	-7.41	-0.64
P6xP7	-19.22*	-5.96	-1.22*	-28.93**	-9.15*	-1.81**
P6xP8	8.77	5.44	0.91	22.34**	11.63**	1.94**
P7xP8	-17.87	-15.00**	-2.29**	-59.72**	-16.07**	-2.89**
SE	13.54	4.49	0.67	10.82	6.19	0.73
CD @ 5%	27.78	9.22	1.37	22.20	12.71	1.50
CD @ 1%	37.52	12.44	1.85	29.97	17.16	2.03

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation;

IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

4.4.4.1 Morphological parameters

The variance due to additive effects of genes (D), mean F_r values, variance due to dominance effect (H_1), proportion of dominance variance (H_2) were significant for plant height (45, 60 and 90 DAT) in both irrigation regimes. The magnitude of H_1 and H_2 was higher than D in both IR 1 and IR 2 at all the three stages. F_r values were positive in both IR 1 and IR 2. The sum of dominance over all loci was found to be significant in IR 1 at 60 DAT (228.21) and at 45 DAT (36.61) in IR 2. The environment component (E) was non-significant in both IR 1 and IR 2. The mean degree of dominance was ranged from 1.61 to 1.70 in IR 1 and from 1.33 to 1.69 in IR 2 during 45 to 90 DAT. The proportion of genes with positive and negative effect was highest at 60 DAT in both IR 1 (0.18) and IR 2 (0.16). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.08 to 0.39 in IR 1 and 0.28 to 0.39 in IR 2 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.14 to 0.27 in IR 1 and from 0.17 to 0.29 in IR 2 during 45 to 90 DAT (Table 61).

Variance due to additive effect was significant in IR 1 and IR 2 for number of branches in all growth stages except at 60 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D . F_r values, sum of dominance over all loci and environment component were non-significant in IR 1 and IR 2, except for environment component at 90 DAT in IR 2. Mean degree of dominance was ranged from 1.14 to 1.39 in IR 1 and from 1.46 to 2.21 in IR 2 during 45 to 90 DAT. The proportion of genes with positive and negative effect was highest at 60 DAT in IR 1 (0.21) and at 45 DAT in IR 2 (0.23). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from -0.04 to 0.08 in IR 1 and -0.08 to 0.03 in IR 2 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.49 to 0.56 in IR 1 and from 0.35 to 0.50 in IR 2 during 45 to 90 DAT (Table 61).

Variance due to additive effect for stem girth was significant in both IR 1 and IR 2 in all growth stages. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D . F_r values were positive and were significant

Table 61. Estimates of genetic components of variation for plant height, number of branches and stem girth under two irrigation regimes

Genetic components	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1									
D (Additive Effect)	32.83*	148.96*	383.40*	6.33*	18.81*	33.47*	0.65*	1.15*	2.91*
F (Mean F _r over arrays)	54.16*	238.59*	638.07*	3.54	1.22	17.05	0.78*	1.77*	4.43*
H ₁ (Dominance Effect)	88.17*	429.37*	990.02*	8.16*	36.12*	46.23*	1.40*	3.12*	6.56*
H ₂	55.60*	304.13*	679.38*	5.92*	29.88*	37.52*	1.07*	2.38*	4.29*
h ² (dominance effects over loci)	15.78	228.21*	267.17	-0.21	0.35	3.04	-0.02	-0.05	0.36
E (Environ. Comp.)	1.52	3.15	4.96	0.52	2.00	3.96	0.06	0.30*	0.09
(H ₁ /D) ^{1/2}	1.64	1.70	1.61	1.14	1.39	1.18	1.46	0.49	1.50
H ₂ /4H ₁	0.16	0.18	0.17	0.18	0.21	0.20	0.19	0.19	0.16
KD/KH	3.03	2.79	3.15	1.66	1.05	1.55	2.37	2.45	3.05
h ² / H ₂ (No. of Gene Groups)	0.28	0.08	0.39	-0.04	0.01	0.08	-0.02	-0.02	0.08
h ² (Heritability in Narrow Sense)	0.27	0.18	0.14	0.56	0.56	0.49	0.23	0.18	0.24
IR 2									
D (Additive Effect)	69.37*	101.60*	458.49*	3.15*	4.15	6.08*	0.67*	0.39	1.35*
F (Mean F _r over arrays)	112.14*	165.43*	649.82*	0.34	4.75	-6.46	0.70	0.20	1.94*
H ₁ (Dominance Effect)	148.03*	289.58*	807.61*	6.69*	20.22*	22.22*	1.06*	2.12*	2.93*
H ₂	94.89*	185.89*	546.27*	6.07*	14.42*	18.69*	0.81*	1.78*	1.95*
h ² (dominance effects over loci)	36.61*	51.75	211.59	0.19	-0.16	-1.51	-0.05	0.13	0.16
E (Environ. Comp.)	2.26	2.73	2.35	0.22	1.15	4.52*	0.13*	0.09	0.13
(H ₁ /D) ^{1/2}	1.46	1.69	1.33	1.46	2.21	1.91	1.25	2.32	1.47
H ₂ /4H ₁	0.16	0.16	0.17	0.23	0.18	0.21	0.19	0.21	0.17
KD/KH	3.48	2.86	3.29	1.08	2.61	0.57	2.41	1.24	2.90
h ² / H ₂ (No. of Gene Groups)	0.39	0.28	0.39	0.03	-0.01	-0.08	-0.06	0.07	0.08
h ² (Heritability in Narrow Sense)	0.17	0.29	0.20	0.50	0.35	0.47	0.25	0.33	0.24

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

at all stages in IR 1 and only at 90 DAT in IR 2. Sum of dominance over all loci was non-significant in IR 1 and IR 2. Environment component at 60 DAT in IR 1 and at 45 DAT in IR 2 was significant. Mean degree of dominance was ranged from 0.49 to 1.50 in IR 1 and from 1.25 to 2.32 in IR 2 during 45 to 90 DAT. The proportion of genes with positive and negative effect was highest at 45 and 60 DAT in IR 1 (0.19) and at 60 DAT in IR 2 (0.21). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from -0.02 to 0.08 in IR 1 and -0.06 to 0.08 in IR 2 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.18 to 0.24 in IR 1 and from 0.24 to 0.33 in IR 2 during 45 to 90 DAT (Table 61).

Variance due to additive effect for root length was significant in both IR 1 and IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values, sum of dominance over all loci and environment component were non-significant in IR 1 and IR 2. Mean degree of dominance was 1.75 in IR 1 and 1.67 in IR 2. The proportion of genes with positive and negative effect was 0.20 in IR 1 and 0.21 in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.19 in IR 1 and 0.09 in IR 2. Narrow sense heritability was 0.34 in IR 1 and 0.39 in IR 2 (Table 62).

Significant variance due to additive was observed for root volume both in IR 1 (45.55) and IR 2 (54.33). H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values and sum of dominance over all loci were non-significant in IR 1 and IR 2. Environment component was significant only in IR 1 (11.69). Mean degree of dominance was 1.79 in IR 1 and 1.97 in IR 2. The proportion of genes with positive and negative effect was 0.22 in IR 1 and 0.21 in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.03 in IR 1 and 0.02 in IR 2. Narrow sense heritability was 0.29 in IR 1 and 0.33 in IR 2 (Table 62).

Table 62. Estimates of genetic components of variation for root length, root volume, stomata count and number of pubescence under two irrigation regimes

Genetic components	Root length (cm)	Root volume (cc)	Stomata count	Number of pubescence	
				AB	AD
IR 1					
D (Additive Effect)	31.95*	45.55*	3.38	15224.11*	52567.48*
F (Mean F _r over arrays)	22.96	31.07	6.63	28385.14	107409.20
H ₁ (Dominance Effect)	97.82*	146.60*	14.61	85273.83*	328495.00*
H ₂	79.58*	126.48*	11.02*	64463.20*	242041.70*
h ² (dominance effects over loci)	15.29	4.03	0.02*	2151.91	17274.96
E (Environ. Comp.)	6.99	11.69*	0.45	65.70	120.41
(H ₁ /D) ^{1/2}	1.75	1.79	2.08	2.37	2.50
H ₂ /4H ₁	0.20	0.22	0.19	0.19	0.18
KD/KH	1.52	1.47	2.79	2.30	2.38
h ² / H ₂ (No. of Gene Groups)	0.19	0.03	0.00	0.03	0.07
h ² (Heritability in Narrow Sense)	0.34	0.29	0.05	0.19	0.21
IR 2					
D (Additive Effect)	127.03*	54.33*	3.28*	4559.51	-122662.80
F (Mean F _r over arrays)	73.69	42.30	6.65	124634.10	-670317.00
H ₁ (Dominance Effect)	353.08*	211.05*	12.74*	695862.60	31700.10
H ₂	298.39*	174.49*	9.03*	474429.90	160815.80
h ² (dominance effects over loci)	27.96	4.18	0.19	-50780.09	29190.70
E (Environ. Comp.)	8.83	5.13	0.08	462539.10*	360118.60*
(H ₁ /D) ^{1/2}	1.67	1.97	1.97	12.35	0.51
H ₂ /4H ₁	0.21	0.21	0.18	0.17	1.27
KD/KH	1.42	1.49	3.12	-19.81	-0.69
h ² / H ₂ (No. of Gene Groups)	0.09	0.02	0.02	-0.11	0.18
h ² (Heritability in Narrow Sense)	0.39	0.33	0.07	0.08	0.34

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

Significant variance due to additive was observed for stomata count only in IR 2 (54.33) and it was non-significant in IR 1. H_1 and H_2 estimates were significant only in IR 2 and in IR 1 only H_2 was significant. F_r values were non-significant in IR 1 and 2. Sum of dominance over all loci were significant in IR 1. Environment component was non-significant both in IR 1 and 2. Mean degree of dominance was 2.08 in IR 1 and 1.97 in IR 2. The proportion of genes with positive and negative effect was 0.19 in IR 1 and 0.18 in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.00 in IR 1 and 0.02 in IR 2. Narrow sense heritability was 0.05 in IR 1 and 0.07 in IR 2 (Table 62).

Significant variance due to additive was observed for number of pubescence (abaxial and adaxial) only in IR 1 and it was non-significant in IR 2. H_1 and H_2 estimates were significant only in IR 1 and in IR 2 these were non-significant. F_r values and sum of dominance over all loci were non-significant in IR 1 and 2. Environment component was significant in IR 2 (for both abaxial and adaxial) and it was non-significant in IR 2. Mean degree of dominance was 2.37 and 2.50 (abaxial and adaxial respectively) in IR 1 and 12.35 and 0.51 (abaxial and adaxial respectively) in IR 2. The proportion of genes with positive and negative effect was 0.19 and 0.18 (abaxial and adaxial respectively) in IR 1 and it was 0.17 and 1.27 (abaxial and adaxial respectively) in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in IR 1, while it was less than unity in IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.03 and 0.07 (abaxial and adaxial respectively) in IR 1 and -0.11 and 0.18 (abaxial and adaxial respectively) in IR 2. Narrow sense heritability was 0.19 and 0.21 (abaxial and adaxial respectively) in IR 1 and 0.08 and 0.34 (abaxial and adaxial respectively) in IR 2 (Table 62).

4.4.4.2 Growth parameters

Variance due to additive effect for number of leaves was significant at 60 and 90 DAT in IR 1 and at 45 and 90 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values were positive and significant only in IR 1 (60 DAT). Sum of dominance over all loci was significant in IR 1 (45, 60 and 90 DAT) and at 45 and 90 DAT in IR 2. Environment component

was non-significant in IR 1 and IR 2. Mean degree of dominance was ranged from 2.76 to 3.97 in IR 1 and from 2.26 to 2.73 in IR 2 during 45 to 90 DAT. The highest value for proportion of genes with positive and negative effect (0.19) was observed at 45 DAT in IR 1 and at 45 and 90 DAT in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.62 to 1.15 in IR 1 and from 0.19 to 1.24 in IR 2 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.26 to 0.34 in IR 1 and from 0.19 to 0.37 in IR 2 during 45 to 90 DAT (Table 63).

Variance due to additive effect for leaf area was significant at 90 DAT in IR 1 and at 45 and 90 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values and environment components were non-significant in IR 1 and IR 2. Sum of dominance over all loci was significant in IR 1 (45, 60 and 90 DAT) and at 45 DAT in IR 2. Mean degree of dominance was ranged from 2.24 to 2.87 in IR 1 and from 2.03 to 2.37 in IR 2 during 45 to 90 DAT. The highest value for proportion of genes with positive and negative effect was observed at 90 DAT in IR 1 (0.21) and it was same for 45, 60 and 90 DAT in IR 2 (0.20). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.32 to 0.50 in IR 1 and from 0.17 to 0.25 in IR 2 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.29 to 0.40 in IR 1 and from 0.29 to 0.32 in IR 2 during 45 to 90 DAT (Table 63).

Variance due to additive effect for absolute growth rate was significant at all growth stages in IR 1 and at 90 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values were significant only at 90 DAT in both IR 1 and IR2. Sum of dominance over all loci was non-significant in both IR 1 and IR 2. Environment components were significant only at 60-90 DAT in IR 1. Mean degree of dominance was ranged from 1.51 to 2.69 in IR 1 and from 2.00 to 3.04 in IR 2. The highest value for proportion of genes with positive and negative effect was observed at 45-60 DAT in IR 1 (0.20) and at 45 - 90 DAT in IR 2 (0.21). The proportion of dominant and recessive genes (KD/KH) in the parents

Table 63. Estimates of genetic components of variation for number of leaves and leaf area under two irrigation regimes

Genetic components	Number of leaves			Leaf area (cm ²)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
IR 1						
D (Additive Effect)	6.12	76.24*	83.19*	768.68	3952.58	19936.45*
F (Mean F _r over arrays)	11.32	191.46*	163.60	984.63	4167.18	10601.07
H ₁ (Dominance Effect)	96.38*	580.90*	728.49*	6330.22*	26238.98*	99809.41*
H ₂	74.64*	396.23*	515.58*	5050.83*	19395.84*	82998.77*
h ² (dominance effects over loci)	52.02*	247.29*	591.48*	1631.72*	8927.42*	41691.45*
E (Environ. Comp.)	4.82	2.19	1.62	43.14	93.45	270.84
(H ₁ /D) ^{1/2}	3.97	2.76	2.96	2.87	2.58	2.24
H ₂ /4H ₁	0.19	0.17	0.18	0.20	0.19	0.21
KD/KH	1.61	2.67	2.00	1.58	1.51	1.27
h ² / H ₂ (No. of Gene Groups)	0.70	0.62	1.15	0.32	0.46	0.50
h ² (Heritability in Narrow Sense)	0.26	0.26	0.34	0.29	0.40	0.38
IR 2						
D (Additive Effect)	20.97*	103.43	170.22*	1123.01*	6483.74	19254.27*
F (Mean F _r over arrays)	34.74	136.73	286.14	1212.10	6635.78	26084.62
H ₁ (Dominance Effect)	122.05*	770.72*	868.55*	5588.82*	36507.73*	79103.92*
H ₂	94.68*	567.52*	670.97*	4514.84*	29429.55*	61910.16*
h ² (dominance effects over loci)	117.36*	109.03	492.59*	1131.66*	4933.27	12213.10
E (Environ. Comp.)	4.41	2.54	2.60	89.01	66.65	51.46
(H ₁ /D) ^{1/2}	2.41	2.73	2.26	2.23	2.37	2.03
H ₂ /4H ₁	0.19	0.18	0.19	0.20	0.20	0.20
KD/KH	2.05	1.64	2.19	1.64	1.55	2.00
h ² / H ₂ (No. of Gene Groups)	1.24	0.19	0.73	0.25	0.17	0.20
h ² (Heritability in Narrow Sense)	0.20	0.37	0.19	0.29	0.32	0.25

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

was more than unity in both IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance was same (0.09) at all the growth stages in IR 1 and it varied from -0.01 to 0.03 in IR 2. Narrow sense heritability ranged from 0.01 to 0.45 in IR 1 and from 0.07 to 0.26 in IR 2 (Table 64).

Variance due to additive effect for relative growth rate was significant only at 45-60 in IR 1 and at 45-60 and 60-90 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values and environment components were non-significant in both IR 1 and IR2. Sum of dominance over all loci was significant at 45-60 and 45-90 DAT in both IR 1 and at all stages in IR 2. Mean degree of dominance was ranged from 1.75 to 2.71 in IR 1 and from 1.82 to 5.41 in IR 2. The highest value for proportion of genes with positive and negative effect was observed at 60-90 DAT in IR 1 (0.21) and at 45-60 and 45-90 DAT in IR 2 (0.21). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in IR 2 at all stages and at 45-60 and 45-90 DAT in IR 1. The number of groups of genes controlling the character and exhibiting dominance was ranged from 0.20 to 0.66 in IR 1 and from 0.42 to 0.68 in IR 2. Narrow sense heritability ranged from 0.23 to 0.60 in IR 1 and from 0.22 to 0.25 in IR 2 (Table 64).

Variance due to additive effect for crop growth rate was significant all stages in IR 1 and at 45-60 and 60-90 DAT in IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values and environment components were non-significant in IR 1 and significant at 45-60 DAT in IR2. Sum of dominance over all loci was significant at all stages in IR 1 and at 45-60 and 60-90 DAT in IR 2. Mean degree of dominance was ranged from 1.94 to 2.24 in IR 1 and from 1.66 to 2.12 in IR 2. The highest value for proportion of genes with positive and negative effect was observed at 60-90 DAT in IR 1 (0.22) and at 45-60 DAT in IR 2 (2.54). The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in IR 1 and IR 2 at all stages. The number of groups of genes controlling the character and exhibiting dominance was ranged from 0.18 to 0.91 in IR 1 and from 0.02 to 0.97 in IR 2. Narrow sense heritability ranged from 0.24 to 0.41 in IR 1 and from 0.15 to 0.35 in IR 2 (Table 64).

Table 64. Estimates of genetic components of variation for absolute growth rate, relative growth rate and crop growth rate under two irrigation regimes

Genetic components	Absolute growth rate			Relative growth rate			Crop growth rate		
	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90	45 - 60	45 - 90	60 - 90
IR 1									
D (Additive Effect)	0.01*	0.01*	0.04*	0.24*	0.02	0.04	0.07*	0.01*	0.81*
F (Mean F _r over arrays)	0.01	0.00	0.06*	0.28	0.03	-0.05	0.11	0.01	0.69
H ₁ (Dominance Effect)	0.08*	0.02*	0.09*	0.72*	0.13*	0.20*	0.31*	0.07*	3.04*
H ₂	0.07*	0.01*	0.07*	0.58*	0.11*	0.17*	0.24*	0.06*	2.68*
h ² (dominance effects over loci)	0.01	0.00	0.01	0.38*	0.07*	0.03	0.13*	0.01*	2.44*
E (Environ. Comp.)	0.00	0.00	0.01*	0.00	0.00	0.00	0.01	0.00	0.00
(H ₁ /D) ^{1/2}	2.69	1.86	1.51	1.75	2.71	2.23	2.07	2.24	1.94
H ₂ /4H ₁	0.20	0.19	0.19	0.20	0.20	0.21	0.19	0.20	0.22
KD/KH	1.46	1.33	2.85	2.03	1.75	0.59	2.07	1.29	1.57
h ² / H ₂ (No. of Gene Groups)	0.09	0.09	0.09	0.66	0.64	0.20	0.54	0.18	0.91
h ² (Heritability in Narrow Sense)	0.32	0.45	0.10	0.25	0.23	0.60	0.24	0.41	0.26
IR 2									
D (Additive Effect)	0.01	0.00	0.04*	0.13*	0.00	0.08*	0.12*	0.01	0.20*
F (Mean F _r over arrays)	0.01	0.00	0.07*	0.15	0.01	0.12	0.20*	0.01	0.12
H ₁ (Dominance Effect)	0.06*	0.02*	0.15*	0.43*	0.10*	0.33*	0.45*	0.05*	0.56*
H ₂	0.05*	0.01*	0.12*	0.35*	0.08*	0.25*	0.33*	0.04*	0.49*
h ² (dominance effects over loci)	0.00	0.00	0.00	0.24*	0.05*	0.10*	0.15*	0.00	0.48*
E (Environ. Comp.)	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01
(H ₁ /D) ^{1/2}	3.04	2.49	2.00	1.82	5.41	2.03	1.96	2.12	1.66
H ₂ /4H ₁	0.20	0.21	0.20	0.21	0.21	0.20	0.19	0.21	0.22
KD/KH	1.67	1.50	2.52	1.91	1.57	2.11	2.54	1.49	1.45
h ² / H ₂ (No. of Gene Groups)	-0.01	0.03	0.02	0.68	0.64	0.42	0.44	0.02	0.97
h ² (Heritability in Narrow Sense)	0.24	0.26	0.07	0.24	0.22	0.25	0.15	0.27	0.35

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

4.4.4.3 Biochemical parameters

Variance due to additive effect for proline content was significant only in IR 1. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values, sum of dominance over all loci and environment component were non-significant in IR 1 and IR 2. Mean degree of dominance was 2.11 in IR 1 and 2.69 in IR 2. The proportion of genes with positive and negative effect was 0.18 in IR 1 and 0.19 in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.17 in IR 1 and 0.14 in IR 2. Narrow sense heritability was 0.33 in IR 1 and 0.28 in IR 2 (Table 65).

Variance due to additive effect for chlorophyll content (a, b and total) was significant in IR 2 and only for chlorophyll b in IR 1. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r values were non-significant in IR 1 and significant for chlorophyll b in IR 2. Sum of dominance over all loci and environment component were non-significant in IR 1 and IR 2. Mean degree of dominance was high for total chlorophyll (2.99) in IR 1 and for chlorophyll a (2.50) in IR 2. The proportion of genes with positive and negative effect was 0.21, 0.19 and 0.20 (chlorophyll a, b and total respectively) in IR 1 and 0.21, 0.19 and 0.21 (chlorophyll a, b and total respectively) in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.18, 0.00 and 0.11 for chlorophyll a, b and total respectively in IR 1 and 0.08, 0.07 and 0.10 for chlorophyll a, b and total respectively in IR 2. Narrow sense heritability was highest for chlorophyll b (0.27) in IR 1 and for total chlorophyll 0.19 in IR 2 (Table 65).

4.4.4.4 Yield parameters

Variance due to additive effect for yield parameters viz., number of fruits, average fruit weight and yield per plant was significant both in IR 1 and IR 2. H_1 and H_2 estimates were significant at both irrigation regimes and the magnitude was more than D. F_r value was non-significant for number of fruits, while it was significant for average fruit weight and yield per plant. Sum of dominance over all loci and environment

Table 65. Estimates of genetic components of variation for biochemical and yield parameters under two irrigation regimes

Genetic components	Proline content ($\mu\text{g g}^{-1}$)	Chlorophyll content (mg/100g)			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
		A	B	Total			
IR 1							
D (Additive Effect)	2732.55*	0.16	0.04*	0.24	622.79*	369.17*	7.87*
F (Mean F_r over arrays)	3855.22	0.20	0.05	0.36	300.19	496.29*	9.63*
H_1 (Dominance Effect)	12126.73*	1.15*	0.20*	2.15*	1244.58*	748.69*	20.23*
H_2	8793.03*	0.96*	0.15*	1.74*	1062.84*	547.71*	16.12*
h^2 (dominance effects over loci)	1498.54	0.17	0.00	0.20	152.79	181.28	2.46
E (Environ. Comp.)	9.58	0.01	0.00	0.01	128.59*	17.76	0.48
$(H_1/D)^{1/2}$	2.11	2.72	2.36	2.99	1.41	1.42	1.60
$H_2/4H_1$	0.18	0.21	0.19	0.20	0.21	0.18	0.20
KD/KH	2.01	1.60	1.95	1.68	1.41	2.79	2.23
h^2 / H_2 (No. of Gene Groups)	0.17	0.18	0.00	0.11	0.14	0.33	0.15
h^2 (Heritability in Narrow Sense)	0.33	0.24	0.27	0.24	0.39	0.19	0.21
IR 2							
D (Additive Effect)	6248.41	0.16*	0.02*	0.26*	767.23*	364.69*	10.74*
F (Mean F_r over arrays)	10185.80	0.23	0.03*	0.35	343.88	588.88*	16.35*
H_1 (Dominance Effect)	45197.81*	1.03*	0.07*	1.38*	3856.00*	847.12*	29.24*
H_2	34572.73*	0.86*	0.05*	1.16*	3482.80*	568.41*	21.10*
h^2 (dominance effects over loci)	4774.34	0.07	0.00	0.11	164.22	103.38	3.08
E (Environ. Comp.)	18.97	0.00	0.00	0.00	71.21	24.59	0.41
$(H_1/D)^{1/2}$	2.69	2.50	1.75	2.32	2.24	1.52	1.65
$H_2/4H_1$	0.19	0.21	0.19	0.21	0.23	0.17	0.18
KD/KH	1.87	1.80	2.59	1.82	1.22	3.25	2.71
h^2 / H_2 (No. of Gene Groups)	0.14	0.08	0.07	0.10	0.05	0.18	0.15
h^2 (Heritability in Narrow Sense)	0.28	0.18	0.17	0.19	0.30	0.14	0.18

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

component were non-significant in IR 1 and IR 2 except environment component for number of fruits in IR 1. Mean degree of dominance was 1.41, 1.42 and 1.60 for number of fruits, average fruit weight and yield per plant respectively in IR 1. The values were 2.24, 1.52 and 1.65 average fruit weight and yield per plant respectively in IR 2. The proportion of genes with positive and negative effect was 0.21, 0.18 and 0.20 for number of fruits, average fruit weight and yield per plant respectively in IR 1. It was 0.23, 0.17 and 0.18 for number of fruits, average fruit weight and yield per plant respectively in IR 2. The proportion of dominant and recessive genes (KD/KH) in the parents was more than unity in both IR 1 and IR 2. The number of groups of genes controlling the character and exhibiting dominance was 0.14, 0.33 and 0.15 for number of fruits, average fruit weight and yield per plant respectively in IR 1 and 0.05, 0.18 and 0.15 for number of fruits, average fruit weight and yield per plant respectively in IR 2. Narrow sense heritability was 0.39, 0.19 and 0.21 for number of fruits, average fruit weight and yield per plant respectively in IR 1 and 0.30, 0.14 and 0.18 for number of fruits, average fruit weight and yield per plant respectively in IR 2 (Table 65).

4.4.5 Heterosis

Exploitation of hybrid vigour in the field of agriculture is one of the most promising developments in crop breeding programs. Relative heterosis, heterobeltiosis and standard heterosis are some types of heterosis which plant breeders use to evaluate hybrid performance. Here in this experiment we have used heterobeltiosis (improvement over better parent) to evaluate tomato hybrids. Observations for plant height, number of branches, stem girth, number of leaves and leaf area at 60 DAT are considered for evaluation. For absolute, relative and crop growth rate observations from 45 to 60 DAT were considered.

4.4.5.1 Morphological parameters

Performance of parents, hybrids and heterobeltiosis values for morphological traits viz., plant height, number of branches, stem girth, root length, root volume, stomata count and number of pubescence on abaxial and adaxial layer are presented in Tables 66 to 73.

Table 66. Estimates of heterobeltiosis for plant height (cm) at 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	64.37	64.95	64.66	-2.82	50.74	32.82	41.78	-17.70**
P1xP3	64.37	54.57	43.10	-33.04**	50.74	34.01	32.17	-36.57**
P1xP4	64.37	66.37	38.82	-42.44**	50.74	51.03	30.47	-41.58**
P1xP5	64.37	45.54	54.96	-14.63**	50.74	45.47	48.11	-5.20
P1xP6	64.37	56.78	71.93	11.78**	50.74	45.59	57.29	12.99**
P1xP7	64.37	54.91	65.13	1.16	50.74	43.88	51.70	1.92
P1xP8	64.37	65.48	64.70	-1.95	50.74	49.84	50.47	-2.07
P2xP3	64.95	54.57	59.76	-7.79**	32.82	34.01	33.42	-7.19*
P2xP4	64.95	66.37	59.17	-12.99**	32.82	51.03	38.64	-24.19**
P2xP5	64.95	45.54	48.75	-24.72**	32.82	45.47	35.86	-21.00**
P2xP6	64.95	56.78	49.51	-23.76**	32.82	45.59	30.09	-33.68**
P2xP7	64.95	54.91	55.44	-14.47**	32.82	43.88	32.86	-24.75**
P2xP8	64.95	65.48	61.97	-6.14*	32.82	49.84	39.69	-20.29**
P3xP4	54.57	66.37	62.18	-5.91*	34.01	51.03	43.20	-15.40**
P3xP5	54.57	45.54	52.88	-3.08	34.01	45.47	41.33	-8.93**
P3xP6	54.57	56.78	94.15	63.93**	34.01	45.59	67.55	48.16**
P3xP7	54.57	54.91	59.59	5.78*	34.01	43.88	40.13	-8.39**
P3xP8	54.57	65.48	63.52	-2.82	34.01	49.84	42.93	-13.70**
P4xP5	66.37	45.54	60.33	-8.97**	51.03	45.47	49.42	-3.14
P4xP6	66.37	56.78	61.89	-6.61**	51.03	45.59	48.08	-5.79
P4xP7	66.37	54.91	60.30	-9.06**	51.03	43.88	46.76	-8.37**
P4xP8	66.37	65.48	63.49	-6.23*	51.03	49.84	48.69	-5.90
P5xP6	45.54	56.78	45.85	-18.99**	45.47	45.59	43.23	-7.95*
P5xP7	45.54	54.91	44.96	-18.08**	45.47	43.88	42.38	-6.80*
P5xP8	45.54	65.48	51.01	-21.94**	45.47	49.84	45.96	-7.83*
P6xP7	56.78	54.91	61.24	3.67	45.59	43.88	49.04	7.56*
P6xP8	56.78	65.48	67.54	3.17	45.59	49.84	52.46	5.32
P7xP8	54.91	65.48	64.06	-2.00	43.88	49.84	50.07	0.45
CD @ 5%	5.50				6.04			
CD @ 1%	7.32				8.04			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 67. Estimates of heterobeltiosis for number of branches at 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	22.14	15.73	29.98	35.96**	11.85	8.42	16.04	37.40**
P1xP3	22.14	24.34	34.64	42.54**	11.85	13.15	18.62	32.44**
P1xP4	22.14	20.65	30.64	37.14**	11.85	9.92	15.63	33.28**
P1xP5	22.14	15.33	25.65	16.03**	11.85	14.12	17.21	18.39**
P1xP6	22.14	16.45	24.50	10.76*	11.85	14.24	15.72	8.72
P1xP7	22.14	18.03	25.98	17.62**	11.85	10.58	14.38	21.71**
P1xP8	22.14	18.11	25.48	15.85**	11.85	12.60	15.06	11.89*
P2xP3	15.73	24.34	24.59	1.74	8.42	13.15	13.23	1.05
P2xP4	15.73	20.65	19.93	-3.51	8.42	9.92	10.13	2.32
P2xP5	15.73	15.33	20.50	28.46**	8.42	14.12	14.93	6.29
P2xP6	15.73	16.45	19.93	18.91**	8.42	14.24	13.87	-2.32
P2xP7	15.73	18.03	20.86	15.60**	8.42	10.58	11.71	11.28
P2xP8	15.73	18.11	20.55	12.89**	8.42	12.60	12.65	1.67
P3xP4	24.34	20.65	27.54	14.07**	13.15	9.92	14.07	7.52
P3xP5	24.34	15.33	23.16	-4.41	13.15	14.12	15.95	13.13*
P3xP6	24.34	16.45	26.88	10.70*	13.15	14.24	17.09	19.95**
P3xP7	24.34	18.03	28.72	18.49**	13.15	10.58	15.97	22.02**
P3xP8	24.34	18.11	29.13	20.72**	13.15	12.60	17.31	30.43**
P4xP5	20.65	15.33	22.62	9.55*	9.92	14.12	14.65	4.28
P4xP6	20.65	16.45	21.77	5.44	9.92	14.24	13.44	-5.47
P4xP7	20.65	18.03	22.69	9.90*	9.92	10.58	11.82	12.13*
P4xP8	20.65	18.11	23.46	13.60**	9.92	12.60	13.30	6.76
P5xP6	15.33	16.45	20.35	23.55**	14.12	14.24	18.15	25.26**
P5xP7	15.33	18.03	20.35	12.49**	14.12	10.58	18.15	28.88**
P5xP8	15.33	18.11	20.89	13.33**	14.12	12.60	16.70	18.00**
P6xP7	16.45	18.03	21.22	17.55**	14.24	10.58	15.76	10.77
P6xP8	16.45	18.11	20.54	8.55	14.24	12.60	16.30	14.15*
P7xP8	18.03	18.11	22.94	19.51**	10.58	12.60	14.42	16.06**
CD @ 5%	8.59				11.64			
CD @ 1%	11.43				15.51			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 68. Estimates of heterobeltiosis for stem girth (cm) at 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	5.00	5.33	6.40	19.36*	4.67	2.47	4.49	-3.41
P1xP3	5.00	5.17	5.94	13.35	4.67	3.30	4.75	2.56
P1xP4	5.00	5.20	6.47	24.51**	4.67	2.93	4.85	4.82
P1xP5	5.00	5.60	6.22	11.47	4.67	3.90	5.10	9.44
P1xP6	5.00	5.07	5.43	3.45	4.67	4.29	4.87	4.44
P1xP7	5.00	6.67	6.72	0.74	4.67	2.27	4.21	-9.33
P1xP8	5.00	6.73	6.28	-6.94	4.67	3.57	4.64	-0.53
P2xP3	5.33	5.17	6.27	14.11	2.47	3.30	3.31	2.17
P2xP4	5.33	5.20	6.65	21.89**	2.47	2.93	3.35	14.40*
P2xP5	5.33	5.60	7.03	20.63	2.47	3.90	3.97	2.01
P2xP6	5.33	5.07	6.58	17.13*	2.47	4.29	4.06	-5.06
P2xP7	5.33	6.67	6.95	4.28	2.47	2.27	2.85	7.92
P2xP8	5.33	6.73	7.99	12.92	2.47	3.57	3.97	11.50
P3xP4	5.17	5.20	5.70	8.82	3.30	2.93	3.45	5.50
P3xP5	5.17	5.60	5.62	0.04	3.30	3.90	3.74	-7.22
P3xP6	5.17	5.07	6.43	20.18*	3.30	4.29	5.01	17.24*
P3xP7	5.17	6.67	6.40	-3.94	3.30	2.27	2.79	-14.78*
P3xP8	5.17	6.73	6.78	0.08	3.30	3.57	3.82	-2.14
P4xP5	5.20	5.60	6.41	14.00	2.93	3.90	4.12	5.91
P4xP6	5.20	5.07	6.05	12.56	2.93	4.29	4.39	2.73
P4xP7	5.20	6.67	6.87	3.00	2.93	2.27	2.92	-0.09
P4xP8	5.20	6.73	7.85	14.60	2.93	3.57	4.25	17.23*
P5xP6	5.60	5.07	7.03	21.38**	3.90	4.29	5.49	28.06**
P5xP7	5.60	6.67	6.95	4.47	3.90	2.27	3.46	-10.85
P5xP8	5.60	6.73	8.06	17.66*	3.90	3.57	4.78	22.67**
P6xP7	5.07	6.67	8.18	22.55**	4.29	2.27	4.74	10.71
P6xP8	5.07	6.73	9.05	43.29**	4.29	3.57	5.03	17.65*
P7xP8	6.67	6.73	8.30	12.40	2.27	3.57	3.41	-3.71
CD @ 5%	15.99				14.22			
CD @ 1%	21.29				18.94			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 69. Estimates of heterobeltiosis for root length (cm) under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	26.33	22.67	29.74	13.21	43.00	43.67	52.89	19.42**
P1xP3	26.33	29.33	36.13	12.98	43.00	45.33	57.15	26.15**
P1xP4	26.33	25.00	36.01	31.96**	43.00	46.33	63.43	35.09**
P1xP5	26.33	30.00	40.81	36.01**	43.00	54.67	71.52	31.00**
P1xP6	26.33	29.00	38.21	30.59**	43.00	53.67	67.44	26.12**
P1xP7	26.33	29.33	38.77	32.61**	43.00	41.67	58.26	28.22**
P1xP8	26.33	28.33	38.81	32.89**	43.00	44.67	62.03	36.82**
P2xP3	22.67	29.33	40.57	40.60**	43.67	45.33	68.66	51.37**
P2xP4	22.67	25.00	36.23	45.33**	43.67	46.33	68.23	41.26**
P2xP5	22.67	30.00	40.83	36.19**	43.67	54.67	75.94	38.95**
P2xP6	22.67	29.00	40.25	38.31**	43.67	53.67	75.61	41.58**
P2xP7	22.67	29.33	40.84	40.44**	43.67	41.67	65.47	43.92**
P2xP8	22.67	28.33	35.98	26.39**	43.67	44.67	61.88	35.56**
P3xP4	29.33	25.00	41.99	43.81**	45.33	46.33	71.59	48.33**
P3xP5	29.33	30.00	45.74	38.93**	45.33	54.67	77.75	42.28**
P3xP6	29.33	29.00	41.36	22.60**	45.33	53.67	71.71	34.22**
P3xP7	29.33	29.33	37.25	10.17	45.33	41.67	55.30	20.81**
P3xP8	29.33	28.33	37.48	15.04*	45.33	44.67	58.50	27.17**
P4xP5	25.00	30.00	39.10	30.55**	46.33	54.67	71.77	30.90**
P4xP6	25.00	29.00	41.28	41.98**	46.33	53.67	76.45	42.58**
P4xP7	25.00	29.33	41.55	43.02**	46.33	41.67	66.28	38.73**
P4xP8	25.00	28.33	41.54	45.14**	46.33	44.67	70.13	46.39**
P5xP6	30.00	29.00	43.09	38.96**	54.67	53.67	79.24	35.95**
P5xP7	30.00	29.33	42.51	37.10**	54.67	41.67	67.49	23.04**
P5xP8	30.00	28.33	33.85	6.88	54.67	44.67	57.71	5.61
P6xP7	29.00	29.33	41.66	41.91**	53.67	41.67	69.78	31.14**
P6xP8	29.00	28.33	41.96	36.32**	53.67	44.67	70.20	31.94**
P7xP8	29.33	28.33	33.72	8.17	41.67	44.67	50.55	12.00**
CD @ 5%	14.79				10.71			
CD @ 1%	19.70				14.26			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 70. Estimates of heterobeltiosis for root volume (cc) under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	20.79	17.73	25.15	21.19*	27.57	25.48	34.83	17.48**
P1xP3	20.79	22.94	28.59	24.65**	27.57	27.39	35.71	17.78**
P1xP4	20.79	32.87	30.26	-5.07	27.57	28.92	31.91	10.54
P1xP5	20.79	28.07	39.73	41.15**	27.57	32.63	48.74	49.88**
P1xP6	20.79	20.88	32.71	41.92**	27.57	32.26	47.03	45.72**
P1xP7	20.79	18.79	25.74	17.85**	27.57	25.27	34.32	22.10**
P1xP8	20.79	22.26	25.98	10.04	27.57	25.55	32.23	7.19
P2xP3	17.73	22.94	25.77	13.00	25.48	27.39	33.75	21.14**
P2xP4	17.73	32.87	41.57	30.04**	25.48	28.92	43.98	45.11**
P2xP5	17.73	28.07	37.90	38.38**	25.48	32.63	47.75	42.31**
P2xP6	17.73	20.88	29.36	41.40**	25.48	32.26	44.19	34.19**
P2xP7	17.73	18.79	22.05	12.13	25.48	25.27	30.71	9.91
P2xP8	17.73	22.26	28.93	31.66**	25.48	25.55	36.75	27.42**
P3xP4	22.94	32.87	32.70	2.05	27.39	28.92	32.95	6.36
P3xP5	22.94	28.07	38.54	34.34**	27.39	32.63	45.27	36.21**
P3xP6	22.94	20.88	33.05	33.34**	27.39	32.26	45.92	41.01**
P3xP7	22.94	18.79	26.00	10.99	27.39	25.27	32.71	14.67*
P3xP8	22.94	22.26	29.38	22.64*	27.39	25.55	34.41	20.96**
P4xP5	32.87	28.07	46.05	40.72**	28.92	32.63	47.31	43.79**
P4xP6	32.87	20.88	39.68	26.70**	28.92	32.26	46.67	41.39**
P4xP7	32.87	18.79	33.11	4.81	28.92	25.27	34.28	16.96*
P4xP8	32.87	22.26	36.93	13.81	28.92	25.55	36.50	16.42*
P5xP6	28.07	20.88	42.03	52.86**	32.63	32.26	55.85	67.54**
P5xP7	28.07	18.79	37.10	36.58**	32.63	25.27	45.41	39.49**
P5xP8	28.07	22.26	37.19	33.42**	32.63	25.55	43.05	31.86**
P6xP7	20.88	18.79	28.77	37.61**	32.26	25.27	42.27	31.33**
P6xP8	20.88	22.26	29.56	21.67*	32.26	25.55	43.45	35.02**
P7xP8	18.79	22.26	25.79	11.55	25.27	25.55	32.01	17.94**
CD @ 5%	17.07				12.89			
CD @ 1%	22.73				17.17			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 71. Estimates of heterobeltiosis for stomata count under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	8.98	8.32	8.91	-0.61	7.48	6.73	7.33	-1.77
P1xP3	8.98	10.34	9.88	-4.46	7.48	9.19	8.49	-7.60*
P1xP4	8.98	9.54	9.16	-6.28	7.48	8.10	7.69	-6.70
P1xP5	8.98	6.34	8.38	-6.65	7.48	4.82	6.75	-9.25*
P1xP6	8.98	6.86	7.76	-13.63**	7.48	5.13	6.39	-14.51**
P1xP7	8.98	13.08	11.13	-14.04*	7.48	10.44	9.08	-13.04**
P1xP8	8.98	12.77	10.00	-19.84**	7.48	10.58	8.31	-21.52**
P2xP3	8.32	10.34	9.49	-8.21	6.73	9.19	7.98	-13.19**
P2xP4	8.32	9.54	8.87	-6.94	6.73	8.10	7.28	-9.95**
P2xP5	8.32	6.34	7.50	-9.88	6.73	4.82	6.01	-10.54**
P2xP6	8.32	6.86	7.64	-8.15	6.73	5.13	6.04	-10.17**
P2xP7	8.32	13.08	10.55	-18.12**	6.73	10.44	8.48	-18.70**
P2xP8	8.32	12.77	10.15	-18.18**	6.73	10.58	8.30	-21.57**
P3xP4	10.34	9.54	9.20	-11.03**	9.19	8.10	8.05	-12.44**
P3xP5	10.34	6.34	7.67	-25.80**	9.19	4.82	6.54	-28.90**
P3xP6	10.34	6.86	8.06	-22.06**	9.19	5.13	6.86	-25.37**
P3xP7	10.34	13.08	10.23	-20.52**	9.19	10.44	8.72	-16.46**
P3xP8	10.34	12.77	10.59	-17.82**	9.19	10.58	9.16	-13.14**
P4xP5	9.54	6.34	8.65	-9.33	8.10	4.82	7.14	-11.84**
P4xP6	9.54	6.86	8.90	-6.63	8.10	5.13	7.30	-9.77**
P4xP7	9.54	13.08	10.79	-15.84**	8.10	10.44	8.91	-14.59**
P4xP8	9.54	12.77	11.76	-5.65	8.10	10.58	9.86	-6.42
P5xP6	6.34	6.86	5.88	-13.86*	4.82	5.13	4.44	-15.84**
P5xP7	6.34	13.08	8.89	-30.95**	4.82	10.44	6.88	-34.09**
P5xP8	6.34	12.77	8.66	-29.77**	4.82	10.58	6.80	-35.31**
P6xP7	6.86	13.08	9.02	-30.42**	5.13	10.44	6.92	-33.74**
P6xP8	6.86	12.77	8.77	-28.65**	5.13	10.58	6.71	-36.28**
P7xP8	13.08	12.77	13.29	-6.46	10.44	10.58	10.75	-1.15
CD @ 5%	11.88				7.11			
CD @ 1%	15.83				9.47			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 72. Estimates of heterobeltiosis for number of pubescence on abaxial layer under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	258.44	263.05	290.83	6.55*	351.71	1552.95	1047.75	-8.48
P1xP3	258.44	150.48	245.91	-4.94	351.71	188.07	323.70	-7.72
P1xP4	258.44	159.21	234.33	-9.37**	351.71	206.75	313.48	-10.69
P1xP5	258.44	367.73	393.29	7.00*	351.71	449.34	501.76	12.12
P1xP6	258.44	363.97	473.63	30.19**	351.71	1745.97	1588.23	23.23*
P1xP7	258.44	50.69	211.14	-18.32**	351.71	86.49	296.89	-15.51
P1xP8	258.44	37.39	173.77	-32.76**	351.71	69.50	244.50	-30.37**
P2xP3	263.05	150.48	263.60	0.69	1552.95	188.07	1174.13	-12.02
P2xP4	263.05	159.21	287.33	9.73**	1552.95	206.75	1281.63	-2.88
P2xP5	263.05	367.73	514.90	39.98**	1552.95	449.34	1565.12	29.72**
P2xP6	263.05	363.97	474.52	30.32**	1552.95	1745.97	2456.75	41.31**
P2xP7	263.05	50.69	204.36	-22.19**	1552.95	86.49	1066.37	-24.25*
P2xP8	263.05	37.39	207.37	-21.11**	1552.95	69.50	1119.60	-22.18*
P3xP4	150.48	159.21	171.08	7.45**	188.07	206.75	217.90	5.40
P3xP5	150.48	367.73	276.66	-24.71**	188.07	449.34	340.28	-24.16*
P3xP6	150.48	363.97	370.45	1.85	188.07	1745.97	1472.82	-3.90
P3xP7	150.48	50.69	121.81	-18.90**	188.07	86.49	167.32	-10.96
P3xP8	150.48	37.39	115.18	-23.25**	188.07	69.50	158.19	-15.73
P4xP5	159.21	367.73	335.96	-8.59**	206.75	449.34	418.69	-6.64
P4xP6	159.21	363.97	271.99	-25.18**	206.75	1745.97	931.56	-30.91**
P4xP7	159.21	50.69	131.31	-17.34**	206.75	86.49	184.00	-11.00
P4xP8	159.21	37.39	126.48	-20.34**	206.75	69.50	180.07	-12.84
P5xP6	367.73	363.97	603.57	63.25**	449.34	1745.97	1783.14	36.04**
P5xP7	367.73	50.69	347.45	-5.49*	449.34	86.49	437.36	-2.61
P5xP8	367.73	37.39	342.53	-6.85*	449.34	69.50	432.25	-3.81
P6xP7	363.97	50.69	328.13	-9.84**	1745.97	86.49	1488.63	-9.40
P6xP8	363.97	37.39	329.64	-9.43**	1745.97	69.50	1494.47	-8.98
P7xP8	50.69	37.39	53.57	6.05*	86.49	69.50	94.55	9.41
CD @ 5%	5.39				21.47			
CD @ 1%	7.17				28.59			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 73. Estimates of heterobeltiosis for number of pubescence on adaxial layer under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	567.20	446.93	567.14	0.07	2476.28	558.31	1716.09	-7.66
P1xP3	567.20	351.89	553.86	-2.31	2476.28	411.21	1680.91	-12.49
P1xP4	567.20	251.51	460.77	-18.71**	2476.28	276.99	1562.87	-26.46**
P1xP5	567.20	779.55	845.14	8.41**	2476.28	813.12	1993.48	-3.79
P1xP6	567.20	690.69	957.90	38.68**	2476.28	825.27	2529.44	18.11*
P1xP7	567.20	154.24	486.84	-14.17**	2476.28	222.96	1879.78	-14.92
P1xP8	567.20	105.05	391.27	-31.01**	2476.28	152.18	1576.12	-32.32**
P2xP3	446.93	351.89	500.35	12.07**	558.31	411.21	609.56	9.29
P2xP4	446.93	251.51	477.43	7.05**	558.31	276.99	575.37	3.21
P2xP5	446.93	779.55	1007.39	29.24**	558.31	813.12	1120.79	37.82**
P2xP6	446.93	690.69	868.08	25.72**	558.31	825.27	1052.28	27.50**
P2xP7	446.93	154.24	392.07	-12.18**	558.31	222.96	509.71	-8.64
P2xP8	446.93	105.05	381.03	-14.67**	558.31	152.18	490.47	-11.89
P3xP4	351.89	251.51	336.48	-4.45	411.21	276.99	384.29	-6.52
P3xP5	351.89	779.55	603.92	-22.53**	411.21	813.12	653.33	-19.65*
P3xP6	351.89	690.69	740.80	7.26**	411.21	825.27	879.88	6.62
P3xP7	351.89	154.24	308.11	-12.45**	411.21	222.96	387.88	-5.67
P3xP8	351.89	105.05	280.35	-20.34**	411.21	152.18	346.01	-15.78
P4xP5	251.51	779.55	654.57	-16.04**	276.99	813.12	692.57	-14.81
P4xP6	251.51	690.69	482.23	-30.20**	276.99	825.27	560.43	-32.09**
P4xP7	251.51	154.24	255.83	2.37	276.99	222.96	316.39	13.38
P4xP8	251.51	105.05	234.54	-6.43**	276.99	152.18	285.87	3.19
P5xP6	779.55	690.69	1214.51	55.79**	813.12	825.27	1351.05	63.69**
P5xP7	779.55	154.24	760.96	-2.39	813.12	222.96	826.08	1.58
P5xP8	779.55	105.05	740.97	-4.95*	813.12	152.18	797.38	-1.92
P6xP7	690.69	154.24	654.32	-5.27*	825.27	222.96	802.90	-2.71
P6xP8	690.69	105.05	657.71	-4.78	825.27	152.18	807.30	-2.18
P7xP8	154.24	105.05	158.18	2.58	222.96	152.18	228.84	3.30
CD @ 5%	4.80				16.83			
CD @ 1%	6.40				22.42			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

The estimates of heterobeltiosis ranged from -41.58 to 48.16 per cent in IR 2 and -42.44 to 63.93 per cent in IR 1. Heterobeltiosis was significant for plant height and positive heterobeltiosis is preferred for this trait. Three hybrids had significant positive heterobeltiosis for this trait in IR 1 and IR 2. P3 x P6 (69.93% and 48.16% respectively in IR 1 and IR 2) and P1 x P6 (11.78% and 12.99% respectively in IR 1 and IR 2) were found to be the best hybrids which were consistently best at both irrigation regimes. Other than these two, P3 x P7 (5.78%) and P6 x P7 (7.56%) hybrids had significant positive heterosis in IR 1 and IR 2 respectively. Seventeen hybrids each showed significant negative heterosis in IR 1 and IR 2. The cross P1 x P4 consistently had highest negative significant heterosis in IR 1 (-42.44%) and IR 2 (-41.58%).

Range of heterosis over better parent was from -5.47 to 37.40 per cent in IR 2 and -4.41 to 42.54 per cent in IR 1 for number of branches. Twenty three hybrids had significant positive heterobeltiosis in IR 1 and 16 hybrids in IR 2. Values in negative direction were non-significant. P1 x P2 (37.40%), P1 x P4 (33.28%) and P1 x P3 (32.44%) performed well under stressed condition. The same hybrids were top performing even under non-stressed condition.

Heterobeltiosis for stem girth was ranged from -14.78 to 28.06 per cent in IR 2 and -6.94 to 43.29 per cent in IR 1. Six hybrids had significant positive values under IR 2 and 10 had the same under IR 1. P5 x P6 (28.06%), P5 x P8 (22.67%) and P6 x P8 (17.65%) were the three best performing hybrids under stressed condition. These hybrids also had positive significant heterobeltiosis under non-stressed condition.

None of the crosses showed negative heterosis for root length. Out of the 28 hybrids, 27 hybrids had significant positive heterobeltiosis under stressed condition and 23 hybrids under non-stressed condition for this trait. The crosses P2 x P3, P3 x P4, P4 x P8, P2 x P7 and P4 x P6 were best performing under stressed condition. These hybrids had positive significant heterosis in non-stressed condition also. Range of heterobeltiosis was from 5.61 to 51.37 per cent in IR 2 and from 6.88 to 45.33 in IR 1.

Heterobeltiosis for root volume was ranged from 6.36 to 67.54 and from -5.07 to 52.86 per cent in IR 2 and IR 1 respectively. Under stressed condition, 24 hybrids had significant positive heterosis over better parent and under non-stressed condition, 19 had the same. P5 x P6, P1 x P5, P1 x P6, P2 x P4 and P4 x P5 were the best performing hybrids under both drought stressed and non-stressed conditions. The cross P5 x P6 had highest significant heterosis under both stressed (67.54%) and non-stressed (52.86%) conditions.

Significant positive heterobeltiosis is preferred for stomata count. Positive heterobeltiosis was noticed neither in IR 2 (-36.28 to -1.15%) nor in IR 1 (-30.95 to -0.61%). Fifteen hybrids had significant negative heterosis under non stressed condition and 24 had that under stressed condition.

Heterobeltiosis for number of pubescence on abaxial layer was ranged from -30.91 to 41.31 per cent in IR 2 and from -32.76 to 63.25 per cent in IR 1. Four hybrids had significant positive heterobeltiosis under stressed condition and nine had the same under non-stressed contortion. P2 x P6, P5 x P6, P2 x P5 and P1 x P6 were found to be the best heterotic hybrids for this trait as these had highest heterosis under both stressed and non stressed condition.

Heterobeltiosis for number of pubescence on adaxial layer was ranged from -32.32 to 63.69 per cent in IR 2 and from -31.01 to 55.79 per cent in IR 1. Four hybrids had significant positive heterobeltiosis for the trait under stressed condition and eight had the same under non-stressed condition. Hybrids P5 x P6, P2 x P5, P2 x P6 and P1 x P6 were the best heterotic hybrids for this trait. Hybrid P5 x P6 had highest heterosis under stressed (63.69%) and non-stressed (55.79%) condition.

4.4.5.2 Growth parameters

Performance of parents, hybrids and heterobeltiosis values for growth traits viz., number of leaves, leaf area, absolute, relative and crop growth rate are presented in Table 74 to 78.

Heterobeltiosis was ranged from -17.67 to 33.71 per cent in IR 2 and from -17.88 to 32.50 per cent in IR 1 for number of leaves. Nine hybrids had significant positive heterobeltiosis for this trait under stressed condition and 19 had the same

Table 74. Estimates of heterobeltiosis for number of leaves at 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	70.00	52.00	63.30	-9.50**	63.00	35.33	51.81	-17.67**
P1xP3	70.00	70.00	71.40	1.03	63.00	65.00	65.16	0.34
P1xP4	70.00	65.33	83.67	19.58**	63.00	68.33	81.69	19.62**
P1xP5	70.00	53.33	72.43	3.45	63.00	42.33	61.73	-1.98
P1xP6	70.00	48.00	69.66	-0.50	63.00	45.67	64.22	2.01
P1xP7	70.00	61.67	84.30	20.49**	63.00	34.67	60.87	-3.20
P1xP8	70.00	64.33	76.57	9.44**	63.00	33.67	55.10	-12.58**
P2xP3	52.00	70.00	75.78	8.28*	35.33	65.00	61.43	-5.19
P2xP4	52.00	65.33	65.81	0.74	35.33	68.33	56.45	-17.39**
P2xP5	52.00	53.33	71.67	29.66**	35.33	42.33	53.02	25.30**
P2xP6	52.00	48.00	58.76	12.49**	35.33	45.67	46.71	2.29
P2xP7	52.00	61.67	73.27	18.76**	35.33	34.67	45.15	24.10**
P2xP8	52.00	64.33	76.26	18.62**	35.33	33.67	45.19	23.52**
P3xP4	70.00	65.33	92.73	32.50**	65.00	68.33	91.32	33.71**
P3xP5	70.00	53.33	79.77	13.93**	65.00	42.33	69.83	7.58
P3xP6	70.00	48.00	57.48	-17.88**	65.00	45.67	53.82	-17.09**
P3xP7	70.00	61.67	92.37	31.97**	65.00	34.67	68.60	5.83
P3xP8	70.00	64.33	91.18	30.24**	65.00	33.67	66.15	1.73
P4xP5	65.33	53.33	81.11	24.31**	68.33	42.33	75.42	10.44**
P4xP6	65.33	48.00	82.65	26.55**	68.33	45.67	82.77	21.15**
P4xP7	65.33	61.67	76.46	17.06**	68.33	34.67	64.16	-6.17
P4xP8	65.33	64.33	78.51	17.21**	68.33	33.67	63.96	-6.35
P5xP6	53.33	48.00	57.87	8.69**	42.33	45.67	50.09	9.72*
P5xP7	53.33	61.67	66.00	7.10*	42.33	34.67	44.39	5.11
P5xP8	53.33	64.33	68.14	5.98	42.33	33.67	44.17	4.45
P6xP7	48.00	61.67	63.13	2.41	45.67	34.67	46.14	0.99
P6xP8	48.00	64.33	63.74	-0.57	45.67	33.67	46.48	1.75
P7xP8	61.67	64.33	73.75	13.50**	34.67	33.67	39.96	9.14*
CD @ 5%	6.37				7.60			
CD @ 1%	8.48				10.13			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 75. Estimates of heterobeltiosis for leaf area (cm²) at 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	501.12	401.30	466.22	-6.93**	451.36	177.63	337.21	-25.29**
P1xP3	501.12	529.84	524.07	-1.22	451.36	441.34	455.88	-0.82
P1xP4	501.12	485.17	610.70	20.44**	451.36	291.90	452.85	0.34
P1xP5	501.12	391.89	524.69	4.75	451.36	313.06	448.24	-0.69
P1xP6	501.12	404.98	536.73	7.12**	451.36	309.64	449.25	-0.47
P1xP7	501.12	329.93	523.19	4.41	451.36	154.06	368.20	-18.42**
P1xP8	501.12	332.89	475.39	-5.06*	451.36	168.41	353.27	-21.74**
P2xP3	401.30	529.84	578.91	9.40**	177.63	441.34	374.13	-15.02**
P2xP4	401.30	485.17	498.58	2.82	177.63	291.90	258.49	-11.53**
P2xP5	401.30	391.89	539.09	34.34**	177.63	313.06	337.73	7.92**
P2xP6	401.30	404.98	471.43	15.25**	177.63	309.64	276.47	-10.78**
P2xP7	401.30	329.93	472.00	17.68**	177.63	154.06	214.06	20.07**
P2xP8	401.30	332.89	480.55	19.75**	177.63	168.41	226.61	22.92**
P3xP4	529.84	485.17	695.50	31.51**	441.34	291.90	503.02	14.17**
P3xP5	529.84	391.89	596.81	12.75**	441.34	313.06	489.23	11.02**
P3xP6	529.84	404.98	452.16	-14.59**	441.34	309.64	365.27	-17.10**
P3xP7	529.84	329.93	595.14	12.31	441.34	154.06	403.96	-8.34**
P3xP8	529.84	332.89	580.75	9.68**	441.34	168.41	406.44	-7.73**
P4xP5	485.17	391.89	599.39	23.62**	291.90	313.06	414.71	32.49**
P4xP6	485.17	404.98	653.10	34.72**	291.90	309.64	446.38	44.16**
P4xP7	485.17	329.93	499.92	3.19	291.90	154.06	277.23	-5.03*
P4xP8	485.17	332.89	504.82	4.13	291.90	168.41	286.51	-1.84
P5xP6	391.89	404.98	453.96	12.09**	313.06	309.64	355.00	13.02**
P5xP7	391.89	329.93	415.98	6.18*	313.06	154.06	270.98	-13.44**
P5xP8	391.89	332.89	420.96	7.42**	313.06	168.41	280.70	-10.34**
P6xP7	404.98	329.93	422.20	4.27	309.64	154.06	265.85	-14.14**
P6xP8	404.98	332.89	425.50	5.09	309.64	168.41	267.39	-13.64**
P7xP8	329.93	332.89	387.79	13.19**	154.06	168.41	188.86	12.24**
CD @ 5%	5.01				4.76			
CD @ 1%	6.67				6.34			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 76. Estimates of heterobeltiosis for absolute growth rate at 45 to 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	0.50	0.53	0.60	11.95*	0.38	0.36	0.43	11.93
P1xP3	0.50	0.66	0.70	5.18	0.38	0.53	0.55	3.41
P1xP4	0.50	0.24	0.45	-10.59*	0.38	0.22	0.36	-3.93
P1xP5	0.50	0.56	0.77	37.37**	0.38	0.41	0.57	38.33**
P1xP6	0.50	0.37	0.70	40.79**	0.38	0.33	0.57	42.43**
P1xP7	0.50	0.31	0.52	4.11	0.38	0.17	0.36	-4.19
P1xP8	0.50	0.48	0.52	3.38	0.38	0.46	0.44	-3.86
P2xP3	0.53	0.66	0.76	14.52**	0.36	0.53	0.56	6.16
P2xP4	0.53	0.24	0.56	4.79	0.36	0.22	0.41	16.76*
P2xP5	0.53	0.56	0.87	55.00**	0.36	0.41	0.61	49.22**
P2xP6	0.53	0.37	0.64	19.83**	0.36	0.33	0.49	22.89**
P2xP7	0.53	0.31	0.51	-4.82	0.36	0.17	0.32	-8.85
P2xP8	0.53	0.48	0.63	17.62**	0.36	0.46	0.49	8.27
P3xP4	0.66	0.24	0.54	-19.14**	0.53	0.22	0.44	-16.37**
P3xP5	0.66	0.56	0.83	24.95**	0.53	0.41	0.63	19.73**
P3xP6	0.66	0.37	0.71	7.14	0.53	0.33	0.59	10.66
P3xP7	0.66	0.31	0.57	-13.36*	0.53	0.17	0.42	-21.60**
P3xP8	0.66	0.48	0.72	8.14	0.53	0.46	0.62	17.35*
P4xP5	0.24	0.56	0.63	12.91*	0.22	0.41	0.49	20.68**
P4xP6	0.24	0.37	0.47	24.60**	0.22	0.33	0.41	26.44**
P4xP7	0.24	0.31	0.33	7.37	0.22	0.17	0.24	9.24
P4xP8	0.24	0.48	0.47	-1.47	0.22	0.46	0.44	-3.21
P5xP6	0.56	0.37	0.78	39.92**	0.41	0.33	0.61	42.70**
P5xP7	0.56	0.31	0.67	19.61**	0.41	0.17	0.46	12.95
P5xP8	0.56	0.48	0.74	32.39**	0.41	0.46	0.60	23.85**
P6xP7	0.37	0.31	0.49	29.47**	0.33	0.17	0.37	14.20*
P6xP8	0.37	0.48	0.49	2.27	0.33	0.46	0.37	-18.90**
P7xP8	0.31	0.48	0.51	5.85	0.17	0.46	0.41	-10.71
CD @ 5%	10.16				14.15			
CD @ 1%	13.53				18.84			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 77. Estimates of heterobeltiosis for relative growth rate at 45 to 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	1.24	0.80	1.13	-9.03	1.02	0.52	0.85	-14.42
P1xP3	1.24	1.34	1.58	15.03	1.02	0.97	1.21	10.91
P1xP4	1.24	0.06	0.74	-40.12**	1.02	0.04	0.60	-40.49*
P1xP5	1.24	0.94	1.54	26.11*	1.02	0.70	1.20	22.10
P1xP6	1.24	0.05	1.00	-19.27	1.02	0.05	0.83	-18.39
P1xP7	1.24	1.13	1.47	19.33	1.02	0.91	1.20	13.08
P1xP8	1.24	0.09	0.80	-35.43**	1.02	0.06	0.65	-35.88
P2xP3	0.80	1.34	1.26	-5.93	0.52	0.97	0.87	-10.19
P2xP4	0.80	0.06	0.63	-21.05	0.52	0.04	0.41	-21.06
P2xP5	0.80	0.94	1.40	48.88**	0.52	0.70	0.98	40.54*
P2xP6	0.80	0.05	0.54	-32.29**	0.52	0.05	0.37	-29.28
P2xP7	0.80	1.13	1.15	1.90	0.52	0.91	0.85	-6.80
P2xP8	0.80	0.09	0.60	-24.13*	0.52	0.06	0.39	-24.01
P3xP4	1.34	0.06	0.81	-39.00**	0.97	0.04	0.59	-39.42*
P3xP5	1.34	0.94	1.17	-12.79	0.97	0.70	0.85	-12.03
P3xP6	1.34	0.05	0.81	-39.68**	0.97	0.05	0.60	-38.27
P3xP7	1.34	1.13	1.41	5.49	0.97	0.91	1.07	10.42
P3xP8	1.34	0.09	0.88	-34.22**	0.97	0.06	0.63	-34.73
P4xP5	0.06	0.94	0.83	-12.37	0.04	0.70	0.61	-13.09
P4xP6	0.06	0.05	0.08	18.33	0.04	0.05	0.07	32.42
P4xP7	0.06	1.13	0.69	-38.95**	0.04	0.91	0.55	-39.66*
P4xP8	0.06	0.09	0.10	6.39	0.04	0.06	0.07	9.08
P5xP6	0.94	0.05	0.84	-10.63	0.70	0.05	0.64	-8.75
P5xP7	0.94	1.13	1.49	32.02**	0.70	0.91	1.14	25.89
P5xP8	0.94	0.09	0.88	-7.04	0.70	0.06	0.64	-7.68
P6xP7	0.05	1.13	0.63	-44.38**	0.05	0.91	0.51	-43.29
P6xP8	0.05	0.09	0.67	605.51**	0.05	0.06	0.54	656.55**
P7xP8	1.13	0.09	0.79	-30.44*	0.91	0.06	0.62	-31.32
CD @ 5%	24.02				38.91			
CD @ 1%	32.00				51.82			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 78. Estimates of heterobeltiosis for crop growth rate at 45 to 60 DAT under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	0.83	0.83	0.94	5.21	0.84	0.45	0.73	-13.47
P1xP3	0.83	1.19	1.27	7.32	0.84	1.18	1.27	9.33
P1xP4	0.83	0.56	0.83	-3.64	0.84	0.29	0.67	-19.53
P1xP5	0.83	1.05	1.35	29.14**	0.84	0.85	1.21	28.04
P1xP6	0.83	0.68	1.19	43.98**	0.84	0.40	0.97	17.54
P1xP7	0.83	1.45	1.43	-1.34	0.84	1.22	1.29	7.54
P1xP8	0.83	0.64	0.82	-0.60	0.84	0.31	0.67	-20.18
P2xP3	0.83	1.19	1.28	8.39	0.45	1.18	0.98	-15.93
P2xP4	0.83	0.56	0.95	13.84	0.45	0.29	0.51	13.30
P2xP5	0.83	1.05	1.51	44.72**	0.45	0.85	1.06	26.34
P2xP6	0.83	0.68	1.09	32.47**	0.45	0.40	0.61	10.69
P2xP7	0.83	1.45	1.36	-5.95	0.45	1.22	0.98	-18.73
P2xP8	0.83	0.64	1.00	18.18*	0.45	0.31	0.52	14.91
P3xP4	1.19	0.56	1.07	-8.49	1.18	0.29	0.88	-26.19
P3xP5	1.19	1.05	1.11	-8.25	1.18	0.85	1.02	-12.37
P3xP6	1.19	0.68	1.25	5.52	1.18	0.40	1.01	-14.99
P3xP7	1.19	1.45	1.49	2.78	1.18	1.22	1.36	7.96
P3xP8	1.19	0.64	1.14	-4.18	1.18	0.31	0.92	-22.56
P4xP5	0.56	1.05	1.22	16.51*	0.29	0.85	0.89	3.00
P4xP6	0.56	0.68	0.93	21.67**	0.29	0.40	0.52	35.24
P4xP7	0.56	1.45	1.17	-19.04*	0.29	1.22	0.88	-29.76
P4xP8	0.56	0.64	0.77	0.99	0.29	0.31	0.39	16.87
P5xP6	1.05	0.68	1.46	39.86**	0.85	0.40	1.06	20.91
P5xP7	1.05	1.45	1.74	19.93*	0.85	1.22	1.44	18.81
P5xP8	1.05	0.64	1.28	22.90**	0.85	0.31	0.92	7.06
P6xP7	0.68	1.45	1.36	-6.12	0.40	1.22	0.99	-21.52
P6xP8	0.68	0.64	1.40	93.65**	0.40	0.31	1.02	253.79**
P7xP8	1.45	0.64	1.31	-10.09	1.22	0.31	0.97	-21.85
CD @ 5%	15.36				79.01			
CD @ 1%	20.46				105.23			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01;

IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

under non-stressed condition. P3 x P4, P2 x P5 and P4 x P6 were the best heterotic hybrids for this trait as these had the highest value under both stressed and non stressed conditions. Hybrid P3 x P4 had the highest heterobeltiosis under stressed (33.71%) and non-stressed (92.73%) conditions. Hybrid P1 x P2 had the highest negative heterosis (-17.67%) under stressed condition.

Heterobeltiosis was ranged from -25.29 to 44.16 per cent in IR 2 and from -14.59 to 34.72 per cent in IR 1 for leaf area. Nine hybrids had significant positive heterobeltiosis for this trait under stressed condition and 18 had the same under non-stressed condition. P4 x P6 (44.16% and 34.72% in IR 2 and IR 1 respectively), P4 x P5 (32.49% and 23.62% in IR 2 and IR 1 respectively) and P3 x P4 (14.17% and 35.51% in IR 2 and IR 1 respectively) had highest significant positive heterosis for this trait under both stressed and non-stressed conditions.

Heterobeltiosis was ranged from -21.60 (P3 x P7) to 49.22 (P2 x P5) per cent in IR 2 and from -19.14 (P3 x P4) to 55.00 (P2 x P5) per cent in IR 1 for absolute growth rate. Twelve hybrids had significant positive heterobeltiosis for this trait under stressed condition and 14 had the same under non-stressed condition. P2 x P5, P5 x P6, P1 x P6 and P1 x P5 were the best heterotic hybrids having highest positive heterosis in both the conditions.

Heterobeltiosis was ranged from -43.29 (P6 x P7) to 656.55 (P6 x P8) per cent in IR 2 and from -44.48 (P6 x P7) to 605.51 (P6 x P8) per cent in IR 1 for relative growth rate. Only two hybrids had significant positive heterobeltiosis for this trait under stressed condition and 4 had the same under non-stressed condition. P6 x P8 and P2 x P5 were the best heterotic hybrids for this trait. These hybrids had significant positive heterosis for the trait under both stressed and non-stressed conditions.

Heterobeltiosis was ranged from -29.76 (P4 x P7) to 253.79 (P6 x P8) per cent in IR 2 and from -19.04 (P4 x P7) to 93.65 (P6 x P8) per cent in IR 1 for absolute growth rate. Only one hybrid (P6 x P8) had significant positive heterobeltiosis for this trait under stressed condition. This hybrid also had highest significant positive heterosis under non-stressed condition. Eleven hybrids had the same under non-stressed condition.

4.4.5.3 Biochemical parameters

Performance of parents, hybrids and heterobeltiosis values for biochemical traits viz., proline content and chlorophyll (a, b and total) content are presented in Table 79 to 82.

Heterobeltiosis was ranged from -17.27 to 61.56 per cent in IR 2 and from -17.13 to 66.78 per cent in IR 1 for proline content. Twenty three hybrids had significant positive heterobeltiosis for this trait under stressed condition and 22 had the same under non-stressed condition. P5 x P6 (61.56% and 66.78% in IR 2 and IR 1 respectively), P1 x P6 (41.29% and 50.75% in IR 2 and IR 1 respectively), P2 x P5 (36.48% and 50.54% in IR 2 and IR 1 respectively) and P2 x P6 (29.32% and 35.11% in IR 2 and IR 1 respectively) were the top four heterotic hybrids under both stressed and non-stressed conditions for this trait.

Heterobeltiosis was ranged from -44.53 (P3 x P5) to 67.18 (P5 x P6) per cent in IR 2 and from -28.02 (P3 x P5) to 57.40 (P5 x P6) per cent in IR 1 for chlorophyll a content. Thirteen hybrids had significant positive heterobeltiosis for this trait under stressed condition and 22 had the same under non-stressed condition. The best heterotic hybrids for this trait were P5 x P6, P1 x P6, P2 x P5, P2 x P4 and P4 x P6.

Range of heterobeltiosis was from -28.83 to 60.39 per cent in IR 2 and from -44.62 to 59.19 per cent in IR 1 for chlorophyll b content. Twenty hybrids had significant positive heterobeltiosis for this trait under stressed condition and 5 had the same under non-stressed condition. The best heterotic hybrids for this trait were P5 x P6, P1 x P6, P2 x P5, P4 x P6 and P2 x P6.

Heterobeltiosis was ranged from -41.30 to 69.69 per cent in IR 2 and from -31.99 to 60.00 per cent in IR 1 for total chlorophyll content. Nineteen hybrids had significant positive heterobeltiosis for this trait under stressed condition and 23 had the same under non-stressed condition. The hybrids P5 x P6, P2 x P5, P1 x P6, P4 x P5 and P4 x P6 were the best heterotic hybrids for this trait.

Table 79. Estimates of heterobeltiosis for proline content ($\mu\text{g g}^{-1}$) under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	196.34	166.65	209.50	6.80**	284.86	245.50	306.13	7.47**
P1xP3	196.34	153.15	227.57	15.97**	284.86	206.76	318.51	11.84**
P1xP4	196.34	137.01	189.36	-3.53	284.86	212.24	282.34	-0.85
P1xP5	196.34	205.54	244.03	18.73**	284.86	389.04	410.70	5.56**
P1xP6	196.34	211.50	318.81	50.75**	284.86	353.98	499.89	41.29**
P1xP7	196.34	146.21	221.65	12.90**	284.86	206.24	318.27	11.76**
P1xP8	196.34	94.58	162.72	-17.13**	284.86	177.89	254.54	-10.63**
P2xP3	166.65	153.15	201.14	20.83**	245.50	206.76	285.70	16.42**
P2xP4	166.65	137.01	203.83	22.47**	245.50	212.24	306.27	24.80**
P2xP5	166.65	205.54	308.61	50.14**	245.50	389.04	530.98	36.48**
P2xP6	166.65	211.50	285.75	35.11**	245.50	353.98	457.53	29.32**
P2xP7	166.65	146.21	209.68	26.08**	245.50	206.24	302.55	23.32**
P2xP8	166.65	94.58	176.01	5.83**	245.50	177.89	284.17	15.75**
P3xP4	153.15	137.01	162.21	5.94**	206.76	212.24	233.61	10.09**
P3xP5	153.15	205.54	193.32	-5.95**	206.76	389.04	321.86	-17.27**
P3xP6	153.15	211.50	238.64	12.82**	206.76	353.98	371.15	4.87**
P3xP7	153.15	146.21	180.37	17.85**	206.76	206.24	248.96	20.01**
P3xP8	153.15	94.58	153.52	0.33	206.76	177.89	239.15	15.71**
P4xP5	137.01	205.54	226.51	10.20**	212.24	389.04	397.18	2.10
P4xP6	137.01	211.50	190.19	-10.08**	212.24	353.98	306.87	-13.27**
P4xP7	137.01	146.21	183.26	25.35**	212.24	206.24	270.21	27.11**
P4xP8	137.01	94.58	154.11	12.54**	212.24	177.89	261.81	23.34**
P5xP6	205.54	211.50	352.75	66.78**	389.04	353.98	628.47	61.56**
P5xP7	205.54	146.21	260.78	26.88**	389.04	206.24	454.37	16.79**
P5xP8	205.54	94.58	231.00	12.39**	389.04	177.89	436.61	12.23**
P6xP7	211.50	146.21	255.99	21.04**	353.98	206.24	407.02	14.99**
P6xP8	211.50	94.58	253.59	19.90**	353.98	177.89	403.79	14.08**
P7xP8	146.21	94.58	149.43	2.19	206.24	177.89	236.36	14.66**
CD @ 5%	4.04				3.29			
CD @ 1%	5.87				4.38			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 80. Estimates of heterobeltiosis for chlorophyll a (mg/100g) content under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	1.53	1.17	1.55	1.53	0.99	0.88	1.07	7.99**
P1xP3	1.53	0.92	1.47	-3.42	0.99	0.25	0.73	-26.33**
P1xP4	1.53	1.05	1.57	3.36	0.99	0.84	1.13	13.53**
P1xP5	1.53	1.85	2.45	32.21**	0.99	1.35	1.71	27.03**
P1xP6	1.53	1.58	2.47	46.99**	0.99	1.30	1.82	40.42**
P1xP7	1.53	0.88	1.60	4.85	0.99	0.45	0.97	-2.54
P1xP8	1.53	0.76	1.28	-16.24**	0.99	0.46	0.81	-17.96**
P2xP3	1.17	0.92	1.33	13.58**	0.88	0.25	0.75	-14.62**
P2xP4	1.17	1.05	1.50	28.20**	0.88	0.84	1.16	31.48**
P2xP5	1.17	1.85	2.46	32.68**	0.88	1.35	1.81	34.13**
P2xP6	1.17	1.58	2.08	32.04**	0.88	1.30	1.66	27.42**
P2xP7	1.17	0.88	1.25	6.65*	0.88	0.45	0.82	-6.59**
P2xP8	1.17	0.76	1.30	10.83**	0.88	0.46	0.90	2.73
P3xP4	0.92	1.05	1.24	18.80**	0.25	0.84	0.72	-14.77**
P3xP5	0.92	1.85	1.33	-28.02**	0.25	1.35	0.75	-44.53**
P3xP6	0.92	1.58	1.86	18.29**	0.25	1.30	1.24	-4.28*
P3xP7	0.92	0.88	1.02	10.74**	0.25	0.45	0.39	-12.00**
P3xP8	0.92	0.76	1.05	14.01**	0.25	0.46	0.45	-1.63
P4xP5	1.05	1.85	2.28	23.51**	0.84	1.35	1.71	27.36**
P4xP6	1.05	1.58	2.05	30.37**	0.84	1.30	1.67	28.73**
P4xP7	1.05	0.88	1.14	9.13**	0.84	0.45	0.77	-8.03**
P4xP8	1.05	0.76	1.15	10.02**	0.84	0.46	0.82	-1.85
P5xP6	1.85	1.58	2.92	57.40**	1.35	1.30	2.25	67.18**
P5xP7	1.85	0.88	2.07	11.99**	1.35	0.45	1.41	4.67*
P5xP8	1.85	0.76	2.05	10.91**	1.35	0.46	1.44	6.91**
P6xP7	1.58	0.88	1.78	13.08**	1.30	0.45	1.32	1.37
P6xP8	1.58	0.76	1.80	13.88**	1.30	0.46	1.33	1.97
P7xP8	0.88	0.76	0.99	12.78**	0.45	0.46	0.54	18.59**
CD @ 5%	6.40				3.61			
CD @ 1%	8.52				4.81			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 81. Estimates of heterobeltiosis for chlorophyll b (mg/100g) content under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	0.24	0.15	0.22	-9.58	0.37	0.46	0.47	3.46
P1xP3	0.24	0.11	0.21	-7.73	0.37	0.17	0.32	-13.21**
P1xP4	0.24	0.11	0.22	-8.95	0.37	0.49	0.54	10.21*
P1xP5	0.24	0.58	0.63	8.78	0.37	0.35	0.51	32.58**
P1xP6	0.24	0.56	0.65	16.61*	0.37	0.40	0.61	51.73**
P1xP7	0.24	0.23	0.31	9.62	0.37	0.46	0.53	15.05**
P1xP8	0.24	0.54	0.40	-26.76**	0.37	0.44	0.42	-3.88
P2xP3	0.15	0.11	0.16	11.24	0.46	0.17	0.41	-10.00*
P2xP4	0.15	0.11	0.18	21.40**	0.46	0.49	0.63	27.72**
P2xP5	0.15	0.58	0.60	3.71	0.46	0.35	0.64	41.66**
P2xP6	0.15	0.56	0.57	1.98	0.46	0.40	0.62	36.98**
P2xP7	0.15	0.23	0.22	-2.50	0.46	0.46	0.55	17.22**
P2xP8	0.15	0.54	0.45	-16.86*	0.46	0.44	0.60	31.56**
P3xP4	0.11	0.11	0.14	21.24**	0.17	0.49	0.43	-11.94**
P3xP5	0.11	0.58	0.32	-44.62**	0.17	0.35	0.25	-28.83**
P3xP6	0.11	0.56	0.54	-4.04	0.17	0.40	0.43	8.95*
P3xP7	0.11	0.23	0.19	-17.26*	0.17	0.46	0.35	-23.71**
P3xP8	0.11	0.54	0.42	-23.34**	0.17	0.44	0.39	-12.04**
P4xP5	0.11	0.58	0.57	-1.32	0.49	0.35	0.63	29.64**
P4xP6	0.11	0.56	0.56	-0.59	0.49	0.40	0.67	37.34**
P4xP7	0.11	0.23	0.20	-12.44	0.49	0.46	0.56	11.86**
P4xP8	0.11	0.54	0.43	-20.54**	0.49	0.44	0.59	20.72**
P5xP6	0.58	0.56	0.97	59.19**	0.35	0.40	0.64	60.39**
P5xP7	0.58	0.23	0.62	7.80	0.35	0.46	0.55	18.80**
P5xP8	0.58	0.54	0.82	39.42**	0.35	0.44	0.56	27.33**
P6xP7	0.56	0.23	0.59	5.55	0.40	0.46	0.58	25.91**
P6xP8	0.56	0.54	0.59	-3.33	0.40	0.44	0.59	32.84**
P7xP8	0.23	0.54	0.45	-17.79*	0.46	0.44	0.54	17.68**
CD @ 5%	15.13				8.25			
CD @ 1%	20.15				10.99			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 82. Estimates of heterobeltiosis for total chlorophyll (mg/100g) content under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	1.77	1.32	1.77	0.56	1.36	1.33	1.54	11.71**
P1xP3	1.77	1.03	1.68	-4.48	1.36	0.42	1.05	-22.75**
P1xP4	1.77	1.16	1.79	1.86	1.36	1.33	1.66	20.10**
P1xP5	1.77	2.43	3.07	26.42**	1.36	1.70	2.22	30.77**
P1xP6	1.77	2.14	3.11	45.18**	1.36	1.70	2.43	43.27**
P1xP7	1.77	1.10	1.90	8.00*	1.36	0.91	1.50	10.26**
P1xP8	1.77	1.30	1.67	-4.97	1.36	0.90	1.24	-8.83**
P2xP3	1.32	1.03	1.49	13.27**	1.33	0.42	1.16	-13.04**
P2xP4	1.32	1.16	1.68	27.45**	1.33	1.33	1.79	33.96**
P2xP5	1.32	2.43	3.05	25.78**	1.33	1.70	2.45	44.23**
P2xP6	1.32	2.14	2.65	23.72**	1.33	1.70	2.28	34.23**
P2xP7	1.32	1.10	1.47	11.57**	1.33	0.91	1.37	2.95*
P2xP8	1.32	1.30	1.75	32.66**	1.33	0.90	1.50	12.56**
P3xP4	1.03	1.16	1.38	19.19**	0.42	1.33	1.14	-13.91**
P3xP5	1.03	2.43	1.65	-31.99**	0.42	1.70	1.00	-41.30**
P3xP6	1.03	2.14	2.40	12.09**	0.42	1.70	1.68	-1.20
P3xP7	1.03	1.10	1.21	9.87**	0.42	0.91	0.75	-17.92**
P3xP8	1.03	1.30	1.47	12.94**	0.42	0.90	0.84	-6.71**
P4xP5	1.16	2.43	2.85	17.59**	1.33	1.70	2.34	37.90**
P4xP6	1.16	2.14	2.61	21.83**	1.33	1.70	2.34	37.81**
P4xP7	1.16	1.10	1.34	15.53**	1.33	0.91	1.33	0.44
P4xP8	1.16	1.30	1.58	21.60**	1.33	0.90	1.42	6.81**
P5xP6	2.43	2.14	3.89	60.00**	1.70	1.70	2.89	69.69**
P5xP7	2.43	1.10	2.69	10.97**	1.70	0.91	1.96	15.22**
P5xP8	2.43	1.30	2.87	18.14**	1.70	0.90	2.00	17.79**
P6xP7	2.14	1.10	2.37	10.64**	1.70	0.91	1.90	11.76**
P6xP8	2.14	1.30	2.39	11.39**	1.70	0.90	1.91	12.53**
P7xP8	1.10	1.30	1.43	10.22**	0.91	0.90	1.09	18.63**
CD @ 5%	6.71				2.81			
CD @ 1%	8.94				3.75			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

4.4.5.4 Yield parameters

Performance of parents, hybrids and heterobeltiosis values for yield parameters viz., number of fruits per plant, average fruit weight and yield per plant are presented in Table 83 to 85.

Heterobeltiosis was ranged from -25.89 to 41.85 per cent in IR 2 and from -5.27 to 46.63 per cent in IR 1 for number of fruits per plant. Thirteen hybrids had significant positive heterobeltiosis for this trait under stressed condition and 22 had the same under non-stressed condition. The best heterotic hybrids for this trait were P3 x P4, P2 x P6, P1 x P7, P3 x P5 and P1 x P4.

Heterobeltiosis was ranged from -34.65 to 11.14 per cent in IR 2 and from -34.11 to 10.05 per cent in IR 1 for average fruit weight. No hybrid had significant positive heterobeltiosis for this trait under stressed and non-stressed condition.

Heterobeltiosis was ranged from -41.17 to 71.56 per cent in IR 2 and from -16.44 to 68.06 per cent in IR 1 for yield per plant. Eight hybrids had significant positive heterobeltiosis for this trait under stressed condition and 12 had the same under non-stressed condition. The best heterotic hybrids for this trait were P4 x P8, P1 x P4, P3 x P4, P3 x P8 and P2 x P5.

4.5 Evaluation of hybrids and parents in diallel approach for TyLCV tolerance

4.5.1 Analysis of variance

Analysis of variance for morphological characters viz., plant height, number of branches and stem girth (at 45, 60 and 90 DAT) and number of pubescence (abaxial and adaxial) showed highly significant differences in treatments, parents and hybrids. Parents vs. hybrids had highly significant difference only plant height (at 45, 60 and 90 DAT) and pubescence (abaxial and adaxial). Among growth parameters viz., number of leaves (at 45, 60 and 90 DAT) and leaf area (at 45, 60 and 90 DAT), highly significant difference was observed in treatments, parents and hybrids. The difference was highly significant in parents vs. hybrids for number of leaves (90 DAT) and leaf area (at 45, 60 and 90 DAT). Disease index parameters viz., per cent plant survival

Table 83. Estimates of heterobeltiosis for number of fruits under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	112.60	133.13	147.74	11.22	74.33	138.13	120.14	-13.07
P1xP3	112.60	106.75	135.86	17.12**	74.33	94.53	100.52	6.22
P1xP4	112.60	111.77	162.71	43.37**	74.33	81.33	112.47	27.45**
P1xP5	112.60	142.40	157.60	10.85	74.33	132.00	122.66	-5.64
P1xP6	112.60	126.60	157.46	23.07**	74.33	151.00	141.03	-6.21
P1xP7	112.60	116.00	163.23	33.01**	74.33	59.67	96.76	30.87**
P1xP8	112.60	118.27	155.24	16.18*	74.33	122.67	127.90	5.68
P2xP3	133.13	106.75	148.17	11.56	138.13	94.53	144.98	4.95
P2xP4	133.13	111.77	174.83	31.67**	138.13	81.33	154.04	11.82
P2xP5	133.13	142.40	181.94	25.35**	138.13	132.00	178.23	24.17**
P2xP6	133.13	126.60	185.28	34.08**	138.13	151.00	207.57	37.74**
P2xP7	133.13	116.00	177.02	32.67**	138.13	59.67	136.33	-1.19
P2xP8	133.13	118.27	158.68	12.75*	138.13	122.67	164.61	13.48
P3xP4	106.75	111.77	167.54	46.57**	94.53	81.33	133.55	41.85**
P3xP5	106.75	142.40	184.73	29.97**	94.53	132.00	168.19	28.51**
P3xP6	106.75	126.60	178.26	41.06**	94.53	151.00	191.31	26.89**
P3xP7	106.75	116.00	144.79	14.84*	94.53	59.67	100.23	6.17
P3xP8	106.75	118.27	152.17	10.93	94.53	122.67	147.31	21.93**
P4xP5	111.77	142.40	185.96	30.72**	81.33	132.00	157.45	19.10**
P4xP6	111.77	126.60	185.03	46.63**	81.33	151.00	185.86	23.55**
P4xP7	111.77	116.00	165.36	33.68**	81.33	59.67	101.03	25.53**
P4xP8	111.77	118.27	167.13	23.74**	81.33	122.67	150.17	23.05**
P5xP6	142.40	126.60	144.78	1.68	132.00	151.00	150.36	-0.49
P5xP7	142.40	116.00	174.50	20.40**	132.00	59.67	124.42	-5.21
P5xP8	142.40	118.27	171.53	14.76*	132.00	122.67	168.65	22.66**
P6xP7	126.60	116.00	173.08	25.36**	151.00	59.67	137.98	-8.07
P6xP8	126.60	118.27	162.64	14.95*	151.00	122.67	132.61	-15.89*
P7xP8	116.00	118.27	120.52	-5.27	59.67	122.67	90.44	-25.89**
CD @ 5%	12.66				14.07			
CD @ 1%	16.86				18.74			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 84. Estimates of heterobeltiosis for average fruit weight (g) under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	14.83	14.42	14.64	-14.08	18.33	17.67	18.03	-30.09**
P1xP3	14.83	11.03	13.12	-13.64	18.33	14.67	16.68	-23.24**
P1xP4	14.83	20.87	22.14	10.05	18.33	15.33	20.36	-3.14
P1xP5	14.83	22.00	18.19	-18.42*	18.33	26.33	22.07	-29.76**
P1xP6	14.83	68.67	45.92	-33.35**	18.33	67.00	46.93	-29.29**
P1xP7	14.83	14.33	17.47	4.51	18.33	10.00	16.58	1.43
P1xP8	14.83	23.67	21.64	-8.38	18.33	13.33	17.68	-8.63
P2xP3	14.42	11.03	15.90	7.76	17.67	14.67	20.11	10.72
P2xP4	14.42	20.87	21.06	-5.07	17.67	15.33	20.07	3.22
P2xP5	14.42	22.00	24.11	8.68	17.67	26.33	29.13	9.59
P2xP6	14.42	68.67	46.45	-31.42**	17.67	67.00	47.66	-27.78**
P2xP7	14.42	14.33	17.11	1.33	17.67	10.00	16.88	-5.14
P2xP8	14.42	23.67	22.63	-4.26	17.67	13.33	18.95	5.52
P3xP4	11.03	20.87	18.46	-1.42	14.67	15.33	18.09	6.47
P3xP5	11.03	22.00	18.83	-13.86	14.67	26.33	23.55	-9.17
P3xP6	11.03	68.67	45.09	-34.11**	14.67	67.00	46.11	-29.74**
P3xP7	11.03	14.33	15.62	9.05	14.67	10.00	15.43	6.83
P3xP8	11.03	23.67	19.24	-18.57*	14.67	13.33	16.33	11.14
P4xP5	20.87	22.00	26.74	-2.34	15.33	26.33	25.55	-1.81
P4xP6	20.87	68.67	48.31	-30.76**	15.33	67.00	43.77	-34.03**
P4xP7	20.87	14.33	21.58	4.27	15.33	10.00	15.57	2.57
P4xP8	20.87	23.67	27.94	0.29	15.33	13.33	18.14	7.12
P5xP6	22.00	68.67	51.43	-24.31**	26.33	67.00	53.06	-19.69*
P5xP7	22.00	14.33	21.87	0.06	26.33	10.00	21.74	-15.47
P5xP8	22.00	23.67	27.65	9.18	26.33	13.33	23.80	-7.64
P6xP7	68.67	14.33	46.45	-32.07**	67.00	10.00	43.29	-34.65**
P6xP8	68.67	23.67	47.74	-30.14**	67.00	13.33	44.19	-33.18**
P7xP8	14.33	23.67	22.13	-6.32	10.00	13.33	13.57	3.76
CD @ 5%	17.04				16.68			
CD @ 1%	22.69				22.22			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 85. Estimates of heterobeltiosis for yield (Kg) per plant under two irrigation regimes

Hybrids	IR 1				IR 2			
	Parents		Hybrid	Heterobeltiosis (%)	Parents		Hybrid	Heterobeltiosis (%)
	Female	Male			Female	Male		
P1xP2	1.68	1.89	2.17	3.04	1.24	2.44	2.13	-16.41
P1xP3	1.68	1.18	1.78	1.17	1.24	1.40	1.63	-6.11
P1xP4	1.68	2.32	3.61	60.11**	1.24	1.27	2.28	55.48**
P1xP5	1.68	3.15	2.87	-7.52	1.24	3.46	2.71	-18.51
P1xP6	1.68	8.56	7.18	-16.44	1.24	9.93	6.51	-34.34*
P1xP7	1.68	1.65	2.89	60.14**	1.24	0.59	1.53	31.77*
P1xP8	1.68	2.75	3.40	26.85	1.24	1.57	2.17	17.42
P2xP3	1.89	1.18	2.34	23.49	2.44	1.40	2.92	23.97
P2xP4	1.89	2.32	3.70	43.21**	2.44	1.27	3.09	34.16*
P2xP5	1.89	3.15	4.39	38.73*	2.44	3.46	5.16	50.10**
P2xP6	1.89	8.56	8.59	0.61	2.44	9.93	9.76	-0.44
P2xP7	1.89	1.65	3.02	52.79**	2.44	0.59	2.31	0.29
P2xP8	1.89	2.75	3.60	37.31*	2.44	1.57	3.14	33.12*
P3xP4	1.18	2.32	3.07	47.06**	1.40	1.27	2.41	52.58**
P3xP5	1.18	3.15	3.48	12.30	1.40	3.46	3.93	17.24
P3xP6	1.18	8.56	7.96	-7.09	1.40	9.93	8.71	-10.88
P3xP7	1.18	1.65	2.26	38.43*	1.40	0.59	1.55	13.18
P3xP8	1.18	2.75	2.91	14.15	1.40	1.57	2.38	50.85**
P4xP5	2.32	3.15	4.95	38.44*	1.27	3.46	4.03	16.95
P4xP6	2.32	8.56	8.79	1.89	1.27	9.93	8.11	-18.68
P4xP7	2.32	1.65	3.67	63.93**	1.27	0.59	1.59	28.58
P4xP8	2.32	2.75	4.80	68.06**	1.27	1.57	2.71	71.56**
P5xP6	3.15	8.56	7.40	-13.19	3.46	9.93	7.96	-20.11
P5xP7	3.15	1.65	3.81	22.61	3.46	0.59	2.71	-20.32
P5xP8	3.15	2.75	4.74	35.59*	3.46	1.57	4.01	17.49
P6xP7	8.56	1.65	8.08	-6.13	9.93	0.59	5.96	-40.10*
P6xP8	8.56	2.75	7.80	-9.39	9.93	1.57	5.84	-41.17**
P7xP8	1.65	2.75	2.64	-0.81	0.59	1.57	1.19	-23.28
CD @ 5%	29.23				30.26			
CD @ 1%	38.93				40.29			

* Significant at 0.05; ** Significant at 0.01; IR 1 - Normal Irrigation; IR 2 - Restricted Irrigation
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

(30, 45 and 60 DAT), disease severity index on vegetative parts (30, 45 and 60 DAT), disease severity index on flowering and fruiting parts (30, 45 and 60 DAT) and vector population (30, 45 and 60 DAT) had highly significant difference in treatments, parents and hybrids. The difference was highly significant in parents vs. hybrids in per cent plant survival (30, 45 and 60 DAT) and vector population (45 and 60 DAT). Among the yield parameters viz., number of fruits per plant, average fruit weight and plant yield, the difference was highly significant in treatments, parents and hybrids. Highly significant in parents vs. hybrids was observed for average fruit weight and plant yield (Table 86 to 89).

4.5.2 Analysis of variance for combining ability and genetic components of various characters

Analysis of variance for general (GCA) and specific (SCA) combining ability showed highly significant differences for all the morphological, growth, disease index and yield parameters. This indicates importance of both additivity and non-additivity in the inheritance of these characters (Table 86 to 89).

Variance due to SCA (V_s) was found to higher for all the growth parameters viz., plant height (45, 60 and 90 DAT), number of branches (45, 60 and 90 DAT), stem girth (45, 60 and 90 DAT) and number of pubescence (abaxial and adaxial). The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for all the morphological characters. Dominance variation was high for plant height (45, 60 and 90 DAT), number of branches (60 and 90 DAT), stem girth (45 and 90 DAT) and number of pubescence (abaxial and adaxial). Additive variance was found to be higher for number of branches (45 DAT) and stem girth (60 DAT). Ratio of additive to dominant variation was found to be less than unity in plant height (45, 60 and 90 DAT), number of branches (60 and 90 DAT), stem girth (45 and 90 DAT) and number of pubescence (abaxial and adaxial). It was more than unity for number of branches (45 DAT) and stem girth (60 DAT). Broad sense heritability was found to be high for all morphological characters (Table 90 and 91).

Among the growth parameters, viz., number of leaves (45, 60 and 90 DAT) and leaf area (45, 60 and 90 DAT), variance due to SCA was higher for number of leaves (45, 60 and 90 DAT) and leaf area (45 and 60 DAT) except for leaf area

Table 86. Analysis of variance for diallel, GCA and SCA effects for plant height, number of branches and stem girth in TyLCV tolerance trial

Source of Variation	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
Replication	8.47	26.83	24.37	11.50	62.32	15.09	75.15	361.61	2.16
Treatments	94.59**	769.01**	513.97**	15.40**	19.37**	30.22**	11.91**	20.58**	60.22**
Parents	71.37**	892.36**	631.89**	25.76**	10.33**	40.26**	18.27**	32.47**	74.93**
Hybrids	100.50**	760.16**	492.63**	12.90**	22.43**	28.70**	10.69**	17.35**	58.60**
Parents Vs. Hybrids	27.66*	144.43**	264.72**	10.42	0.15	1.06	0.23	24.39*	1.06
Error	5.96	5.51	3.81	3.80	2.83	0.68	0.79	6.07	2.63
GCA	39.99**	647.69**	459.42**	13.68**	14.01**	18.22**	4.64**	18.74**	49.69**
SCA	29.42**	458.50**	99.30**	3.00**	4.57**	8.04**	3.80**	3.89**	12.67**
Error	1.99	1.84	1.27	1.27	0.94	0.23	0.26	2.02	0.88

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Table 87. Analysis of variance for diallel, GCA and SCA effects for number of pubescence, number of leaves and leaf area in TyLCV tolerance trial

Source of Variation	Number of pubescence		Number of leaves			Leaf area (cm ²)		
	AB	AD	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
Replication	126.16	996.39	348.65	39.45	22.65	1436.67	923.54	31094.80
Treatments	42849.38**	180015.80**	412.77**	203.47**	230.58**	2322.46**	6278.41**	4045.49**
Parents	78282.76**	174667.50**	154.00**	304.49**	342.14**	2123.76**	7598.40**	5717.05**
Hybrids	42483.60**	183914.90**	143.80**	184.35**	206.32**	2321.62**	6075.56**	36.06.04**
Parents Vs. Hybrids	13641.14**	112178.20**	36.40	12.78	104.59**	3735.96**	2515.47**	4209.45*
Error	88.38	261.21	11.26	4.83	3.15	62.85	34.98	955.44
GCA	19097.68**	79590.14**	146.93**	159.41**	184.84**	1847.89**	6290.36**	4019.81**
SCA	13066.99**	55109.06**	22.76**	44.93**	49.87**	505.72**	1043.42**	680.67**
Error	29.46	87.07	3.76	1.61	1.05	20.95	11.66	318.48

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Table 88. Analysis of variance for diallel, GCA and SCA effects for Per cent plant survival and disease severity index on vegetative and fruiting parts in TyLCV tolerance trial

Source of Variation	Per cent plant survival			Disease Severity Index (V)			Disease Severity Index (F)		
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
Replication	3.74	9.39	71.57	1.64	0.86	0.97	0.15	0.37	0.86
Treatments	96.27**	942.91**	1986.36**	0.41**	1.98**	4.01**	0.50**	1.56**	4.25**
Parents	141.51**	1030.20**	3254.19**	0.36**	1.18**	3.94**	0.64**	1.28**	4.32**
Hybrids	80.95**	921.27**	1912.38**	0.44**	2.26**	4.09**	0.47**	1.65**	4.36**
Parents Vs. Hybrids	193.33**	916.38**	1408.86**	0.15	0.11	2.85**	0.19**	0.37**	0.82**
Error	1.99	6.92	6.43	0.10	0.10	0.04	0.01	0.03	0.04
GCA	41.41**	510.26**	1204.65**	0.22**	1.36**	2.81**	0.25**	0.92**	2.36**
SCA	29.76**	265.32**	526.48**	0.12**	0.48**	0.97**	0.14**	0.41**	1.18**
Error	0.66	2.31	2.14	0.03	0.03	0.01	0.00	0.01	0.01

V - Vegetative parts; F - Flowering and fruiting parts; DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Table 89. Analysis of variance for diallel, GCA and SCA effects for vector population and yield parameters in TyLCV tolerance trial

Source of Variation	Vector Population			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
	30 DAT	45 DAT	60 DAT			
Replication	1.77	7.27	38.16	4700.88	95.99	8.07
Treatments	20.03**	50.67**	457.16**	1927.31**	482.27**	2.33**
Parents	16.17**	32.48**	142.53**	2894.76**	607.08**	2.58**
Hybrids	21.75**	57.04**	166.45**	1747.53**	459.54**	2.28**
Parents Vs. Hybrids	0.49	5.96*	8.72*	9.34	222.41**	2.20**
Error	0.42	0.95	1.84	97.46	7.94	0.16
GCA	10.33**	21.97**	89.85**	2118.36**	91.96**	2.08**
SCA	5.76**	15.63**	43.02**	273.46**	177.96**	0.45**
Error	0.14	0.39	0.64	32.49	2.47	0.05

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Table 90. Genetic components of variation for plant height, number of branches and stem girth in TyLCV trial

Source of Variation	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
V_g	3.80	64.59	45.82	1.24	1.31	1.80	0.44	1.67	4.88
V_s	27.43	156.66	98.03	1.73	3.63	7.81	3.54	1.86	11.79
V_g/V_s	0.14	0.41	0.47	0.72	0.36	0.23	0.12	0.90	0.41
V_A	7.60	129.17	91.63	2.48	2.61	3.60	0.88	3.34	9.76
V_D	27.43	156.66	98.03	1.73	3.63	7.81	3.54	1.86	11.79
V_A/V_D	0.28	0.82	0.93	1.44	0.72	0.46	0.25	1.79	0.83
h^2 NS	0.21	0.45	0.48	0.45	0.36	0.31	0.19	0.46	0.44
h^2 BS	0.95	0.99	0.99	0.77	0.87	0.98	0.94	0.72	0.96

DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h^2 -heritability; NS- narrow sense; BS- broad sense

Table 91. Genetic components of variation for number of pubescence, number of leaves and leaf area in TyLCV trial

Source of Variation	Number of pubescence		Number of leaves			Leaf area (cm ²)		
	AB	AD	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
V _g	1906.82	7950.31	14.32	15.78	18.38	182.69	627.87	370.13
V _s	13037.53	55021.99	19.00	43.32	48.82	484.77	1031.76	362.19
V _g /V _s	0.15	0.14	0.75	0.36	0.38	0.38	0.61	1.02
V _A	3813.64	15900.61	28.64	31.56	36.76	365.39	1255.74	740.27
V _D	13037.53	55021.99	19.00	43.32	48.82	484.77	1031.76	362.19
V _A /V _D	0.29	0.29	1.51	0.73	0.75	0.75	1.22	2.04
h ² NS	0.23	0.22	0.56	0.41	0.42	0.42	0.55	0.52
h ² BS	1.00	1.00	0.93	0.98	0.99	0.98	1.00	0.78

DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h² -heritability; NS- narrow sense; BS- broad sense

(90 DAT) which had higher variance due to GCA effects. The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for number of leaves (45, 60 and 90 DAT) and leaf area (45 and 60 DAT) except for leaf area (90 DAT). Additive variance was found to high for number of leaves (45 DAT) and leaf area (60 and 90 DAT). Dominant variance was found to higher for number of leaves (60 and 90 DAT) and leaf area (45 DAT). Ratio of additive to dominant variance was found to less than unity for number of leaves (60 and 90 DAT) and leaf area (45 DAT). Heritability (broad sense) was found to be higher for all the growth parameters (Table 91).

Variance due to SCA was higher for all the disease index parameters *viz.*, per cent plant survival (30, 45 and 60 DAT), disease severity index on vegetative parts number of leaves (60 and 90 DAT) and leaf area (45 DAT), disease severity index on flowering and fruiting parts number of leaves (60 and 90 DAT) and leaf area (45 DAT) and vector population number of leaves (60 and 90 DAT) and leaf area (45 DAT). The genetic component ratio of GCA to SCA (V_g/V_s) was less than unity for all the disease index parameters. Dominant variance was high for all the disease index parameters. Ratio of additive to dominant variance was found to less than unity for all the disease index parameters. Broad sense heritability was found to be high (Table 92 and 93).

SCA variance was high compared to GCA variance for all the yield parameters *viz.*, number of fruits per plant, average fruit weight and yield per plant. Genetic component ratio (V_g/V_s) was less than unity. Dominant variance was found to be high and ratio of additive to dominant variance was less than unity for average fruit weight. Additive variance was found to be high and ratio of additive to dominant variance was more than unity for number of fruits and yield per plant. Broad sense heritability was found to be high in both conditions (Table 93).

4.5.3 Combining Ability analysis for TyLCV tolerance

4.5.3.1 Morphological parameters

General and specific combining ability estimates of parents and hybrids for morphological parameters are presented in Table 94 to 97.

Out of eight parents, two, three and three parents had significant positive GCA for plant height at 45, 60 and 90 DAT respectively. L 01942 may be considered as

Table 92. Genetic components of variation for Per cent plant survival and disease severity index on vegetative and fruiting parts for in TyLCV trial

Source of Variation	Per cent plant survival			Disease Severity Index (V)			Disease Severity Index (F)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
V _g	4.07	50.80	120.25	0.02	0.13	0.28	0.03	0.09	0.24
V _s	29.10	263.01	524.34	0.08	0.45	0.96	0.14	0.40	1.17
V _g /V _s	0.14	0.19	0.23	0.23	0.30	0.29	0.18	0.23	0.20
V _A	8.15	101.59	240.50	0.04	0.27	0.56	0.05	0.18	0.47
V _D	29.10	263.01	524.34	0.08	0.45	0.96	0.14	0.40	1.17
V _A /V _D	0.28	0.39	0.46	0.47	0.59	0.58	0.35	0.45	0.40
h ² NS	0.22	0.28	0.31	0.25	0.36	0.37	0.26	0.31	0.29
h ² BS	0.98	0.99	1.00	0.78	0.96	0.99	0.98	0.99	0.99

V - Vegetative parts; F - Flowering and fruiting parts; DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h² -heritability; NS- narrow sense; BS- broad sense

Table 93. Genetic components of variation for vector population and yield parameters in TyLCV trial

Source of Variation	Vector Population			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
	45 DAT	60 DAT	90 DAT			
V_g	1.02	2.17	8.92	208.59	8.93	0.20
V_s	5.62	15.30	42.41	240.97	175.31	0.40
V_g/V_s	0.18	0.14	0.21	0.87	0.05	0.51
V_A	2.04	4.33	17.85	417.17	17.86	0.41
V_D	5.62	15.30	42.41	240.97	175.31	0.40
V_A/V_D	0.36	0.28	0.42	1.73	0.10	1.02
h^2 NS	0.26	0.22	0.29	0.60	0.09	0.47
h^2 BS	0.98	0.98	0.99	0.95	0.99	0.94

DAT - Days after transplanting; V_g - gca variance; V_s - sca variance; V_A - additive variance; V_D - dominance variance; h^2 -heritability; NS- narrow sense; BS- broad sense

Table 94. GCA estimates of tomato parents under TyLCV trial for plant height, number of branches and stem girth

Parents	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 01942	0.02	15.17**	13.23**	1.79**	1.77**	1.55**	-0.95**	1.88**	3.40**
L 06052	-1.63**	5.80**	6.37**	1.57**	1.24**	0.96**	0.44**	1.72**	2.77**
L 02079	-3.68**	-8.67**	-5.80**	0.55	-0.40	-0.62**	0.76**	0.58	1.09**
LA 3913	3.24**	-3.09**	-4.33**	-0.47	0.40	0.62**	0.83**	0.20	-0.95**
TLB 133	0.94*	5.18**	2.42**	-0.79*	0.62*	1.55**	0.37*	-0.06	0.31
L 06231	0.05	-6.95**	-4.68**	-0.36	-1.45**	-2.04**	-0.68**	-1.27**	-2.03**
L 02692	0.42	-2.68**	-3.59**	-0.93**	-1.11**	-0.83**	-0.46**	-1.58**	-1.11**
BL 1188	0.47	-4.77**	-3.62**	-1.34**	-1.06**	-1.19**	-0.31*	-1.46**	-2.84**
SE	0.63	0.61	0.50	0.50	0.43	0.21	0.23	0.64	0.42
CD @ 5%	1.49	1.43	1.19	1.19	1.03	0.50	0.54	1.50	0.99
CD @ 1%	2.21	1.12	1.76	1.76	1.52	0.76	0.80	2.23	1.47

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Table 95. SCA estimates of tomato parents under TyLCV trial for plant height and number of branches

Hybrids	Plant height (cm)			Number of branches		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-1.51	-10.86**	-10.42**	1.55	0.70	-1.13*
P1xP3	0.83	0.79	1.81	0.44	-1.87*	-1.63**
P1xP4	4.42**	6.07**	3.47**	0.32	-0.78	-1.08*
P1xP5	-2.44	-0.53	-0.10	1.16	2.80**	3.86**
P1xP6	1.09	5.44**	3.34**	-1.11	-0.14	2.06**
P1xP7	-1.08	-1.13	1.14	-1.16	1.50	0.00
P1xP8	-2.75*	2.27	3.04**	4.20**	3.80**	2.35**
P2xP3	5.92**	19.11**	14.19**	-1.20	0.55	1.25**
P2xP4	-0.19	13.37**	8.44**	-1.82	0.33	2.31**
P2xP5	1.33	0.57	2.86**	-0.88	-1.18	-0.02
P2xP6	2.24	14.01**	11.56**	-1.63	3.30**	3.11**
P2xP7	-8.57**	-23.67**	-15.69**	1.49	-2.03*	-3.96**
P2xP8	-2.90*	-16.00**	-15.02**	-0.16	-2.04*	-3.49**
P3xP4	-7.59**	-6.64**	-2.82*	0.67	-0.22	-0.57
P3xP5	-4.31**	-14.36**	-8.81**	-0.08	0.15	-3.63**
P3xP6	3.51*	-0.18	0.51	0.51	-1.08	-0.73
P3xP7	1.35	-1.35	-0.87	0.99	1.21	2.33**
P3xP8	-1.70	-6.60**	-1.89	1.93	0.40	2.10**
P4xP5	0.52	-3.20**	-8.51**	-2.00	-2.99**	-2.75**
P4xP6	9.51**	6.72**	1.87	0.34	0.78	2.10**
P4xP7	9.01**	2.12	0.88	0.72	3.10**	0.80
P4xP8	2.54	9.53**	-0.84	0.80	3.67**	6.97**
P5xP6	-1.07	-13.75**	-8.14**	-1.39	0.94	0.78
P5xP7	-0.45	27.45**	26.06**	1.73	-1.06	-2.27**
P5xP8	-1.53	24.47**	24.69**	0.69	-1.54	-1.82**
P6xP7	-7.56**	-12.95**	-3.08**	1.75	-2.52**	-2.60**
P6xP8	10.72**	7.40**	-0.01	-2.04	-3.19**	-3.07**
P7xP8	-1.78	-8.11**	-3.83**	-1.20	-1.89*	0.21
SE	1.89	1.82	1.51	1.51	1.30	0.64
CD @ 5%	3.88	3.73	3.10	3.10	2.67	1.31
CD @ 1%	5.24	5.04	4.19	4.19	3.61	1.77

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 96. SCA estimates of tomato parents under TyLCV trial for stem girth and number of pubescence

Hybrids	Stem girth (cm)			Number of pubescence	
	45 DAT	60 DAT	90 DAT	AB	AD
P1xP2	-2.06**	-3.37*	-2.78**	-48.17**	-16.83
P1xP3	-1.24*	-0.43	0.15	-17.66**	-61.73**
P1xP4	0.13	1.23	1.68	132.00**	311.58**
P1xP5	2.25**	2.80*	5.25**	95.77**	191.31**
P1xP6	-0.05	-0.25	-3.32**	-64.60**	-94.11**
P1xP7	-0.73	0.91	-2.84**	-99.09**	-157.25**
P1xP8	1.77**	2.69*	5.33**	36.47**	12.88**
P2xP3	0.54	1.51	0.98	145.89**	308.13**
P2xP4	0.03	-1.76	1.16	83.59**	115.10**
P2xP5	-1.06*	-1.99	-4.30**	-73.34**	-150.88**
P2xP6	1.04*	2.99*	0.52	-32.54**	-84.36**
P2xP7	-0.09	0.50	1.20	-100.07**	-203.55**
P2xP8	0.93	0.86	1.58	78.71**	235.27**
P3xP4	-1.86**	-1.79	-3.28**	-159.14**	-275.59**
P3xP5	-1.81**	-0.76	-3.14**	-140.01**	-244.86**
P3xP6	1.49**	2.65*	3.06**	53.83**	68.50**
P3xP7	2.30**	1.75	3.36**	62.95**	72.14**
P3xP8	-0.50	-0.39	-2.47**	-64.78**	-154.09**
P4xP5	1.39**	-0.55	2.01*	146.16**	297.34**
P4xP6	0.78	0.39	-1.58	92.95**	232.95**
P4xP7	0.51	2.15	-0.89	56.79**	164.63**
P4xP8	3.65**	2.64	3.01**	81.25**	157.57**
P5xP6	-1.21*	-2.78*	-7.51**	-171.69**	-316.65**
P5xP7	-4.87**	-0.17	2.93**	7.21	56.90**
P5xP8	-1.21*	1.08	5.25**	44.37**	-5.27
P6xP7	-0.72	-0.66	1.41	-37.43**	-168.58**
P6xP8	1.00*	0.59	2.10*	197.78**	426.78**
P7xP8	-1.12*	-2.83*	-7.35**	-138.98**	-234.97**
SE	0.69	1.91	1.26	7.28	12.52
CD @ 5%	1.41	3.92	2.58	14.94	25.69
CD @ 1%	1.91	5.29	3.48	20.18	34.69

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 97. GCA estimates of tomato parents under TyLCV trial for number of pubescence, number of leaves and leaf area

Parents	Number of pubescence		Number of leaves			Leaf area (cm ²)		
	AB	AD	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 01942	70.88**	158.15**	5.89**	5.56**	6.97**	23.92**	45.69**	37.69**
L 06052	31.85**	27.57**	3.84**	4.52**	4.13**	11.73**	28.85**	19.59**
L 02079	-16.57**	-43.76**	1.43*	-0.20	-0.33	-5.03**	-8.18**	-10.77*
LA 3913	34.31**	82.44**	1.08	0.81*	0.43	2.92*	-9.84**	-13.95*
TLB 133	3.31*	12.98**	-0.02	1.95**	2.05**	5.78**	5.43**	9.10
L 06231	-45.96**	-81.41**	-3.83**	-4.42**	-5.04**	-13.84**	-22.77**	-11.81*
L 02692	-19.82**	-44.28**	-3.86**	-5.21**	-3.76**	-12.93**	-18.17**	-18.91**
BL 1188	-58.00**	-111.69**	-4.54**	-3.01**	-4.44**	-12.56**	-21.01**	-10.94*
SE	2.43	4.17	0.87	0.57	0.46	2.05	1.53	7.98
CD @ 5%	5.74	9.97	2.05	1.34	1.08	4.84	3.61	18.87
CD @ 1%	8.50	14.60	3.03	1.99	1.60	7.16	5.34	27.93

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01; AB - Abaxial; AD - Adaxial

good general combiner, TLB 133 and L06052 may be considered as average general combiners for plant height. Two, five and five parents each had significant negative GCA for this trait. Out of 28 hybrids, 6, 10 and 9 hybrids had positive significant SCA for plant height at 45, 60 and 90 DAT respectively. P2 x P3, P1 x P4, P6 x P8, P4 x P6, P2 x P6 and P1 x P6 may be considered as good specific combiners for this trait.

Two, three and four parents show significant positive GCA for number of branches at 45, 60 and 90 DAT respectively. L 01942 may be considered as good general combiner and L 06052 as average general combiner for this trait. Three, three and four parents showed significant negative GCA for this trait. Out of 28 hybrids, 1, 5 and 10 hybrids show significant SCA for this trait. P1 x P8, P4 x P 8, P1 x P5 and P2 x P6 may be considered as good specific combiners for this trait.

For stem girth, four, two and three parents had significant positive GCA at 45, 60 and 90 DAT respectively. L 06052 may be considered as good general combiner, L 01942 and L 02079 as average general combiner and LA 3913 as poor general combiner for this trait. Out of 28 hybrids, 8, 4 and 9 hybrids had significant positive SCA at 45, 60 and 90 DAT respectively. P1, P5, P1 x P8, P3 x P6, P2 x P6, P4 x P8, P3 x P7 and P6 x P8 may be considered as good specific combiners for this trait.

Out of eight parents, four parents each had significant positive GCA for number of pubescence on adaxial and adaxial layer respectively. L 01942 may be considered as good general combiner, L 06052 and LA 3913 as average general combiners and TLB 133 as poor general combiner for this trait. Among the 28 hybrids, 14 hybrids each had significant positive SCA for number of pubescence on adaxial and adaxial layer respectively. Among these hybrids, P6 x P8, P1 x P4, P2 x P3, P4 x P5 and P2 x P8 had high significant positive SCA effects.

4.5.3.2 Growth parameters

General and specific combining ability estimates of parents and hybrids for growth parameters are presented in Table 97 and 98.

Among the eight parents, three, four and three had significant positive GCA for number of leaves at 45, 60 and 90 DAT respectively. L 01942 may be considered

Table 98. SCA estimates of tomato parents under TyLCV trial for number of leaves and leaf area

Hybrids	Number of leaves			Leaf area (cm ²)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	-5.31**	-10.21**	-9.67**	-26.48**	-42.44**	-16.73
P1xP3	-3.34	-4.26**	-5.69**	-6.04	-3.09	-16.16
P1xP4	1.04	-5.15**	4.02**	17.72**	10.27**	3.56
P1xP5	8.41	2.86	9.80	33.16**	32.81**	-0.92
P1xP6	-1.52**	4.20*	1.19**	2.68	-10.04**	19.82
P1xP7	5.30**	11.00**	-1.71	7.74	0.26	-5.95
P1xP8	4.79*	4.22**	3.02**	-0.30	24.63**	21.61
P2xP3	2.23	2.71*	9.91**	55.95**	63.27**	39.40*
P2xP4	0.15	0.29	8.22**	10.05*	30.88**	18.83
P2xP5	-4.99**	1.93	-2.29*	-7.42	-12.15**	19.64
P2xP6	7.83**	16.88**	5.32**	26.05**	41.66**	14.59
P2xP7	-1.68	-5.49**	-9.84**	-30.21**	-39.36**	-27.43
P2xP8	2.69	-7.95**	1.10	-7.44	-32.32**	-25.66
P3xP4	-7.68**	-4.05**	-8.62**	-28.39**	-28.47**	27.96
P3xP5	2.20	4.49**	-10.03**	-27.72**	-33.55**	-25.16
P3xP6	4.21*	-0.21	4.83**	15.26**	13.00**	-16.97
P3xP7	5.97**	4.68**	6.86**	6.23	9.54**	-13.58
P3xP8	-1.80	3.22**	-3.06**	-12.50**	-20.02**	-2.67
P4xP5	-3.85*	-12.63**	0.56	10.55*	0.74	-24.35
P4xP6	0.84	1.93	5.39**	14.99**	-1.95	16.58
P4xP7	6.65**	7.53**	2.58**	18.44**	6.72*	-5.09
P4xP8	3.08	3.43**	8.36**	19.05**	13.86**	13.45
P5xP6	-2.79	5.25**	-7.99**	-13.77**	-38.57**	-17.45
P5xP7	1.65	-1.72	4.29**	18.87**	57.99**	59.50**
P5xP8	-1.97	-0.87	4.67**	8.58*	67.36**	50.65**
P6xP7	-4.57*	-5.82**	-7.22**	-19.87**	-5.82	-24.63
P6xP8	1.62	-7.96**	7.58**	22.25**	9.95**	-12.27
P7xP8	-10.46**	-3.15*	-6.84**	-19.40**	-42.94**	23.88
SE	2.60	1.70	1.38	6.14	4.58	23.94
CD @ 5%	5.33	3.49	2.82	12.60	9.40	49.13
CD @ 1%	7.20	4.72	3.81	17.01	12.69	66.34

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

as good general combiner, L 06052 as average general combiners and TLB 133 as poor general combiner for this trait. Out of the 28 hybrids, 7, 12 and 14 hybrids had significant positive SCA for this trait. P2 x P 6, P4 x P 7, P3 x P7, P1 x P5, P1 x P8, P1 x P7, P4 x P8 and P2 x P3 may be considered as good specific combiners for this trait.

Among eight parents four, three and two parents had significant positive GCA for leaf area at 45, 60 and 90 DAT respectively. L 01942 may be considered as good general combiner, L 06052 as average general combiners and TLB 133 as poor general combiner for this trait. Out of 28 hybrids, 13 hybrids each had significant positive SCA for this trait. P6 x P8, P4 x P5, P1 x P5, P4 x P8, P3 x P7, P3 x P6 and P1 x P8 may be considered as good specific combiners for this trait.

4.5.3.3 Disease index parameters

General and specific combining ability estimates of parents and hybrids for growth parameters are presented in Tables 99 to 102. Combining ability towards negative direction is preferred for these characters except for per cent plant survival.

Out of the eight parents, two, three and three had significant positive GCA at 30 and 45 DAT and five parents had the same at 60 DAT for per cent plant survival. L 01942 may be considered as good general combiner, TLB 133 and L 06052 as average general combiners for this trait. Out of 28 hybrids, 15 hybrids each had significant negative SCA at 30 and 45 DAT and 13 had the same at 60 DAT for this trait. P2 x P3, P6 x P8, P4 x P8, P2 x P4, P5 x P7, P1 x P6, P5 x P8, P1 x P3, P4 x P5 and P2 x P6 may be considered as good specific combiners for this trait.

For disease severity index on vegetative parts, two parents had significant negative GCA at 30 DAT and three parents each had the same at 45 and 60 DAT respectively. L 01942 may be considered as good general combiner, TLB 133 as average general combiner and L 06052 as poor general combiner for this trait. Out of the 28 hybrids, two, seven and ten hybrids had significant negative SCA for this trait. P2 x P3, P2 x P6, P5 x P7, P5 x P8, P2 x P4, P4 x P7 and P4 x P6 may be considered as good specific combiners for this trait.

Table 99. GCA estimates of tomato parents under TyLCV trial for Per cent plant survival and disease severity index on vegetative and fruiting parts

Parents	Per cent plant survival			Disease Severity Index (V)			Disease Severity Index (F)		
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
L 01942	3.60**	12.65**	21.64**	-0.21**	-0.74**	-1.04**	-0.24**	-0.58**	-0.98**
L 06052	0.62*	1.94**	6.58**	0.00	-0.30**	-0.35**	0.00	-0.14**	-0.30**
L 02079	-2.53**	-8.80**	-8.85**	0.22**	0.24**	0.48**	0.23**	0.32**	0.38**
LA 3913	-0.05	0.85	-0.93*	-0.03	0.09	0.04	-0.04*	0.05	0.16**
TLB 133	1.96**	6.65**	6.44**	-0.18**	-0.14*	-0.28**	-0.17**	-0.23**	-0.28**
L 06231	-2.04**	-6.82**	-9.48**	0.13*	0.28**	0.46**	0.18**	0.29**	0.42**
L 02692	-0.66**	-4.60**	-6.63**	0.12*	0.25**	0.33**	0.05*	0.17**	0.26**
BL 1188	-0.92**	-1.87**	-8.78**	-0.05	0.31**	0.36**	-0.02	0.13**	0.34**
SE	0.36	0.68	0.65	0.08	0.08	0.05	0.03	0.04	0.05
CD @ 5%	0.86	1.61	1.55	0.20	0.20	0.12	0.07	0.10	0.13
CD @ 1%	1.27	2.38	2.29	0.29	0.29	0.18	0.10	0.14	0.19

V - Vegetative parts; F- Flowering and fruiting parts; DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01; V - Vegetative parts;
F - Flowering and fruiting parts

Table 100. SCA estimates of tomato parents under TyLCV trial for Per cent plant survival and disease severity index on vegetative parts

Hybrids	Per cent plant survival			Disease severity index (V)		
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
P1xP2	-0.37	0.51	-0.36	0.08	0.27	0.52**
P1xP3	3.29**	10.09**	12.49**	0.03	-0.10	-0.45**
P1xP4	1.66*	3.04*	6.59**	-0.09	-0.33	-0.45**
P1xP5	-0.75	-2.98*	0.09	0.09	0.02	0.13
P1xP6	4.10**	13.60**	17.03**	-0.27	-0.37*	-0.80**
P1xP7	-2.03*	1.67	-4.69*	-0.20	-0.09	-0.15
P1xP8	-2.65**	-8.12**	-0.63	0.25	-0.13	0.30**
P2xP3	7.31**	24.67**	32.70**	-0.53**	-0.89**	-1.48**
P2xP4	4.56**	14.21**	24.23**	-0.27	-0.74**	-0.99**
P2xP5	1.97*	4.87**	-1.91	-0.12	0.54**	0.31**
P2xP6	2.20**	14.28**	13.38**	-0.41*	-0.58**	-0.96**
P2xP7	-13.14**	-44.80**	-55.96**	0.94**	1.31**	2.41**
P2xP8	-4.11**	-12.30**	-6.94**	0.22	-0.12	0.45**
P3xP4	-4.78**	-12.68**	-18.65**	0.16	0.85**	1.54**
P3xP5	-10.01**	-21.73**	-30.36**	0.27	0.45*	1.36**
P3xP6	2.70**	0.72	2.65	0.11	-0.18	-0.69**
P3xP7	1.09	-1.79	-0.10	0.12	-0.16	-0.53**
P3xP8	1.21	-6.72**	-14.96**	0.29	0.83**	0.43**
P4xP5	3.03**	9.91**	24.32**	-0.07	-0.69**	-0.74**
P4xP6	6.47**	19.16**	20.50**	-0.38*	-0.08	-0.56**
P4xP7	0.13	9.96**	10.83**	-0.33	-0.61**	-0.73**
P4xP8	5.04**	13.53**	17.73**	-0.18	0.16	-0.14
P5xP6	-3.47**	-5.65**	-32.93**	-0.12	1.41**	1.43**
P5xP7	4.41**	8.83**	15.46**	-0.20	-1.13**	-1.62**
P5xP8	3.66**	3.44*	18.94**	0.01	-1.15**	-1.29**
P6xP7	-2.59**	-19.04**	-20.95**	0.57**	0.29	0.01
P6xP8	6.34**	13.90**	25.86**	-0.16	-0.34	-0.33**
P7xP8	4.75**	13.02**	-0.32**	-0.32	1.07**	0.57**
SE	1.09	2.04	1.96	0.25	0.25	0.16
CD @ 5%	2.24	4.18	4.03	0.51	0.51	0.32
CD @ 1%	3.03	5.65	5.44	0.69	0.68	0.44

V - Vegetative parts; DAT - Days after transplanting; * Significant at 0.05;

** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 101. SCA estimates of tomato parents under TyLCV trial for disease severity index on fruiting parts and vector population

Hybrids	Disease severity index (F)			Vector Population		
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
P1xP2	0.15*	0.21*	0.25*	0.36	0.90	1.67*
P1xP3	-0.18**	-0.22*	-0.22*	0.03	-0.79	-1.37
P1xP4	-0.10	-0.35**	-0.70**	-0.96**	-2.50**	-4.68**
P1xP5	0.02	-0.01	-0.16	0.14	-1.95**	-2.88**
P1xP6	-0.27**	-0.15	-0.12	-0.63	2.20**	1.87*
P1xP7	-0.10	-0.08	0.25*	-1.32**	0.04	0.49
P1xP8	0.33**	0.18*	-0.08	1.38**	-0.24	-0.45
P2xP3	-0.60**	-1.05**	-1.57**	-3.95**	-5.16**	-9.69**
P2xP4	-0.35**	-0.74**	-1.31**	-2.27**	-4.23**	-7.43**
P2xP5	-0.09	0.30**	0.57**	0.33	3.26**	3.33**
P2xP6	-0.42**	-0.42**	-0.07	-2.91**	-1.65**	-0.51
P2xP7	1.11**	1.58**	2.19**	6.22**	6.91**	12.77**
P2xP8	0.37**	0.15	-0.25*	1.03**	-0.73	-1.49*
P3xP4	0.50**	0.89**	1.11**	2.27**	7.53**	11.35**
P3xP5	0.55**	0.83**	1.48**	1.36**	3.26**	9.99**
P3xP6	-0.18**	-0.25**	-0.27*	0.45	-2.35**	-3.90**
P3xP7	-0.07	-0.12	-0.10	0.78*	-1.31*	-2.69**
P3xP8	0.11	0.70**	1.24**	3.30**	5.20**	6.86**
P4xP5	-0.15*	-0.60**	-1.27**	-1.31**	-5.62**	-10.27**
P4xP6	-0.38**	-0.41**	-0.66**	-1.62**	0.31	-2.39**
P4xP7	-0.22**	-0.46**	-0.42**	-2.55**	-2.27**	-3.03**
P4xP8	-0.18**	-0.05	-0.26*	-0.48	0.01	-2.79**
P5xP6	-0.07	0.73**	1.80**	0.15	5.55**	9.65**
P5xP7	-0.20**	-0.85**	-1.32**	-1.84**	-1.55**	-2.93**
P5xP8	-0.14*	-0.80**	-1.37**	-0.68	-2.86**	-3.23**
P6xP7	0.28**	0.43**	0.78**	4.05**	1.50**	2.08**
P6xP8	-0.19**	-0.69**	-1.48**	-2.69**	-6.48**	-9.73**
P7xP8	-0.17**	0.37**	0.66**	0.33	6.53**	5.15**
SE	0.08	0.12	0.16	0.50	0.76	1.05
CD @ 5%	0.17	0.25	0.33	1.03	1.55	2.15
CD @ 1%	0.23	0.34	0.44	1.39	2.09	2.91

F - Flowering and fruiting parts; DAT - Days after transplanting; * Significant at 0.05;
 ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
 P7 - L 02692; P8 - BL 1188

Table 102. GCA estimates of tomato parents under TyLCV trial for vector population and yield parameters

Parents	Vector Population			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
	30 DAT	45 DAT	60 DAT			
L 01942	-1.53**	-2.97**	-6.12**	28.00**	-1.38**	0.88**
L 06052	-0.10	-1.21**	-2.46**	11.24**	-1.78**	0.31**
L 02079	1.54**	0.13**	2.36**	-6.87**	-3.94**	-0.38**
LA 3913	-0.08	0.32	0.48*	-3.25	3.89**	0.11
TLB 133	-1.09**	-0.14	-0.45	7.37**	-0.32	0.19**
L 06231	0.95**	1.38**	2.41**	-14.57**	1.52**	-0.35**
L 02692	0.57**	0.17	1.44**	-9.00**	-2.48**	-0.37**
BL 1188	-0.26*	1.12**	2.34**	-12.93**	4.48**	-0.39**
SE	0.17	0.25	0.35	2.55	0.73	0.10
CD @ 5%	0.39	0.60	0.83	6.03	172.00	0.25
CD @ 1%	0.58	0.88	1.23	8.92	2.55	0.36

DAT - Days after transplanting * Significant at 0.05; ** Significant at 0.01

Out of the eight parents, three parents each had significant negative GCA at 30 and 60 DAT and four parents had the same at 45 DAT for disease severity index on flowering and fruiting parts. L 01942 may be considered as good general combiner, TLB 133 as average general combiner and L 06052 as poor general combiner for this trait. Out of 28 hybrids, six hybrids had significant negative SCA at 30 DAT and ten hybrids each had the same at 45 and 60 DAT. Hybrids with most proffered SCA are P2 x P3, P5 x P8, P5 x P7, P2 x P4, P6 x P8 and P4 x P5.

Three parents had significant negative GCA at 30 DAT and two each had the same at 45 and 60 DAT for vector population. L 01942 may be considered as good general combiner and L 06052 as average general combiner for this trait. Out of 28 hybrids, 8, 9 and 10 hybrids had significant negative SCA for this trait at 30, 45 and 60 DAT. Hybrids with most proffered SCA are P2 x P3, P4 x P5, P6 x P8, P2 x P4 and P4 x P7.

4.5.3.4 Yield parameters

General and specific combining ability estimates of parents and hybrids for yield parameters are presented in Table 102 and 103.

Three parents had significant positive GCA for number of fruits. L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for this trait. Out of 28 hybrids, seven had significant positive SCA for this trait. P2 x P4, P4 x P8, P1 x P8, P5 x P8 and P2 x P6 may be considered as good specific combiners for this trait.

Three parents had significant positive GCA for average fruit weight. L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for this trait. Fifteen hybrids had significant positive SCA for this trait. P4 x P7, P5 x P6, P4 x P8, P6 x P8, P3 x P4, P1 x P7 and P2 x P3 may be considered as good specific combiners for this trait.

Three parents had significant positive GCA for yield per plant. L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for this trait. P2 x P6, P2 x P3, P4 x P5, P4 x P7, P1 x P7 and P1 x P4 may be considered as good specific combiners for this trait.

Table 103. SCA estimates of tomato parents under TyLCV trial for yield parameters

Hybrids	Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
P1xP2	-14.91**	-2.02	-719.00**
P1xP3	-6.54	-0.66	-0.38
P1xP4	-2.83	7.15**	0.70**
P1xP5	7.85	-4.05*	-0.12
P1xP6	7.91	-5.56**	-0.20
P1xP7	-6.43	13.36**	0.77**
P1xP8	18.96**	11.23**	-0.04
P2xP3	12.23*	12.77**	1.33**
P2xP4	31.95**	10.04**	0.21
P2xP5	3.46	-5.19**	-0.28
P2xP6	15.54**	11.98**	1.47**
P2xP7	-28.68**	-8.65**	-1.23**
P2xP8	-17.05**	9.67**	0.13
P3xP4	-2.94	13.37**	-0.76**
P3xP5	-26.18**	11.29**	-0.30
P3xP6	-8.59	7.41**	0.00
P3xP7	8.95	-1.06	0.19
P3xP8	-4.00	-9.34**	-0.29
P4xP5	11.22*	5.97**	1.12**
P4xP6	0.11	-4.47**	-0.20
P4xP7	-14.03*	33.70**	0.85**
P4xP8	28.07**	18.92**	-0.02
P5xP6	-16.40**	21.80**	0.40
P5xP7	8.49	-3.23*	0.05
P5xP8	16.09**	-12.05**	0.07
P6xP7	-7.65	-8.87**	-0.57*
P6xP8	-7.35	16.68**	0.36
P7xP8	-3.19	-11.63**	-0.38
SE	7.65	2.18	0.31
CD @ 5%	15.69	4.48	0.64
CD @ 1%	21.19	6.05	0.86

* Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

4.5.4 Gene action for TyLCV tolerance traits using diallel analysis

4.5.4.1 Morphological parameters

Variance due to additive effects of genes (D) for plant height was significant at 60 and 90 DAT. Variance due to dominance effect (H_1), proportion of dominance variance (H_2) were significant at all the three stages. Mean F_r values were non-significant but was positive. The magnitude of H_1 and H_2 was higher than D at all the stages. Sum of dominance over all loci and environment component (E) were found to be non-significant at all stages for this trait. Mean degree of dominance was ranged from 1.40 to 2.35 during 45 to 90 DAT. Proportion of genes with positive and negative effect was ranged from 0.17 to 0.23 during 45 to 90 DAT and the highest value was at 90 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.04 to 0.11 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.05 to 0.49 (Table 104).

Variance due to additive effects of genes for number of branches was significant at 45 and 90 DAT. Variance due to dominance effect (H_1), proportion of dominance variance (H_2) were significant at all the three stages. Mean F_r values were non-significant but was positive at 45 and 90 DAT. The magnitude of H_1 and H_2 was higher than D at all the stages. Sum of dominance over all loci and environment component (E) were found to be non-significant at all stages for this trait. Mean degree of dominance was ranged from 1.23 to 2.91 during 45 to 90 DAT. Proportion of genes with positive and negative effect was ranged from 0.16 to 0.21 during 45 to 90 DAT and the highest value was at 60 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from -0.05 to 0.16 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.34 to 0.46 (Table 104).

Variance due to additive effects of genes for stem girth was significant at all stages. Variance due to dominance effect (H_1), proportion of dominance variance (H_2) was significant at 45 and 90 DAT. Only H_2 was significant at 60 DAT. Mean F_r value was significant and positive at 45 DAT. The magnitude of H_1 and H_2 was higher than

Table 104. Genetic components of variations of tomato parents under TyLCV trial for plant height, number of branches and stem girth

Genetic components	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
D (Additive Effect)	25.11	295.42*	209.17*	7.25*	1.95	13.06*	5.14*	5.51*	24.10*
F (Mean F _r over arrays)	47.30	108.42	58.79	5.76	-1.90	14.33	8.93*	-2.02	9.92
H ₁ (Dominance Effect)	138.87*	673.02*	408.23*	10.99*	16.45*	36.55*	16.39*	1.77	51.90*
H ₂	94.87*	595.17*	375.07*	7.15*	13.77*	27.82*	10.76*	3.51*	46.48*
h ² (dominance effects over loci)	3.66	22.81	42.79	1.12	-0.63	0.02	-0.38	1.68	-0.21
E (Environ. Comp.)	2.01	2.03	1.46	1.34*	1.49	0.36	0.95	5.32*	0.88
(H ₁ /D) ^{1/2}	2.35	1.51	1.40	1.23	2.91	1.67	1.79	0.57	1.47
H ₂ /4H ₁	0.17	0.22	0.23	0.16	0.21	0.19	0.16	0.50	0.22
KD/KH	2.34	1.28	1.22	1.95	0.71	1.98	2.90	0.51	1.33
h ² / H ₂ (No. of Gene Groups)	0.04	0.04	0.11	0.16	-0.05	0.00	-0.04	0.48	0.00
h ² (Heritability in Narrow Sense)	0.30	0.05	0.49	0.46	0.40	0.34	0.20	0.32	0.44

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05

D at 45 and 90 DAT. Sum of dominance over all loci was found to be non-significant at all stages. Environment component was significant at 60 DAT. Mean degree of dominance was ranged from 0.57 to 1.79 during 45 to 90 DAT. Proportion of genes with positive and negative effect was ranged from 0.16 to 0.50 during 45 to 90 DAT and the highest value was at 45 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from -0.04 to 0.48 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.20 to 0.44 (Table 104).

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) and mean F_r values were significant for number of pubescence (abaxial and adaxial). The magnitude of H_1 and H_2 was higher than D for both abaxial and adaxial surfaces. Sum of dominance over all loci and environment component (E) were found to be non-significant for this trait. Mean degree of dominance was 1.98 (abaxial) and 2.15 for adaxial surface. Proportion of genes with positive and negative effect was 0.18 (abaxial) and 0.17 for adaxial. The proportion of dominant and recessive genes (KD/KH) was more than unity for both abaxial and adaxial layers. The number of groups of genes controlling the character and exhibiting dominance was 0.05 (abaxial) and 0.10 (adaxial). Narrow sense heritability was 0.29 (abaxial) and 0.31 for adaxial layer (Table 105).

4.5.4.2 Growth parameters

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) for number of leaves was significant at all stages. Mean F_r value was significant and positive at 90 DAT. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci was found to be non-significant at all stages. Environment component was significant at 45 DAT. Mean degree of dominance was ranged from 1.30 to 1.40 during 45 to 90 DAT. Proportion of genes with positive and negative effect was ranged from 0.20 to 0.25 during 45 to 90 DAT and the highest value was at 45 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.01 to 0.09 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.41 to 0.54 (Table 105).

Table 105. Genetic components of variations of tomato parents under TyLCV trial for number of pubescence, number of leaves and leaf area

Genetic components	Number of pubescence		Number of leaves			Leaf area (cm ²)		
	AB	AD	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
D (Additive Effect)	16064.44*	58128.62*	4.46*	99.57*	112.82*	674.25*	2512.91*	1308.14*
F (Mean F _r over arrays)	24762.25*	99651.36*	-15.16	64.40	83.95*	109.37	210.08	-179.27
H ₁ (Dominance Effect)	62580.27*	267947.90*	74.69*	189.23*	220.64*	2001.64*	4230.88*	1250.35
H ₂	44805.15*	184506.90*	74.28*	165.51*	176.99*	1778.24*	3971.94*	1267.45*
h ² (dominance effects over loci)	2224.96	178363.15	2.96	1.25	16.62	598.20*	403.99	429.19
E (Environ. Comp.)	29.81	93.88	6.88*	1.93	1.23	33.67	19.89	597.55*
(H ₁ /D) ^{1/2}	1.98	2.15	1.30	1.38	1.40	1.72	1.30	0.98
H ₂ /4H ₁	0.18	0.17	0.25	0.22	0.20	0.22	0.24	0.25
KD/KH	2.28	2.33	0.77	1.61	1.73	1.10	1.07	0.87
h ² / H ₂ (No. of Gene Groups)	0.05	0.10	0.04	0.01	0.09	0.34	0.10	0.34
h ² (Heritability in Narrow Sense)	0.29	0.31	0.54	0.41	0.44	0.45	0.56	0.45

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) for leaf area was significant at all stages. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci was found to be significant at 45 DAT. Mean F_r value was non-significant and environment component was significant at 90 DAT. Mean degree of dominance was ranged from 0.98 to 1.72 during 45 to 90 DAT. Proportion of genes with positive and negative effect was ranged from 0.22 to 0.25 during 45 to 90 DAT and the highest value was at 90 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at 45 and 60 DAT but was less at 90 DAT. The number of groups of genes controlling the character and exhibiting dominance varied from 0.10 to 0.34 during 45 to 90 DAT. Narrow sense heritability was ranged from 0.45 to 0.56 (Table 105).

4.5.4.3 Disease index parameters

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) for per cent plant survival was significant at all stages. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci and mean F_r value were found to be significant at 30 DAT. Environment component was non-significant. Mean degree of dominance was ranged from 1.69 to 1.89 during 30 to 60 DAT. Proportion of genes with positive and negative effect was ranged from 0.18 to 0.19 during 30 to 60 DAT and the highest value was at 30 and 45 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.16 to 0.31 during 30 to 60 DAT. Narrow sense heritability was ranged from 0.23 to 0.38 (Table 106).

Variance due to additive effects of genes was significant for disease severity index on vegetative parts only at 60 DAT. Variance due to dominance effect (H_1), proportion of dominance variance (H_2) was significant at all stages. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci and mean F_r value were found to be non-significant. Environment component was significant at 30 DAT. Mean degree of dominance was ranged from 1.75 to 2.36 during 30 to 60 DAT. Proportion of genes with positive and negative effect was ranged from 0.20 to 0.23 during 30 to 60 DAT and the highest value was at 30 and 45 DAT. The proportion

Table 106. Genetic components of variations of tomato parents under TyLCV trial for Per cent plant survival and disease severity index on vegetative and fruiting parts

Genetic components	Per cent plant survival (%)			Disease Severity Index (V)			Disease Severity Index (F)		
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
D (Additive Effect)	46.49*	341.07*	781.98*	0.07	0.35	1.29*	0.21*	0.42*	1.42*
F (Mean F _t over arrays)	63.11*	410.78	930.34	0.06	-0.07	0.47	0.25	0.28	1.55
H ₁ (Dominance Effect)	132.55*	1215.88*	2485.94*	0.40*	1.96*	3.96*	0.64*	1.77*	5.36*
H ₂	100.72*	917.44*	1793.15*	0.32*	1.76*	3.64*	0.50*	1.50*	4.18*
h ² (dominance effects over loci)	31.42*	149.32	229.94	0.00	0.00	0.46	0.03	0.06	0.13
E (Environ. Comp.)	0.68	2.33	2.75	0.05*	0.04	0.02	0.01	0.01	0.02
(H ₁ /D) ^{1/2}	1.69	1.89	1.78	2.36	2.36	1.75	1.75	2.06	1.95
H ₂ /4H ₁	0.19	0.19	0.18	0.20	0.23	0.23	0.20	0.21	0.20
KD/KH	2.34	1.94	2.00	1.45	0.92	1.23	2.03	1.38	1.78
h ² / H ₂ (No. of Gene Groups)	0.31	0.16	0.13	0.01	0.00	0.13	0.06	0.04	0.03
h ² (Heritability in Narrow Sense)	0.23	0.33	0.38	0.27	0.39	0.38	0.27	0.34	0.33

V - Vegetative parts; F - Flowering and fruiting parts; DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents;

* Significant at 0.05

of dominant and recessive genes (KD/KH) was more than unity at 30 and 60 DAT but it was less than unity at 45 DAT. The number of groups of genes controlling the character and exhibiting dominance varied from 0.00 to 0.13 during 30 to 60 DAT. Narrow sense heritability was ranged from 0.27 to 0.39 (Table 106).

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) for disease severity index on flowering and fruiting parts was significant at all stages. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci, mean F_r value and environment component were found to be non-significant at all stages. Mean degree of dominance was ranged from 1.75 to 2.06 during 30 to 60 DAT. Proportion of genes with positive and negative effect was ranged from 0.20 to 0.21 during 30 to 60 DAT and the highest value was at 45 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.03 to 0.06 during 30 to 60 DAT. Narrow sense heritability was ranged from 0.27 to 0.34 (Table 106).

Variance due to additive effects of genes for vector population was significant at 45 and 60 DAT. Variance due to dominance effect (H_1), proportion of dominance variance (H_2) were significant at all stages. The magnitude of H_1 and H_2 was higher than D at all stages. Sum of dominance over all loci, mean F_r value and environment component were found to be non-significant at all stages. Mean degree of dominance was ranged from 2.03 to 2.54 during 30 to 60 DAT. Proportion of genes with positive and negative effect was ranged from 0.19 to 0.21 during 30 to 60 DAT and the highest value was at 60 DAT. The proportion of dominant and recessive genes (KD/KH) was more than unity at all stages. The number of groups of genes controlling the character and exhibiting dominance varied from 0.00 to 0.01 during 30 to 60 DAT. Narrow sense heritability was ranged from 0.26 to 0.34 (Table 107).

4.5.4.4 Yield parameters

Variance due to additive effects of genes, variance due to dominance effect (H_1), proportion of dominance variance (H_2) were significant for all the yield parameters viz., number of fruits per plant, average fruit weight and yield per plant. The magnitude of H_1 and H_2 was higher than D for all the yield parameters. Sum of

Table 107. Genetic components of variations of tomato parents under TyLCV trial for vector population and yield parameters

Genetic components	Vector Population			Number of fruits	Average fruit weight (g)	Yield per plant (Kg)
	30 DAT	45 DAT	60 DAT			
D (Additive Effect)	5.24	10.45*	46.56*	889.81*	198.90*	0.73*
F (Mean F _r over arrays)	6.62	10.31	44.16	324.46	343.43*	0.06
H ₁ (Dominance Effect)	26.58*	67.56*	192.64*	1104.69*	803.91*	1.58*
H ₂	20.09*	57.44*	154.44*	798.33*	629.44*	1.41*
h ² (dominance effects over loci)	0.01	0.81	1.02	-31.33	34.98	0.31
E (Environ. Comp.)	0.15	0.38	0.95	75.11	3.46	0.13*
(H ₁ /D) ^{1/2}	2.25	2.54	2.03	1.11	2.01	1.47
H ₂ /4H ₁	0.19	0.21	0.20	0.18	0.20	0.22
KD/KH	1.78	1.48	1.61	1.39	2.51	1.06
h ² / H ₂ (No. of Gene Groups)	0.00	0.01	0.01	-0.04	0.06	0.22
h ² (Heritability in Narrow Sense)	0.33	0.26	0.34	0.61	0.09	0.47

DAT - Days after transplanting; KD/KR - Dominant and recessive genes in parents; * Significant at 0.05

dominance over all loci, mean F_r value and environment component were found to be non-significant. Mean degree of dominance was 1.11, 2.01 and 1.47 (number of fruits per plant, average fruit weight and yield per plant respectively). Proportion of genes with positive and negative effect was 0.18, 0.20 and 0.22 (number of fruits per plant, average fruit weight and yield per plant respectively). The proportion of dominant and recessive genes (KD/KH) was more than unity. The number of groups of genes controlling the character and exhibiting dominance was -0.04, 0.06 and 0.22 (number of fruits per plant, average fruit weight and yield per plant respectively). Narrow sense heritability was 0.61, 0.09 and 0.47 (number of fruits per plant, average fruit weight and yield per plant respectively). The estimates of genetic components of variation for yield parameters are presented in Table 107.

4.5.5 Heterosis

4.5.5.1 Morphological parameters

Performance of parents, hybrids and heterobeltiosis values for morphological traits viz., plant height, number of branches, stem girth and number of pubescence on abaxial and adaxial layer are presented in Tables 108 to 110.

Heterobeltiosis was ranged from -42.95 (P3 x P6) to 3.33 (P5 x P7) per cent for plant height. No hybrid had significant positive heterobeltiosis for this trait.

Hybrid P1 x P6 (37.11%) had highest significant positive heterosis for number of branches and P5 x P6 (-3.96%) had that in negative direction. Seventeen hybrids had significant positive heterobeltiosis for this trait. The crosses P1 x P6, P2 x P4, P2 x P3, P6 x P7 and P5 x P8 were the best heterotic hybrids for this trait.

Heterobeltiosis was ranged from -1.86 to 35.70 per cent for stem girth. Fourteen hybrids had significant positive heterobeltiosis for this trait. Hybrid P1 x P6 (35.70%) had the highest significant positive heterosis and it was followed by P1 x P5 (27.55%) and P3 x P4 (26.73%).

The extent of heterosis was ranged from -28.17 to 46.14 per cent for number of pubescence on abaxial layer. Twelve hybrids had significant positive heterobeltiosis for this trait. Hybrids P1 x P2, P1 x P5, P1 x P3, P5 x P6 and P1 x P6 were the best heterotic hybrids for this trait.

Table 108. Estimates of heterobeltiosis for plant height and number of branches at 60 DAT under TyLCV trial

Hybrids	Plant height (cm)				Number of branches			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	64.23	59.17	63.59	-1.01	14.91	14.49	16.99	7.08
P1xP3	64.23	16.90	44.39	-30.93**	14.91	14.58	20.16	26.71**
P1xP4	64.23	11.70	41.57	-35.26**	14.91	11.38	15.96	7.24
P1xP5	64.23	29.97	52.43	-18.36**	14.91	10.64	17.84	20.06**
P1xP6	64.23	37.73	54.10	-15.77**	14.91	15.09	21.66	37.11**
P1xP7	64.23	18.73	47.94	-25.33**	14.91	12.40	16.65	11.21
P1xP8	64.23	18.27	45.65	-28.92**	14.91	14.81	18.62	13.45*
P2xP3	59.17	16.90	46.95	-20.67**	14.49	14.58	20.97	31.52**
P2xP4	59.17	11.70	47.60	-19.53**	14.49	11.38	19.12	32.53**
P2xP5	59.17	29.97	50.52	-14.61**	14.49	10.64	17.84	23.84**
P2xP6	59.17	37.73	50.36	-14.87**	14.49	15.09	18.42	21.41**
P2xP7	59.17	18.73	45.83	-22.50**	14.49	12.40	17.13	18.30**
P2xP8	59.17	18.27	47.13	-20.33**	14.49	14.81	19.55	24.00**
P3xP4	16.90	11.70	13.73	-17.94**	14.58	11.38	14.55	1.33
P3xP5	16.90	29.97	19.32	-35.55**	14.58	10.64	14.60	2.46
P3xP6	16.90	37.73	21.54	-42.95**	14.58	15.09	16.09	-1.93
P3xP7	16.90	18.73	15.88	-28.38**	14.58	12.40	16.24	7.72
P3xP8	16.90	18.27	16.44	-18.29**	14.58	14.81	16.82	7.28
P4xP5	11.70	29.97	18.49	-38.29**	11.38	10.64	13.53	18.48**
P4xP6	11.70	37.73	21.62	-42.64**	11.38	15.09	16.15	7.13
P4xP7	11.70	18.73	14.25	-23.77**	11.38	12.40	15.40	22.20**
P4xP8	11.70	18.27	15.62	-14.12**	11.38	14.81	15.32	3.74
P5xP6	29.97	37.73	30.18	-19.99**	10.64	15.09	14.48	-3.96
P5xP7	29.97	18.73	30.96	3.33	10.64	12.40	16.18	28.17**
P5xP8	29.97	18.27	30.64	2.24	10.64	14.81	18.84	28.17**
P6xP7	37.73	18.73	35.96	-4.67	15.09	12.40	19.46	28.98**
P6xP8	37.73	18.27	35.68	-5.41	15.09	14.81	19.14	17.79**
P7xP8	18.73	18.27	19.03	-6.78	12.40	14.81	16.58	13.77*
CD @ 5%	7.92				12.38			
CD @ 1%	10.54				16.48			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 109. Estimates of heterobeltiosis for stem girth at 60 DAT and number of pubescence on abaxial layer under TyLCV trial

Hybrids	Stem girth (cm)				Number of pubescence (AB)			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	15.77	17.13	19.54	13.22	260.80	259.79	394.50	46.14**
P1xP3	15.77	13.57	17.81	11.93	260.80	159.04	324.65	24.47**
P1xP4	15.77	14.07	19.61	23.64**	260.80	166.90	306.75	17.63**
P1xP5	15.77	15.43	20.88	27.55**	260.80	363.93	507.28	39.43**
P1xP6	15.77	13.53	22.20	35.70**	260.80	354.77	440.04	24.03**
P1xP7	15.77	11.70	17.93	11.84	260.80	53.31	230.43	-11.66**
P1xP8	15.77	12.33	18.78	19.01*	260.80	36.70	222.07	-14.85**
P2xP3	17.13	13.57	20.67	19.99*	259.79	159.04	319.45	23.25**
P2xP4	17.13	14.07	21.64	25.48**	259.79	166.90	306.75	18.37**
P2xP5	17.13	15.43	21.39	24.36**	259.79	363.93	431.26	18.51**
P2xP6	17.13	13.53	17.73	2.14	259.79	354.77	419.84	18.40**
P2xP7	17.13	11.70	17.25	-0.68	259.79	53.31	231.92	-10.70**
P2xP8	17.13	12.33	21.01	23.03**	259.79	36.70	223.45	-13.93**
P3xP4	13.57	14.07	18.22	26.73**	159.04	166.90	182.06	9.11**
P3xP5	13.57	15.43	18.70	13.64	159.04	363.93	322.66	-11.32**
P3xP6	13.57	13.53	17.42	6.21	159.04	354.77	296.42	-16.46**
P3xP7	13.57	11.70	16.56	19.95*	159.04	53.31	128.70	-19.08**
P3xP8	13.57	12.33	17.35	25.70**	159.04	36.70	116.83	-26.53**
P4xP5	14.07	15.43	19.54	18.51*	166.90	363.93	261.40	-28.17**
P4xP6	14.07	13.53	18.43	12.25	166.90	354.77	296.66	-16.38**
P4xP7	14.07	11.70	16.31	13.55	166.90	53.31	130.75	-21.60**
P4xP8	14.07	12.33	16.82	14.92	166.90	36.70	121.91	-26.95**
P5xP6	15.43	13.53	17.16	9.46	363.93	354.77	453.88	24.11**
P5xP7	15.43	11.70	16.90	1.93	363.93	53.31	351.40	-3.42
P5xP8	15.43	12.33	18.34	18.82*	363.93	36.70	341.38	-6.19**
P6xP7	13.53	11.70	18.96	15.05	354.77	53.31	327.66	-7.64**
P6xP8	13.53	12.33	18.65	22.82**	354.77	36.70	322.50	-9.10**
P7xP8	11.70	12.33	13.46	-1.86	53.31	36.70	55.76	5.01*
CD @ 5%	16.35				4.26			
CD @ 1%	21.77				5.67			

AB - Abaxial layer; DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Table 110. Estimates of heterobeltiosis for number of pubescence on adaxial layer and number of leaves at 60 DAT under TyLCV trial

Hybrids	Number of pubescence (AD)				Number of leaves			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	574.21	444.63	771.97	34.46**	44.02	47.07	58.79	24.95**
P1xP3	574.21	353.51	717.49	24.98**	44.02	33.02	48.86	11.13**
P1xP4	574.21	254.33	601.26	4.77	44.02	33.55	50.10	13.92**
P1xP5	574.21	782.28	1100.76	40.71**	44.02	33.61	50.22	14.13**
P1xP6	574.21	695.39	911.04	31.01**	44.02	35.07	59.37	34.97**
P1xP7	574.21	157.67	531.23	-7.48**	44.02	37.63	54.34	23.72**
P1xP8	574.21	106.14	505.23	-12.00**	44.02	47.50	60.35	27.10**
P2xP3	444.63	353.51	607.95	36.86**	47.07	33.02	55.76	18.70**
P2xP4	444.63	254.33	502.30	13.21**	47.07	33.55	58.96	25.51**
P2xP5	444.63	782.28	840.54	7.45**	47.07	33.61	56.02	19.04**
P2xP6	444.63	695.39	773.71	11.28**	47.07	35.07	54.62	16.28**
P2xP7	444.63	157.67	438.27	-1.37	47.07	37.63	57.39	22.16**
P2xP8	444.63	106.14	410.40	-7.64**	47.07	47.50	65.98	37.02**
P3xP4	353.51	254.33	328.34	-7.20**	33.02	33.55	42.81	27.69**
P3xP5	353.51	782.28	699.76	-10.55**	33.02	33.61	42.55	22.71**
P3xP6	353.51	695.39	604.83	-13.02**	33.02	35.07	45.30	29.19**
P3xP7	353.51	157.67	311.69	-11.83**	33.02	37.63	45.55	21.15**
P3xP8	353.51	106.14	272.96	-22.80**	33.02	47.50	55.23	16.33**
P4xP5	254.33	782.28	491.92	-37.12**	33.55	33.61	44.17	25.44**
P4xP6	254.33	695.39	532.70	-23.41**	33.55	35.07	48.26	37.56**
P4xP7	254.33	157.67	239.07	-5.46*	33.55	37.63	49.00	29.97**
P4xP8	254.33	106.14	211.69	-16.55**	33.55	47.50	54.95	15.74**
P5xP6	782.28	695.39	941.36	20.33**	33.61	35.07	39.13	8.51*
P5xP7	782.28	157.67	782.58	0.04	33.61	37.63	47.31	25.99**
P5xP8	782.28	106.14	751.39	-3.95	33.61	47.50	52.13	9.78**
P6xP7	695.39	157.67	676.92	-2.66	35.07	37.63	50.22	31.66**
P6xP8	695.39	106.14	660.63	-5.00*	35.07	47.50	53.24	12.15**
P7xP8	157.67	106.14	163.52	3.69	37.63	47.50	51.77	9.00**
CD @ 5%	4.89				6.45			
CD @ 1%	6.51				8.59			

AD - Adaxial layer; DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01
P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;
P7 - L 02692; P8 - BL 1188

Heterobeltiosis was ranged from -37.12 to 40.71 per cent for number of pubescence on abaxial layer. Nine hybrids had significant positive heterobeltiosis for this trait. The hybrids P1 x P5, P2 x P3, P1 x P2, P1 x P6 and P1 x P3 were the best heterotic hybrids for this trait.

4.5.5.2 Growth parameters

Performance of parents, hybrids and heterobeltiosis values for growth traits viz., number of leaves and leaf area per plant are presented in Tables 110 and 111.

Heterobeltiosis was ranged from 8.51 to 37.56 per cent for number of leaves. All 28 hybrids had significant positive heterobeltiosis for this trait. The crosses P4 x P6, P2 x P8, P1 x P6, P6 x P7 and P4 x P7 were the best heterotic for this trait.

Heterobeltiosis was ranged from -16.64 to 20.38 per cent for leaf area. Thirteen hybrids had significant positive heterobeltiosis for this trait. Best heterotic hybrids for this trait were P5 x P6, P1 x P6, P1 x P2, P3 x P4 and P2 x P5.

4.5.5.3 Disease index parameters

Performance of parents, hybrids and heterobeltiosis values for disease index parameters viz., per cent plant survival, disease severity index on vegetative parts, disease severity index on flowering and fruiting parts and vector population are presented in Tables 111 to 113.

Heterobeltiosis was ranged from -40.77 to 11.40 per cent for per cent plant survival. Nine hybrids had significant positive heterobeltiosis for this trait. The best heterotic hybrids for this trait were P2 x P5, P5 x P6, P6 x P8, P1 x P7 and P2 x P6.

Heterobeltiosis in negative direction is preferred for disease severity index on vegetative parts. Heterobeltiosis was ranged from -86.96 to 21.09 per cent for this trait. Twenty two hybrids had significant negative heterobeltiosis for this trait. The best heterotic hybrids for this trait were P1 x P7, P1 x P5, P2 x P5, P2 x P6 and P1 x P6.

Table 111. Estimates of heterobeltiosis for leaf area and Per cent plant survival at 60 DAT under TyLCV trial

Hybrids	Leaf area (cm ²)				Per cent plant survival			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	193.03	199.57	232.96	16.24**	87.67	85.00	93.16	5.91*
P1xP3	193.03	98.12	179.89	-6.73*	87.67	44.67	91.88	4.84
P1xP4	193.03	101.02	182.21	-5.62	87.67	46.33	90.71	3.53
P1xP5	193.03	113.96	193.90	0.54	87.67	82.00	93.33	6.50*
P1xP6	193.03	118.24	231.71	20.00**	87.67	83.67	93.10	6.24*
P1xP7	193.03	65.66	160.66	-16.64**	87.67	83.33	96.21	9.37**
P1xP8	193.03	95.51	175.56	-9.04**	87.67	64.67	86.51	-1.27
P2xP3	199.57	98.12	197.09	-1.23	85.00	44.67	79.44	-6.37*
P2xP4	199.57	101.02	200.72	0.57	85.00	46.33	79.95	-5.85
P2xP5	199.57	113.96	231.73	16.09**	85.00	82.00	94.60	11.40**
P2xP6	199.57	118.24	197.68	-0.98	85.00	83.67	93.79	8.22**
P2xP7	199.57	65.66	169.92	-14.83**	85.00	83.33	90.25	5.41
P2xP8	199.57	95.51	195.53	-2.04	85.00	64.67	86.19	1.48
P3xP4	98.12	101.02	119.11	16.11**	44.67	46.33	29.33	-40.77**
P3xP5	98.12	113.96	123.31	8.50**	44.67	82.00	64.55	-21.16**
P3xP6	98.12	118.24	131.08	11.17**	44.67	83.67	62.91	-24.87**
P3xP7	98.12	65.66	101.30	3.26	44.67	83.33	56.15	-32.61**
P3xP8	98.12	95.51	111.48	11.08**	44.67	64.67	52.90	-18.05**
P4xP5	101.02	113.96	129.84	13.29**	46.33	82.00	61.88	-24.40**
P4xP6	101.02	118.24	130.97	10.90**	46.33	83.67	61.59	-26.32**
P4xP7	101.02	65.66	98.58	-2.09	46.33	83.33	59.39	-28.76**
P4xP8	101.02	95.51	112.09	10.20**	46.33	64.67	49.93	-22.77**
P5xP6	113.96	118.24	144.11	20.38**	82.00	83.67	94.20	11.30**
P5xP7	113.96	65.66	113.23	-0.54	82.00	83.33	89.98	5.88*
P5xP8	113.96	95.51	126.50	11.10**	82.00	64.67	83.00	1.31
P6xP7	118.24	65.66	130.79	10.94**	83.67	83.33	89.29	5.06
P6xP8	118.24	95.51	121.33	2.95	83.67	64.67	91.73	9.68**
P7xP8	65.66	95.51	91.88	-3.55	83.33	64.67	70.97	-14.81**
CD @ 5%	5.92				5.56			
CD @ 1%	7.88				7.40			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 112. Estimates of heterobeltiosis for disease severity index on vegetative and flowering and fruit parts at 60 DAT under TyLCV trial

Hybrids	Disease severity index (V)				Disease severity index (F)			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	0.17	0.20	0.06	-22.61*	0.07	0.07	0.02	-24.50**
P1xP3	0.17	1.67	0.42	-74.67**	0.07	1.93	0.46	-76.13**
P1xP4	0.17	2.00	0.59	-70.55**	0.07	1.87	0.48	-74.12**
P1xP5	0.17	1.43	0.20	-85.59**	0.07	0.70	0.09	-87.36**
P1xP6	0.17	1.33	0.32	-75.24**	0.07	0.87	0.15	-82.79**
P1xP7	0.17	2.80	0.36	-86.96**	0.07	1.63	0.53	-67.48**
P1xP8	0.17	1.63	0.60	-63.60**	0.07	1.30	0.48	-62.84**
P2xP3	0.20	1.67	0.62	-62.27**	0.07	1.93	0.69	-64.22**
P2xP4	0.20	2.00	0.69	-65.40**	0.07	1.87	0.67	-64.20**
P2xP5	0.20	1.43	0.24	-82.67**	0.07	0.70	0.10	-85.71**
P2xP6	0.20	1.33	0.24	-81.52**	0.07	0.87	0.14	-84.44**
P2xP7	0.20	2.80	1.29	-53.55**	0.07	1.63	0.90	-44.90**
P2xP8	0.20	1.63	0.58	-64.75**	0.07	1.30	0.70	-45.96**
P3xP4	1.67	2.00	2.44	21.09*	1.93	1.87	2.58	28.65**
P3xP5	1.67	1.43	1.08	-35.43**	1.93	0.70	1.10	-42.91**
P3xP6	1.67	1.33	1.26	-24.64**	1.93	0.87	1.21	-37.32**
P3xP7	1.67	2.80	2.37	-13.70	1.93	1.63	2.22	15.62*
P3xP8	1.67	1.63	1.74	-10.06	1.93	1.30	1.90	-0.34
P4xP5	2.00	1.43	1.53	-24.72**	1.87	0.70	1.33	-28.70**
P4xP6	2.00	1.33	1.51	-24.33**	1.87	0.87	1.34	-28.35**
P4xP7	2.00	2.80	2.56	-6.45	1.87	1.63	2.11	13.50
P4xP8	2.00	1.63	2.09	-1.00	1.87	1.30	1.93	5.07
P5xP6	1.43	1.33	0.45	-71.02**	0.70	0.87	0.19	-77.96**
P5xP7	1.43	2.80	1.47	-46.99**	0.70	1.63	0.91	-44.48**
P5xP8	1.43	1.63	0.91	-50.05**	0.70	1.30	0.73	-43.80**
P6xP7	1.33	2.80	1.74	-37.84**	0.87	1.63	1.09	-32.96**
P6xP8	1.33	1.63	1.18	-38.47**	0.87	1.30	0.72	-43.32**
P7xP8	2.80	1.63	2.74	2.32	1.63	1.30	1.77	9.12
CD @ 5%	17.73				15.65			
CD @ 1%	23.61				20.85			

V - Vegetative parts; F - Flowering and fruiting parts; DAT - Days after transplanting;

* Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Table 113. Estimates of heterobeltiosis for vector population at 60 DAT and number of fruits per plant under TyLCV trial

Hybrids	Vector population				Number of fruits per plant			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	4.30	3.93	1.05	-77.07**	71.26	74.94	118.39	55.61**
P1xP3	4.30	9.03	2.53	-71.78**	71.26	43.48	88.73	28.25**
P1xP4	4.30	8.87	3.40	-61.53**	71.26	33.18	78.99	12.22
P1xP5	4.30	1.83	0.67	-84.52**	71.26	29.55	86.33	20.26**
P1xP6	4.30	1.23	0.75	-82.43**	71.26	67.67	107.62	44.30**
P1xP7	4.30	13.63	6.43	-52.86**	71.26	39.29	85.74	22.57**
P1xP8	4.30	7.33	3.06	-58.00**	71.26	22.61	76.97	8.95
P2xP3	3.93	9.03	3.73	-58.41**	74.94	43.48	98.43	33.44**
P2xP4	3.93	8.87	3.74	-57.66**	74.94	33.18	85.62	14.94*
P2xP5	3.93	1.83	0.79	-79.49**	74.94	29.55	81.01	7.26
P2xP6	3.93	1.23	0.69	-82.30**	74.94	67.67	104.34	36.61**
P2xP7	3.93	13.63	7.72	-43.31**	74.94	39.29	86.48	16.88*
P2xP8	3.93	7.33	4.33	-40.19**	74.94	22.61	76.62	2.88
P3xP4	9.03	8.87	11.69	14.98*	43.48	33.18	37.96	-12.30
P3xP5	9.03	1.83	5.00	-44.51**	43.48	29.55	45.67	1.22
P3xP6	9.03	1.23	5.30	-41.24**	43.48	67.67	64.03	-4.93
P3xP7	9.03	13.63	15.00	10.70	43.48	39.29	51.35	18.19*
P3xP8	9.03	7.33	10.28	13.65*	43.48	22.61	38.73	-10.73
P4xP5	8.87	1.83	6.18	-30.36**	33.18	29.55	34.38	-3.19
P4xP6	8.87	1.23	6.02	-32.10**	33.18	67.67	57.48	-15.10*
P4xP7	8.87	13.63	13.47	-1.31	33.18	39.29	40.94	4.42
P4xP8	8.87	7.33	9.85	7.53	33.18	22.61	32.14	-3.17
P5xP6	1.83	1.23	0.37	-80.22**	29.55	67.67	79.75	17.15*
P5xP7	1.83	13.63	7.82	-42.66**	29.55	39.29	46.70	11.78
P5xP8	1.83	7.33	4.03	-44.76**	29.55	22.61	38.12	22.16**
P6xP7	1.23	13.63	7.26	-46.72**	67.67	39.29	76.29	13.00
P6xP8	1.23	7.33	5.49	-20.41**	67.67	22.61	76.88	13.88
P7xP8	13.63	7.33	12.60	-7.49	39.29	22.61	40.80	3.79
CD @ 5%	11.88				14.87			
CD @ 1%	15.81				19.81			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

Heterobeltiosis in negative direction is preferred for disease severity index on flowering and fruiting parts. Heterobeltiosis was ranged from -87.36 to 28.65 per cent for this trait. Twenty two hybrids had significant negative heterobeltiosis for this trait. The hybrids P1 x P5, P2 x P5, P2 x P6, P1 x P6 and P5 x P6 were the best heterotic hybrids for this trait.

Heterobeltiosis in negative direction is preferred for vector population. Heterobeltiosis was ranged from -84.52 to 14.98 per cent for this trait. Twenty two hybrids had significant negative heterobeltiosis for this trait. The best heterotic hybrids for this trait were P1 x P2, P1 x P5, P1 x P6, P2 x P6 and P5 x P6.

4.4.5.4 Yield parameters

Performance of parents, hybrids and heterobeltiosis values for yield parameters viz., number of fruits per plant, average fruit weight and yield per plant are presented in Tables 113 and 114.

Heterobeltiosis was ranged from -15.10 to 55.61 per cent for number of fruits per plant. Twelve hybrids had significant positive heterobeltiosis for this trait. The hybrids P1 x P2, P1 x P6, P2 x P6, P2 x P3 and P1 x P3 were the best heterotic hybrids for this trait.

Heterobeltiosis was ranged from -57.52 to 16.55 per cent for average fruit weight. Only two hybrids had significant positive heterobeltiosis for this trait. The best heterotic hybrids for this trait were P1 x P2 and P5 x P8.

Heterobeltiosis was ranged from -15.05 to 87.93 per cent for yield per plant. Fourteen hybrids had significant positive heterobeltiosis for this trait. The best heterotic hybrids for this trait were P5 x P6, P1 x P5, P1 x P2, P2 x P8 and P1 x P8.

Table 114. Estimates of heterobeltiosis for average fruit weight and yield per plant under TyLCV trial

Hybrids	Average fruit weight (g)				Yield per plant (Kg)			
	Female	Male	Hybrid	Heterobeltiosis (%)	Female	Male	Hybrid	Heterobeltiosis (%)
P1xP2	27.69	25.83	32.46	16.55**	1.95	1.94	3.82	83.66**
P1xP3	27.69	17.26	28.55	3.44	1.95	0.75	2.54	31.86*
P1xP4	27.69	23.89	27.74	0.35	1.95	0.80	2.19	12.39
P1xP5	27.69	56.40	43.38	-22.96**	1.95	1.70	3.76	85.19**
P1xP6	27.69	21.93	27.98	1.35	1.95	1.50	3.01	55.41**
P1xP7	27.69	24.09	28.31	1.97	1.95	0.94	2.41	25.10*
P1xP8	27.69	61.09	43.22	-28.97**	1.95	1.39	3.35	70.36**
P2xP3	25.83	17.26	25.59	-0.18	1.94	0.75	2.53	33.07*
P2xP4	25.83	23.89	25.89	-0.89	1.94	0.80	2.23	15.43
P2xP5	25.83	56.40	40.76	-27.70**	1.94	1.70	3.33	62.74**
P2xP6	25.83	21.93	25.78	-1.39	1.94	1.50	2.70	34.58*
P2xP7	25.83	24.09	26.43	2.09	1.94	0.94	2.28	19.25
P2xP8	25.83	61.09	45.44	-25.31**	1.94	1.39	3.51	78.55**
P3xP4	17.26	23.89	20.81	-12.56*	0.75	0.80	0.79	-6.97
P3xP5	17.26	56.40	46.09	-18.26**	0.75	1.70	2.12	36.21**
P3xP6	17.26	21.93	22.32	1.91	0.75	1.50	1.44	-3.12
P3xP7	17.26	24.09	20.30	-13.82**	0.75	0.94	1.04	12.26
P3xP8	17.26	61.09	40.76	-33.34**	0.75	1.39	1.58	16.07
P4xP5	23.89	56.40	38.71	-31.42**	0.80	1.70	1.34	-15.05
P4xP6	23.89	21.93	26.24	4.54	0.80	1.50	1.52	3.96
P4xP7	23.89	24.09	24.92	-1.55	0.80	0.94	1.01	4.11
P4xP8	23.89	61.09	41.48	-32.04**	0.80	1.39	1.34	-2.61
P5xP6	56.40	21.93	43.26	-23.23**	1.70	1.50	3.49	87.93**
P5xP7	56.40	24.09	34.66	-38.55**	1.70	0.94	1.63	3.63
P5xP8	56.40	61.09	68.83	12.75*	1.70	1.39	2.67	43.61**
P6xP7	21.93	24.09	23.17	-10.93*	1.50	0.94	1.77	19.91
P6xP8	21.93	61.09	25.81	-57.52**	1.50	1.39	1.99	39.66**
P7xP8	24.09	61.09	56.72	-6.94	0.94	1.39	2.31	65.68**
CD @ 5%	10.21				26.13			
CD @ 1%	13.60				34.80			

DAT - Days after transplanting; * Significant at 0.05; ** Significant at 0.01

P1 - L 01942; P2 - L 06052; P3 - L 02079; P4 - LA 3913; P5 - TLB 133; P6 - L 06231;

P7 - L 02692; P8 - BL 1188

5. DISCUSSION

Present study was aimed at understanding the genetics of tolerance to TyLCV and drought. For this purpose, hundred tomato genotypes were screened for TyLCV and drought stress separately and tolerant and susceptible genotypes were picked up based on their *per se* performance. These were further crossed in diallel mating design and hybrids were produced, which were further exposed to same stresses. Detailed discussion on the results obtained of this study is presented in this chapter.

5.1 Evaluation of tomato genotypes for TyLCV

Hundred genotypes of tomato were studied for tolerance to TyLCV during *rabi* 2011. Field screening was done without taking any crop protection sprays so as to assure spread of disease and to judge natural tolerance of genotypes against the disease.

5.1.1 Morphological characters

Analysis of variance revealed presence of highly significant variability with respect to all morphological characters studied viz., Plant height at 45, 60 and 90 DAT, number of branches at 45, 60 and 90 DAT and stem girth at 45, 60 and 90 DAT (Table 5). This shows presence of high variability among the genotypes which facilitates scope for selection of genotypes for crop improvement under the biotic stress of TyLCV.

Genotypic coefficient of variation was found high for plant height at 60 and 90 DAT except that in 45 DAT which had moderate GCV. This indicates presence of good variability for the character. Further, phenotypic coefficient of variation was found to be higher than GCV which points at the fact that there was an influence of environment on expression of the character. It was found that there was a narrow difference between GCV and PCV at 60 and 90 DAT which indicates that the influence of environment was very little (Table 6). This difference was more at 45 DAT, indicating more influence of environment on expression of this trait at 45 DAT. Heritability and genetic advance over mean were high at 45, 60 and 90 DAT for plant height which indicates that most likely inheritance is due to additive gene effects and

selection may be effective. These results were in accordance with Singh *et al.* (2000), Joshi and Singh (2003), Mohanty (2003), Upadhyay *et al.* (2005).

More number of branches gives a good spread to plant and also it may give rise to more number of flowering shoots which increase plant yield. GCV for number of branches and stem girth was found to be moderate at all the three stages viz., 45, 60 and 90 DAT (Table 6). This shows that moderate variation was present among the genotypes. Among the different growth stages, PCV was high at 45 DAT whereas it was moderate for 60 and 90 DAT. Narrow difference between GCV and PCV was observed which indicates little influence of environment on expression of this trait at 60 and 90 DAT. Influence of environment may be more at 45 DAT, which was indicated by more difference between GCV and PCV at this stage. Heritability and genetic advance over mean was found to be high at 45 and 90 DAT while it was moderate for number of branches and stem girth at 60 DAT. This shows that additive genes are governing inheritance of the trait and selection may be employed for improvement of this trait. The present investigation is in conformity with the results of Singh *et al.* (2000), Tiwari and Lal (2005), Kumar *et al.* (2006), Revanasiddappa (2008) and Sivaprasad (2008) in tomato.

Healthy plant will have a good stem which can withstand weight of all the above ground parts. Variability among the genotypes for stem girth was found to be high at 45 and 90 DAT as the GCV values were high. Moderate variability was observed at 60 DAT. Difference between GCV and PCV were low, which can be attributed to the fact that variability was mostly due to the genetic makeup and environment had little effect on expression of this trait. Heritability along with genetic advance was high which shows that additive genes are mostly governing the inheritance of this trait and simple selection may be effective for crop improvement. The present investigation is in conformity with the results of Singh *et al.* (2000), Tiwari and Lal (2005), Kumar *et al.* (2006), Revanasiddappa (2008) and Sivaprasad (2008) in tomato.

5.1.2 Growth characters

Leaves, as an organ of photosynthesis, are very important for plant growth. Leaf curl disease will cause a reduction in number of leaves and leaf area. Estimation

of number of leaves and leaf area at different stages of plant life will lead to judge the extent of disease infection and genotype's tolerance to the disease. More leaf area may help to trap maximum amount of solar radiation, but TyLCV causes reduction in leaf area by leaf curling. Higher number of leaves and more leaf area helps to select tolerant genotype for the disease stress.

Anova reveals presence of highly significant variations among all the growth characters viz., number of leaves at 45, 60 and 90 DAT and leaf area 45, 60 and 90 DAT (Table 5). Moderate GCV and PCV were found for number of leaves at 45 and 60 DAT. There was less influence of environment on expression of this character which was confirmed by the narrow difference between GCV and PCV (Table 7). High GCV and PCV were found for number of leaves at 90 DAT and leaf area at 45, 60 and 90 DAT. Even though environment had a control on expression of these characters, it seems to be very little. This provides an evidence to believe that the variations were due to genotype. Heritability and GAM were high for all the growth characters studied. This points for the effectiveness of selection for improving this trait as additive genes govern inheritance. These results were in accordance with Singh *et al.* (2000), Parasanna *et al.* (2005) and Revanasiddappa (2008).

5.1.3 Disease indexing for TyLCV

Percentage plant survival against TyLCV depicts the ability of genotypes to tolerate disease at different stages of their life cycle. Mean per cent plant survival was maximum during the initial crop growth stage (82.80% at 30 DAT) and it reached to very low value of 21.56 per cent at 90 DAT. GCV was high at all stages pointing to the fact that genetic makeup was maximum contributor for the variability. The difference between GCV and PCV was found to be less in all stages which shows that environmental variability was less. As the variability estimates were high, it can be believed that high variability was present among the genotypes with respect to this trait. Heritability estimates were also high along with high genetic advance. This shows that this trait may be controlled due to additive genes and selection may be used to improve this trait. Pradeepkumar *et al.* (2001) reported similar results in bacterial wilt of tomato.

Disease severity index helps in monitoring the progress of spread of disease. Analysis of variance showed that the observations were highly significantly different. Disease severity on vegetative parts was less in the initial stages of growth (0.00 - 1.57 at 45 DAT), it gradually increase and reached up to 2.23 - 4.00 at 90 DAT. Increase in disease severity was also observed on flowering and fruiting parts. Vector population showed an increasing trend up to 75 DAT but later there was no further increase in vector population and at 90 DAT it decreased. This may be attributed to the fact that *B. tabaci* prefers young plant parts to feed on and also the environmental conditions may not be congenial for buildup of whitefly population (Muniyappa and Reddy, 1976; Ramappa, 1993; Muniyappa *et al.*, 2000). There was high GCV noticed for the above mentioned traits viz., disease severity index on vegetative parts, flowering and fruiting parts and vector population. The difference between GCV and PCV was observed to be less indicating that the variability may be mostly due to the genetic makeup of genotypes under study. Despite the low and delayed natural infection, it was possible to categorize genotypes into different groups based on their reaction to the infection. These results of field evaluation are in accordance with the findings of Pico *et al.* (1998), Saikia and Muniyappa (1989), Lapidot *et al.* (1997) and Lapidot and Friedmann (2002). No plant protection measures were taken up and it resulted in increase of disease severity.

5.1.4 Yield parameters

Anova results show that there was significant difference the genotypes for all the yield parameters viz., number of fruits per plant, average fruit weight and yield per plant (Table 5). High GCV and PCV were recorded for number of fruits per plant and average fruit weight. It shows that the genetic makeup may be mostly responsible for the high variability among the genotypes studied. Heritability and genetic advance values were also high for this trait. This points for the effectiveness of selection for improving this trait as additive genes govern inheritance. This result was in accordance with Singh *et al.* (2000), Parasanna *et al.* (2005), Joshi and Singh (2003), Joshi *et al.* (2004), Mehta and Asati (2008) and Sivaprasad (2008).

Moderate GCV and high PCV was observed for yield per plant. The difference between GCV and PCV reveals that there is some environmental effect on expression of this character. Heritability estimates were moderate and the genetic advance was

found to be high. It shows that though non additive genes may be governing the trait and environment also controls expression of this trait. By this it can be inferred that simple selection may not be fully reliable to improve this trait. This is in contrast with the findings of Singh *et al.* (2000) and Prashanth (2004). Similar findings are reported by Parvindarsingh *et al.* (2002) and Joshi and Singh (2003). However, non-additive gene action is noticed indicating the selection after hybridization and heterosis breeding are suggested to improve yield parameters (Fig. 4).

5.1.5 Genetic divergence

Genetic architecture of a population is the result of prolonged natural selection. The population which exists in diverse environments might have been strongly diversified genetically. So, it is necessary to understand the extent and rates of genetic divergence existing between the diversified forms or types. Genetic divergence among the parents is important in self pollinated crops because a cross involving genetically diverse parents is likely to produce high heterozygous as well as heterotic effect.

Mahalanobis's D^2 statistics is one of the potent techniques of measuring genetic divergence in various breeding materials. In plant breeding, genetic diversity plays an important role because, hybrids between genotypes of diverse origin, generally display a greater heterosis and throw more recombinants than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability or due to different patterns of evolution.

Since there existed a wide variability among the genotypes, this technique is adopted to group genotypes based on 12 characters. This is a reliable tool and many scientist have already been used this tool in tomato breeding (Dharmatti *et al.*, 2001; Sharma and Verma, 2001; Arun *et al.*, 2003; Prashanth, 2003; Veershetty, 2004; Sekar *et al.*, 2008).

All the hundred genotypes under study are divided into 8 clusters. Genetic diversity study was found to be effective since genotypes responding to TyLCV in similar manner were falling in same group. Inter cluster distances were more than intra cluster distances (Table 14), which also confirms the effectiveness of this tool. Plant height, average fruit weight, leaf area and number of fruits per plant contributed

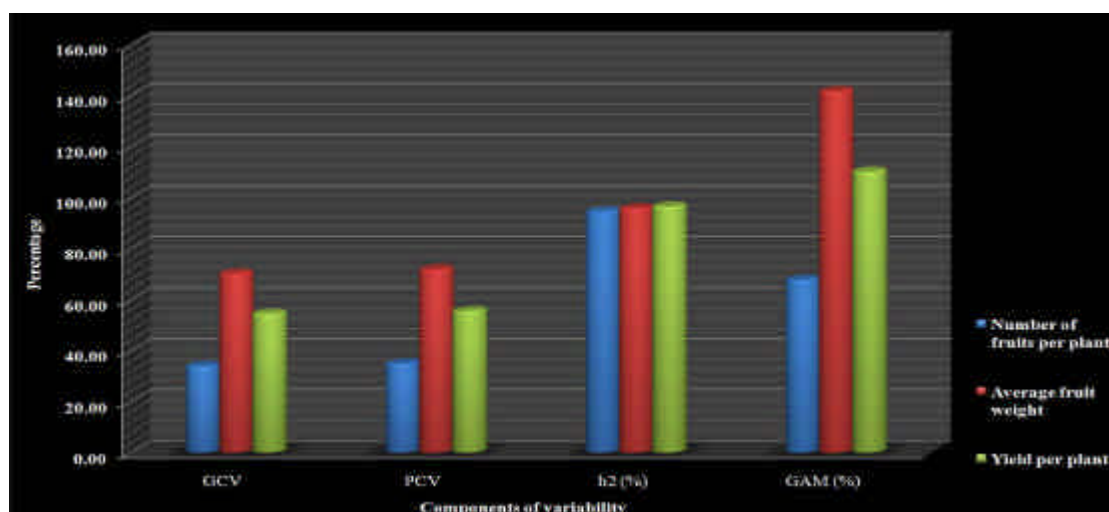


Fig. 4. Components of variability under normal irrigation

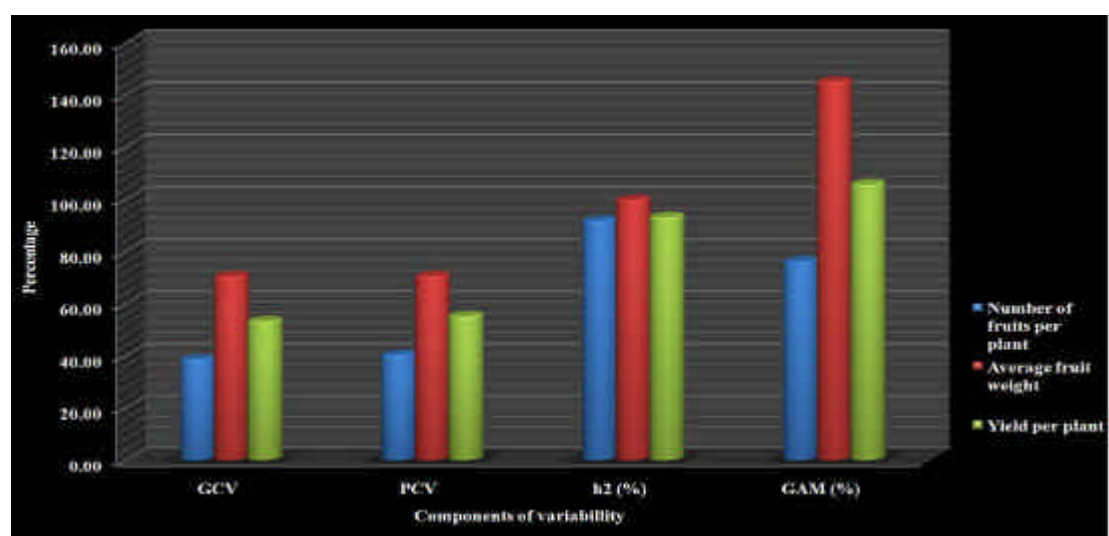


Fig. 5. Components of variability under restricted irrigation

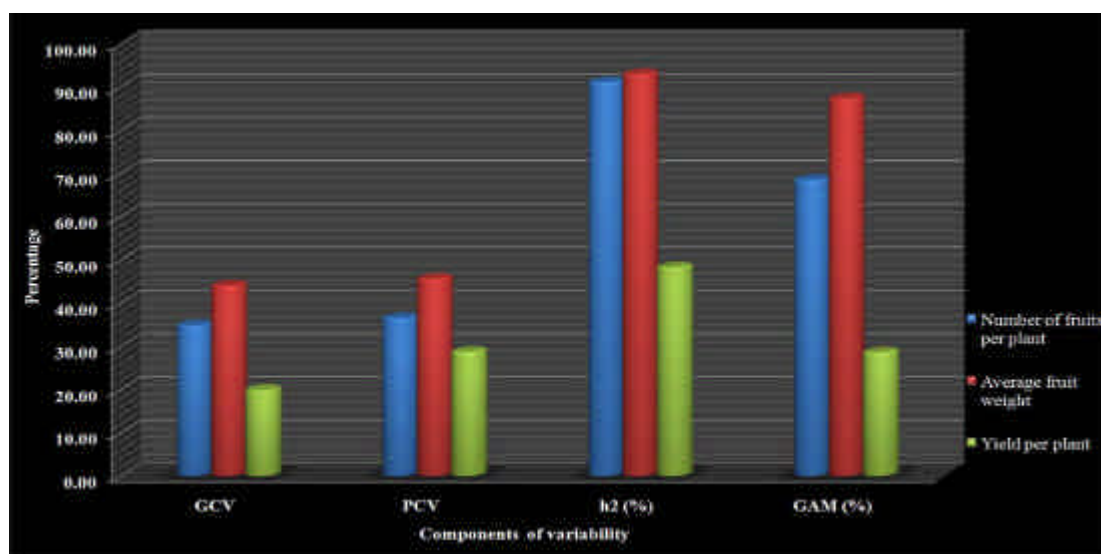


Fig. 6. Components of variability under TyLCV trial

considerably to the divergence. Contributions of other characters were less compared to the above mentioned characters.

5.2 Evaluation of tomato genotypes for drought stress

The same hundred genotypes, which were used for screening for TyLCV resistance, were used for screening for drought resistance. This experiment was conducted in summer 2012. Genotypes were exposed for two types of irrigation treatments, one with normal irrigation (IR1) and the other with restricted irrigation *i.e.*, once in a week (IR2).

5.2.1 Morphological characters

Analysis of variance was performed separately for normal and stressed irrigation treatments to have a deeper look into the variability. Analysis of variance revealed highly significant variation among all the morphological characters studied *viz.*, plant height (45, 60 and 90 DAT), number of branches (45, 60 and 90 DAT), stem girth (45, 60 and 90 DAT), root length and root volume in IR 1 and IR 2 except stem girth at 90 DAT in IR 2 (Table 16).

In the present investigation, when the traits like plant height, number of branches and stem girth were compared between fully irrigated and restricted irrigated condition, it was clear that all the above mentioned parameters were decreased in restricted irrigation condition. It has been established that drought stress is a very important limiting factor for plant growth and development. It affects both elongation and expansion of growth. Water stress greatly suppresses cell expansion and cell growth due to the low turgor pressure. The genotypes which show lesser reduction in these parameters might have maintained cell turgor and volume by osmoregulation (Anjum *et al.*, 2003; Bhatt and Rao, 2005; Kusaka *et al.*, 2005). Reduction in number of branches and stem girth may be attributed to improper availability of water which in turn affected partitioning of photosynthates. Hormonal imbalance and reduction in cell multiplication may also be a reason. This kind of results were reported in *Populus* (Wullscheleger *et al.*, 2005) Soybean (Zhang *et al.*, 2004) and okra (Bhatt and Rao, 2005). GCV was found to be moderate for plant height, number of branches and stem girth in IR 1 and it was found to be low to moderate in IR 2. In fully irrigated

environment (IR 1) the difference between GCV and PCV was found to be less, while in restricted irrigation (IR 2) it was little higher. It means that environment is playing important role in expression of these traits. Heritability and genetic advance values were high for these characters in IR 1. Which reveals that the inheritance of these traits may be governed by non additive genes and simple selection may be practiced to improve these traits. Interestingly, heritability and genetic advance values were decreased in IR 2 for the same traits, as compared with IR 1. This reveals that selection under non stress condition may not identify genotypes that would perform well under stress. Similar results were reported in rice (Sellammal *et al.*, 2014), maize (Smith *et al.*, 1998) and coffee (Montagnon *et al.*, 2003).

Production of strong, adequate and capable root system under drought stress is important for a plant to sustain its life. The importance of roots in acquiring water has long been established. A prolific root system can confer the advantage to support accelerated plant growth during early crop growth stage and extract water from soil that otherwise lost by evaporation. The development of root system increases the water uptake and maintains requisite osmotic pressure. An increase values of root length and volume was noticed when IR 1 and IR 2 were compared. This may be because tomato plants penetrate their roots deeper to pump water from deeper layers of soil when it is not available on top layers in plenty. Such observations were reported in tomato (Chavan, 2007), soybean (Benjamin and Nielsen, 2006), chickpea (Serraj *et al.*, 2004), sunflower (Tahir *et al.*, 2002) and *Catharanthus roseus* (Jaleel *et al.*, 2008). GCV was low for root length and moderate for root volume in IR 1 while both were low in IR 2. This means there was low to moderate variability for root length and volume among the genotypes. Heritability and genetic advance values were high in both IR 1 and IR 2, which means simple selection may be practiced to improve this trait. These values were moderate in IR 1 and less in IR 2. Which means simple selection may not be efficient in improving this character. Also it reveals that selection should be done in stressed condition to select tolerant genotypes.

5.2.2 Growth characters

Analysis variance showed highly significant difference for all the growth characters studied *viz.*, number of leaves (45, 60 and 90 DAT), leaf area (45, 60 and

90 DAT), absolute growth rate (45-60, 45- 90 and 60-90 DAT), relative growth rate (45-60, 45- 90 and 60-90 DAT) and crop growth rate (45-60, 45- 90 and 60-90 DAT).

High amount of variability was observed for number of leaves and leaf area both under IR 1 and IR 2. It was noticed that number of leaves per plant and leaf area per plant were reduced in stressed irrigation as compared with normal irrigation condition. Development of optimal leaf area is important to photosynthesis and dry matter yield. Genotypes might have reduced their growth as a result of reduced availability of water. This may help plant to conserve water from loss due to transpiration. Water deficit stress mostly reduced leaf growth and in turn the leaf areas in tomato (Chavan, 2007) and many species of plant like *Populus* (Wullschleger *et al.*, 2005), soybean (Zhang *et al.*, 2004) and many other species (Farooq *et al.*, 2009). Significant inter-specific differences between two sympatric *Populus* species were found in total number of leaves, total leaf area and total leaf biomass under drought stress (Wullschleger *et al.*, 2005). The leaf growth was more sensitive to water stress in wheat than in maize (Sacks *et al.*, 1997); *Vigna unguiculata* (Manivannan *et al.*, 2007a) and sunflower (Manivannan *et al.*, 2007b & 2008). Moderate to low GCV was observed for number of leaves both in IR 1 and IR 2, which shows that moderate variability was present among genotypes for number of leaves. The difference between GCV and PCV was found to be little, indicating little effect of environment on expression of these characters. Heritability and genetic advance was found to be high for both the characters in IR 1, whereas it was comparatively less in IR 2. It shows that selection should be done in stressed condition for these traits to select tolerant genotypes for crop improvement.

Observations on absolute growth rate (dry matter production per unit time), relative growth rate (rate of increase in the dry weight per unit dry weight already present) and crop growth rate (rate of dry matter production per unit ground area per unit time) give an idea about genotype's capacity to produce dry matter. These are the important characters which influence plant growth. Analysis of variance revealed that the genotypes differed significantly for AGR, RGR and CGR in both IR 1 and IR 2. Absolute growth rate in IR 2 was found to be less during 45-60 and 45-90 DAT when compared with IR 1. Dry matter production is directly related to the production of photosynthates and leaves are the organs which produce photosynthates. It was clear

in this experiment that number of leaves and leaf area are less in IR 2 compared with IR 1. This might be the cause of reduced growth rate in IR 2 than in IR 1. Decreased dry matter production in stressed condition is reported in tomato (Nahar *et al.*, 2011; Chavan, 2007; Rahman *et al.*, 1998; Qasem and Judah, 1985), lentil (Lal *et al.*, 1988). Interestingly AGR during 60-90 DAT was high in IR 2 than IR 1. Mixed response was observed in GCV estimates of AGR, RGR and CGR. GCV was found to be high in IR 1 for AGR 45-90 DAT, RGR 45-60 DAT, RGR 60-90 DAT, CGR 45-90 DAT and CGR 60-90 DAT. For other characters GCV was found high in IR 2 compared to IR 1.

5.2.3 Yield characters

Analysis of variance showed significant difference for all the yield characters studied viz., number of fruits per plant, average fruit weight and yield per plant. There was noticeable difference between IR 1 and IR 2 for yield parameters. Number of fruits per plant, average fruit weight and yield per plant was found to be higher in IR 1 than IR 2. It was known fact that final yield and yield attributing characters are basically governed by vegetative growth, dry matter production and its distribution. As plant growth was found to be retarded in stressed irrigation condition, final yield also had lesser values. Yield reduction in tomato under water stress was reported by many scientists (Chavan, 2007; Verbruggen and Hermans, 2008; Pervez *et al.*, 2009; Shriari *et al.*, 2009; Mafakheri *et al.*, 2010). High GCV was observed for all the yield characters in both IR 1 and IR 2. It indicates that high amount of variability is present among the genotypes for these characters. Heritability and genetic advance values were high for these traits in both IR 1 and IR 2 indicating that these traits may be governed by non additive genes and simple selection may be practiced to improve these traits. Heritability and genetic advance values of IR 1 and IR 2 were almost same, which reveals that selection may be practiced even in normal irrigation condition to select superior genotypes for these traits (Fig. 5 and 6).

5.2.5 Genetic divergence

Genetic divergence study was done separately for IR 1 and IR 2 to have deep information about the genetic difference between the genotypes. This was done on the basis of 13 characters viz., plant height at 60 DAT, number of branches at 60 DAT,

stem girth at 60 DAT, root length, root volume, number of leaves at 60 DAT, leaf area at 60 DAT, absolute growth rate (45-60 DAT), relative growth rate (45-60 DAT), crop growth rate (45-60 DAT), number of fruits per plant, average fruit weight and per plant yield.

All the hundred genotypes under study are divided into 7 clusters in IR 1. Genetic diversity study was found to be effective since genotypes performing in similar manner were falling in same group. Inter cluster distances were more than intra cluster distances, which also confirms the effectiveness of this tool. Yield per plant, leaf area and number of leaves contributed considerably to the divergence. Contributions of other characters were less compared to the above mentioned characters.

In IR 2, genotypes were grouped into 10 clusters. Genetic diversity study was found to be effective since genotypes responding to stress in similar manner were falling in same group. Inter cluster distances were more than intra cluster distances. Average fruit weight and relative growth rate (45 - 60 DAT) contributed considerably to the divergence. Contributions of other characters were less compared to the above mentioned characters.

5.3 Selection of parents for hybridization

The success of any plant breeding program largely depends on the correct choice of good parents. High mean value was the main criterion among the breeders for a long time. Gilbert (1958) suggested that the parents with good *per se* performance would result in better genotypes.

5.3.1 Selection for TyLCV tolerance

Genotypes L 01942 (cluster 6) and L 06052 (cluster 7) were selected as tolerant parents and genotype L 02079 (cluster 2) and LA 3913 (cluster 5) were selected as susceptible parents for the further study.

5.3.2 Selection for drought tolerance

Genotype TLB 133 (cluster 3 in IR 1 and IR 2) and L 06231 (cluster 2 in IR 1 and cluster 1 in IR 2) were selected as tolerant parents. Genotype L 02692 (cluster 6

in IR 1 and cluster 8 in IR 2) and BL 1188 (cluster 4 in IR 1 and cluster 2 in IR 2) were selected as susceptible parents.

5.4 Evaluation of hybrids and parents in diallel approach for drought tolerance

5.4.1 Analysis of variance

Analysis of variance for different morphological, growth, biochemical and yield parameters showed significant difference among the treatments. Variance due to parents and hybrids was significant for all the characters except for number of pubescence both of abaxial and adaxial surfaces. Parents vs. hybrid was significant for plant height (45, 60 and 90 DAT), stem girth (90 DAT), root length, number of leaves (45, 60 and 90 DAT), leaf area (45, 60 and 90 DAT), absolute growth rate (90 DAT), relative growth rate (45, 60 and 90 DAT), crop growth rate (45 and 90 DAT), proline content, chlorophyll a content, total chlorophyll content and yield parameters in both stressed and non-stressed condition. This shows presence of large variation for the above mentioned characters. These results are in accordance with Yashavantakumar (2008), Kulkarni (2003), Prashanth (2004), Sajjan (2001), Joshi and Thakur (2003), Mahendrakar (2004) Singh *et al.* (2005), Chadha *et al.* (2002) and Rai *et al.* (2003). Significant anova results indicate that further analysis is appropriate.

5.4.2 Analysis of variance for combining ability and genetic components of variation

The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942) working on single crosses in maize. Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its progenies. The value of a genotype depends on its ability to produce superior hybrids in combination with other genotypes. Combining ability analysis provides information about the nature and magnitude of various types of gene action involved in the expression of various quantitative characters and thus it helps in deciding the breeding procedures for genetic improvement of such traits. It also helps in evaluation of inbreds or lines or genotypes in terms of their genetic value and in the selection of suitable parents for hybridization and in the identification of superior cross

combinations. There are two types of combining abilities, viz., general combining ability (GCA) and specific combining ability (SCA). Sprague and Tatum (1942) defined GCA as the average performance of a line or population in several hybrid combinations and SCA as those effects in certain combinations which significantly departed from what should be expected on the basis of the average performance of the lines involved. They further attributed GCA to additive effect of genes and SCA to dominance deviation and epistatic interactions. Combining ability analysis gives useful information regarding the selection of parents in terms of the performance of hybrids and in addition it indicates the nature and magnitude of various types of gene action involved in the expression of the quantitative traits (Dhillon, 1975).

Analysis of variance for general and specific combining ability showed it was significant for all the morphological, growth, biochemical and yield parameters. This indicates the importance of both additive and non-additive genetic variances in the inheritance of the characters.

General combining ability variances were higher compared with specific combining ability variances for all the characters in both stressed and non-stressed conditions. This indicated the opulence of additive genetic variance in the improvement of these characters under both stressed and non-stressed conditions. The available additive genetic variance could well be exploited by resorting to simple pure line selection and/or pedigree breeding, whereas the non-additive genetic variance could well be exploited in later generations or by resorting to hybrid breeding. Both the variances could be exploited simultaneously by resorting to population improvement program.

The genetic component variance ratio of gca and sca (V_g/V_s) was less than unity for all the characters under both irrigation regimes. This indicates the predominance of non-additive gene effects in inheritance of these traits. Since the ratio of additive genetic variance to dominance genetic variance is less than unity, inheritance all the traits may be believed to be by dominance gene action. Dominance variance was more than additive variance and the ratio of V_A/V_D was less than unity. Hence, selection may be practiced in segregating population and also intermating the selected plants in segregating population or recurrent selection may be practiced. Higher broad sense heritability compared to narrow sense heritability proves that the

variation among genotypes may be largely due to the genotypic variation. So, it can be stated that heterosis breeding along with the selection of superior plants in the later generations is ideal to improve these traits for drought tolerance in tomato.

5.4.3 Combining Ability analysis for drought tolerance

5.4.3.1 Morphological parameters

Significant positive GCA is preferred for plant height. Out of eight parents, L 02079 and TLB 133 showed highly significant positive GCA effects in all the three stages (45, 60 and 90 DAT) for plant height. These parents are found to be good general combiner for plant height in both IR 1 and IR 2 (Table 44). Hence these parents can be used in breeding programs to improve plant height. Out of 28 hybrids, P4 x P8, P1 x P5, P1 x P6, P2 x P8, P1 x P4 and P6 x P7 had significant positive SCA for this trait in all the stages, consistently for IR 1 and IR 2. These may be considered as good specific combiners for plant height (Table 45). These combinations may be recommended for heterosis breeding.

Combining ability in positive direction is preferred for number of branches. L 01942 and L 2079 were found to be good general combiners for this trait. Hence these parents can be used in breeding programs to improve number of branches. Hybrids P1 x P2, P2 x P8 and P3 x P5 had consistent positive combining ability for number of branches in both IR 1 and IR 2. These may be considered as good specific combiners for this trait (Table 46). These combinations may be recommended for heterosis breeding.

Significant positive combining ability is preferred for stem girth. Parents LA 3913 and TLB 133 were found to be good general combiners for this trait and these may be used in breeding program to improve stem girth. Hybrids P4 x P8, P4 x P5 and P1 x P3 were found to be consistent good specific combiners for this trait (Table 47). These combinations may be recommended for heterosis breeding.

L 06052, L 02079 and LA 3913 found to be good general combiners for root characters. BL 1188 and L 06231 found to be good general combiners for stomatal count. L 01942, L 06052, LA 3913 and TLB 133 were found to be good general combiners for number of pubescence (Table 48). Pubescences are uni or multi-cellular

structures which cover the surface of stem and leaves. They are considered as differentiated epidermal cells. These are reported to protect plants from UV radiations, drought and herbivory (Skaltsa *et al.*, 1994; Huttunen *et al.*, 2010). These parents may be used for breeding programs to improve root characters, stomata count and number of pubescence. Hybrids P2 x P8, P3 x P7 and P1 x P8 were found to be good specific combiners for root length. P4 x P5, P2 x P8, P3 x P6, P3 x P7 and P1 x P4 were found to be good specific combiners for root volume. P5 x P6, P7 x P8, P3 x P5, P3 x P4, P2 x P5, P1 x P6, P3 x P8, P1 x P2, P2 x P7 and P1 x P7 were found to be good specific combiners for stomata count (Table 49). These combinations may be recommended for heterosis breeding program.

5.4.3.2 Growth parameters

L 01942 and TLB 133 had significant positive combining ability for number of pubescence in stressed and non-stressed condition and are considered as good general combiners. Hence, these parents may be used for further breeding programs to improve this trait. Hybrids P2 x P4, P4 x P5, P2 x P3, P6 x P8, P1 x P5, P3 x P6, P4 x P8, P1 x P8, P5 x P8 and P3 x P4 had significant positive SCA for number of pubescence. These may be suggested for heterosis breeding.

Significant positive combining ability is preferred for number of leaves. Parents L 02079, L 01942 and L 06052 had significant positive GCA for number of leaves in both IR 1 and IR 2. These are considered as good general combiners for this trait. These may be used for further breeding program to improve this trait. Hybrids P3 x P7, P2 x P7, P3 x P4, P1 x P8, P2 x P8, P3 x P6 and P1 x P6 had consistent significant positive SCA effects for number of leaves in both IR 1 and IR 2 (Table 52). These may be recommended for heterosis breeding to improve number of leaves. Hybrids P1 x P2, P1 x P3 and P2 x P3 may be recommended for recombination breeding as the parents had significant positive GCA and hybrids had that in negative direction.

Genotypes L 02079, L 02692 and L 06052 found to be good general combiners for leaf area per plant (Table 50). These may be used for further breeding program to improve this trait. Hybrids P2 x P8, P2 x P7, P1 x P5, P1 x P4, P1 s P8, P3

s P6 and P4 x P5 were found to be good specific combiners for leaf area per plant (Table 53). These may be recommended for heterosis breeding to improve number of leaves.

Significant positive combining ability is preferred for absolute, relative and crop growth rate. Parents LA 3913, L 02079 and L 06052 may be considered as good general combiners for these traits in IR 2 (Table 54). These may be used for further breeding program to improve this trait. Hybrids P1 x P8 (for AGR); P2 x P3, P1 x P4, P2 x P8 and P6 x P8 (for RGR); P2 x P3, P4 x P6, P1 x P6, P4 x P7, P1 x P8 and P4 x P5 (for CGR) were found to be good specific combiners for the above mentioned traits (Table 55, 56 and 57). These may be recommended for heterosis breeding to improve number of leaves.

5.4.3.3 Biochemical parameters

Extensive research has revealed proline accumulation as a universal response of plants under stress. Proline accumulation due to water or salt stress results from a stimulated synthesis in the tissue, an inhibited oxidation, or an impaired incorporation of proline into proteins. Clearly, under such conditions, the mechanisms of feedback inhibition cannot function. Indeed, this was proven by Boggess *et al.* (1976), who showed that proline does not inhibit its own synthesis in wilted barley and tobacco leaves. The increased synthesis of proline due to wilting seems to be related to the first step of this synthesis. The reduction in turgor is accepted as the primary trigger of proline accumulation in plants subjected to conditions of drought and salinity. The loss of turgor activates a complex sequence of adaptive events correlated to the level of stress, plant tolerances and plant growth. Proline accumulation can also be observed with other stresses such as high temperature and under starvation (Sairam *et al.*, 2002). Parents L 06052, L 02079, LA 3913 and TLB 133 had highly significant positive GCA effects in both IR 1 and IR 2. So, these may be considered as good general combiners for proline content (Table 58) and may be recommended for further breeding programs to improve this trait. Hybrids P4 x P5, P2 x P3, P1 x P5, P6 x P8, P4 x P6, P3 x P6, P4 x P7, P4 x P8, P2 x P4, P2 x P8 and P1 x P6 were good specific combiners for proline content (Table 59). These may be recommended for heterosis breeding to improve proline content. Rana and Kalloo (1989) also reported significant increase in proline content when tomato plants were exposed to drought stress.

Chlorophyll is one of the basic pigments of plants that its reduction of concentration causing chlorosis, growth reduction and the yield (Kholgh and Ando, 1995). It was also reported that plants under environmental (peripheral) stresses lose their green chlorophyll tissues. Chlorophyll and higher carotenoids are proved to be associated with stress tolerance. It is reliable to measure the changes in chlorophyll, the photosynthetic pigment to analyse the effect of different environmental stress on plant physiology (Kraus *et al.*, 1995). Chlorophyll is one of the basic pigments in plants whose reduction in concentration causes chlorosis and reduction of growth and yield (Khosh and Ando, 1995). For chlorophyll content (a, b and total), LA 3913 and TLB 133 had highly significant positive GCA effects in both IR 1 and IR 2. These two parents may be considered as good general combiners for this trait (Table 58) and may be recommended for further breeding program to improve these traits. P4 x P5, P3 x P6, P6 x P8, P2 x P3, P1 x P5, P3 x P7, P1 x P4, P2 x P4, P4 x P8, P4 x P6 and P4 x P7 were good specific combiners for chlorophyll a content. P3 x P4, P3 x P6, P2 x P6, P2 x P3, P1 x P5, P4 x P8, P2 x P4, P4 x P6 and P4 x P7 were good specific combiners for chlorophyll b. P4 x P5, P3 x P6, P2 x P3, P1 x P5, P3 x P7, P6 x P8, P2 x P4, P1 x P4, P4 x P8, P4 x P6 and P4 x P7 were good specific combiners for total chlorophyll content (Table 59). These may be recommended for heterosis breeding to improve chlorophyll content.

5.4.3.4 Yield parameters

Three parents (L 06052, L 02079 and LA 3913) had highly significant positive GCA effects for number of fruits per plant in IR 1 and IR 2. These parents may be considered as good general combiners for number of fruits per plant. These may be recommended for further breeding program to improve number of fruits per plant. P3 x P7, P3 x P6, P4 x P7, P2 x P4, P1 x P8, P2 x P8, P2 x P6, P1 x P5 and P6 x P8 were good specific combiners for number of fruits. These may be recommended for heterosis breeding to improve number of fruits per plant. Parents L 02079, LA 3913, TLB 133 and L 02692 had highly significant positive GCA effects for average fruit weight in IR 1 and IR 2. These parents may be recommended for further breeding program to improve number of fruits per plant. Parents L 02079, LA 3913 and L 02692 had highly significant positive GCA effects for yield per plant. So, these parents may be considered as good general combiners for yield per plant and may be

recommended for further breeding program to improve this trait. In general L 02079 and LA 3913 had highly significant positive GCA effects for all the yield parameters in both IR 1 and IR 2. So, these two may be considered as good general combiners for overall yield parameters (Table 58) and may be considered for further breeding programs. P2 x P4, P1 x P5, P4 x P5, P4 x P8, P3 x P7 and P6 x P8 were good specific combiners for average fruit weight. P2 x P4, P1 x P5, P4 x P5, P3 x P7, P4 x P8 and P6 x P8 were good specific combiners for yield per plant (Table 60). These parents may be recommended for heterosis breeding to improve yield parameters.

5.4.4 Gene action for drought tolerance traits using diallel analysis

Breeding of plants is an exercise for exploiting and manipulating the genetic system. Williams (1964) has suggested that refined and deliberate methods of breeding can be developed only from a more thorough knowledge and understanding of the genetic basis of traits. In the breeding program, it is desirable to obtain information on the ability to select individuals which when combined together can give rise to superior progeny (Hayward, 1979). Hence, breeders have been giving importance for choice of parents for hybridization based up on the genetic potentiality rather than on their phenotypic performance. The genetic potentiality of parents is assessed based on their mean performance, combining ability and their effects on hybrid performance. Diallel mating design is used to estimate the genetic components of variation and combining ability of inbreds in a series of crosses. The application of diallel cross, procedures of the analysis of polygenic traits in self pollinated species was developed by Jinks (1954) and Hayman (1954a).

The present investigation was done as per Hayman's approach model II. This provides detailed description of the relative genetic properties of the inbred lines, while the Griffing's approach stresses statistical concepts of GCA and SCA at the loss of some genetic information.

The additive genetic variance was significant for plant height (45, 60 and 90 DAT), number of branches (45 and 90 DAT), stem girth (45 and 90 DAT), root length, root volume, stomata count, number of leaves (45 and 90 DAT), leaf area (45 and 90 DAT), absolute growth rate (60 to 90 DAT), relative growth rate (45 to 60 and 60 to 90 DAT), crop growth rate (45 to 60 and 60 to 90 DAT), chlorophyll (a, b and

total) content, number of fruits per plant, average fruit weight and yield per plant in stressed condition. Proline content and number of pubescence (abaxial and adaxial) had significant additive genetic variance in non-stressed condition. This indicated that the component of variation due to additive genetic variance was important for these traits. These characters could be improved by resorting to simple selection. These results are in accordance with Yashavantakumar (2008), Sajjan (2001), Rai *et al.* (2003) Bhatt *et al.* (2004), Singh *et al.* (2005) and Asati *et al.* (2007). The estimates of H_1 and H_2 were positive and significant for all the traits except number of pubescence in stressed condition. While, number of pubescence had significant variation under non-stressed condition. It indicated that the dominance variance component of variation of these traits was due to dominant effect and there were unequal frequency of alleles. Further proof for the unequal distribution of the alleles over loci was obtained by the ratio of $H_2/4H_1$, which was in the range of 0.16 to 0.23 in stressed condition and from 0.16 to 0.22 in non-stressed condition. These values are less than the maximum value of 0.25 and this indicates the asymmetry of alleles. If this value is 0.25, it indicates the symmetry of positive and negative alleles and if H_1 is equal to H_2 (gene frequency of 0.5), the increased and decreased alleles are in equal proportion. In the present study, H_1 is not equal to H_2 .

The estimates of $H_2/4H_1$ are very low, which indicate that the positive and negative alleles at the loci exhibiting dominance were not in equal proportion of the parents of interest. However, this estimate did not permit a determination as to which type of alleles occurred more frequently. The unequal distribution of positive and negative alleles indicated the operation of non-allelic interaction *i.e.*, epistasis. As H_1 is not equal to H_2 in the present study, the observed low regression could be the result of gene frequency other than 0.5 instead of epistasis. The theoretical consideration of Coughtrev and Mather (1970) and the computer stimulation of Feyt (1976) also indicated that Hayman (1956) test for detecting epistasis is reliable only if the genes are distributed independently in the parents involved in the diallel cross. These results made to think whether the observed heterosis is due to dominance or over dominance. Similar results were reported by Thakur and Kohli (2005).

The estimates of F (Mean F_r over arrays) were significant and positive for plant height, stem girth, number of pubescence, number of leaves, absolute growth

rate (60 to 90 DAT), crop growth rate (45 to 60 DAT), chlorophyll b content, average fruit weight and yield per plant. It indicated the predominance of dominant alleles in the parent for these traits, in this generation. The estimates of F were positive but non-significant for number of branches, root length, root volume, stomata count, number of pubescence on abaxial layer, leaf area, relative growth rate, proline content, chlorophyll (a and total) content and number of fruits per plant. This may indicate that the parents of interest had more recessive alleles for these characters. F estimate was negative for number of pubescence on adaxial layer, implying that both dominance and recessive genes contributed equally to this trait in the parents of present study.

Estimates of dominance effect over loci (h^2) were positive and significant for plant height (45 and 60 DAT), number of leaves (45, 60 and 90 DAT), leaf area (45, 60 and 90 DAT), relative growth rate and crop growth rate. It indicated the dominance effect expressed as the algebraic sum over all loci as heterozygous phases in all the crosses.

Average degree of dominance over all loci $(H_1/D)^{1/2}$, was more than unity for all the morphological, growth, biochemical and yield parameters both in stressed and non-stressed conditions. This shows the presence of over dominance for all these characters. Similar results were reported by Thakur and Kohli (2005). The negative effects of alleles in parents were compensated by positive alleles in hybrids resulting over dominance. Hence, selection of parents with high positive alleles, dominant genes, manifests dominance in hybrids. The degree of dominance might be caused either due to presence of correlated gene distribution and/or due to unidirectional dominance with plus or minus effects and seemed to be not due to epistasis. It appeared that the additive and dominance components (Hayman, 1954b) may likely to be confounded due to the presence of correlated gene distribution. Therefore, both the assumptions *i.e.*, no epistasis and no correlated gene distribution underlying diallel analysis seemed to be not valid (Jagtap and Kolhe, 1987).

Estimates of number of dominance and recessive genes in parents (KD/KH) were more than unity for all the characters studied both in stressed and non-stressed conditions. This indicates presence of more of dominant alleles in parents. Estimates of number of genes groups controlling that character and exhibiting dominance (h^2/H_2) were less than unity for all the characters studied both in stressed and non-

stressed conditions. This under estimation may be due to the fact that the dominance effects of the genes affecting these traits are not equal in size and direction.

Narrow sense heritability estimates were high for all the characters both in stressed and non-stressed conditions. These characters may be controlled by additive genetic variance. This indicated that the individual genotype can be evaluated readily from their phenotypic expression. Simple selection will be more effective in these sets of materials exhibiting greater additive genetic variability and desirable mean performance.

It is evidenced from the study that both additive and non additive gene effects are involved in the genetic control of the traits. So, both gene effects must be considered while developing superior lines. Tomato is a homozygous self pollinated crop and thus it does not make use of the dominance effect of genes at individual loci. Therefore, crosses involving high GCA estimates are required for developing lines in advanced generations. It is also evidenced from the study that genotypes must be evaluated under stressed conditions for different traits to design drought tolerant lines as evidenced by importance of both additive and non-additive gene actions.

5.4.5 Heterosis

The impulse of progress in crop improvement through plant breeding was propelled by a better understanding and an appropriate exploitation of heterosis. Heterosis is manifested through greater vigour of F_1 's over the parents resulting into higher yields through their component characters. The term signifies an increased or decreased vigour of F_1 's over mid parent or best parental values Shull (1914). The sector of success of F_1 hybrids lies in the fact that all plants are exceptionally uniform in growth and development, better adaptability to changing and adverse ecological conditions and above all give high total yields.

The ultimate choice of the parents to be used in a breeding program is determined by *per se* performance and their behavior in hybrid combinations. Some idea on the usefulness of the parents may be obtained from their individual performance, particularly in respect of yield components. It is therefore, necessary to assess genetic potentiality of the parents in hybrid combinations through systematic combining abilities. Diallel method has been used in the present study for estimating combining abilities.

The recent trend in tomato breeding has been towards development of hybrids to meet the specific traits (*viz.*, tolerance to biotic and abiotic stresses, earliness, quality parameters *etc.*) coupled with high yield as it may be difficult to develop a hybrid having all the characters. However, it is reasonable to search one which can have maximum number of useful characters keeping yield as primary motto. In the present study, along with yield, tolerance to drought and TyLCV is also considered.

Significant positive and negative heterosis was observed for plant height, number of branches, stem girth, root volume, number of pubescence (abaxial and abaxial), number of leaves, leaf area, absolute growth rate, relative growth rate, crop growth rate, proline content, chlorophyll (a, b and total) content, number of fruits per plant and yield per plant. This indicates that both additive and non additive gene effects are involved in the genetic control of these traits. None of the crosses showed negative heterosis for root length. This shows the predominance of additive gene action in governing this trait. Positive heterosis was not observed for stomata count and average fruit weight neither in IR 1 nor in IR 2. This indicates the predominance of non-additive gene action governing inheritance of this trait. Presence of additive and non-additive gene action was also proved by the diallel results. The observed significant heterosis justify the importance of genetic makeup of the parents involved and the genetic divergence between them. The result also indicates that there is a good scope for improvement of the above mentioned traits by heterosis breeding (Fig. 7 and 8). Similar reports were recorded by Fageria *et al.* (2001), Joshi and Thakur (2003), Asati *et al.* (2007), Singh *et al.* (2007) and Singh *et al.* (2008).

5.5 Evaluation of hybrids and parents in diallel approach for TyLCV tolerance

5.5.1 Analysis of variance

Analysis of variance for different morphological, growth, disease index and yield parameters had significant difference among the treatments, parents and hybrids. Parents vs. hybrids had significant variations in plant height (45, 60 and 90 DAT), stem girth (60 and 90 DAT), number of pubescence (abaxial and adaxial), number of leaves (90 DAT), leaf area (45, 60 and 90 DAT), per cent disease survival (30, 45 and 60 DAT), disease severity index on vegetative parts (60 DAT), disease severity index

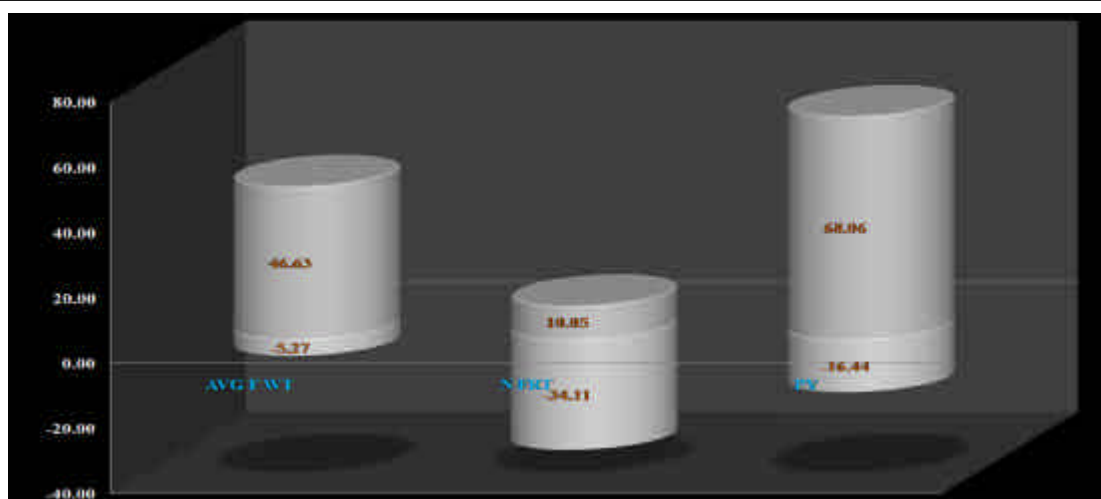


Fig. 7. Range of heterobeltiosis of yield parameters under normal irrigation

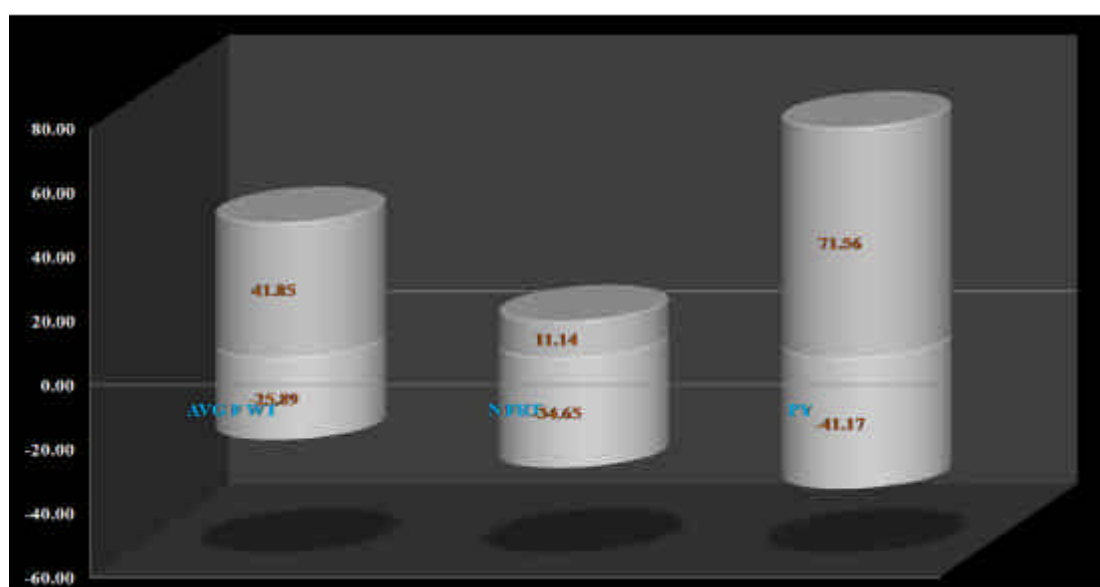


Fig. 8. Range of heterobeltiosis of yield parameters under restricted irrigation

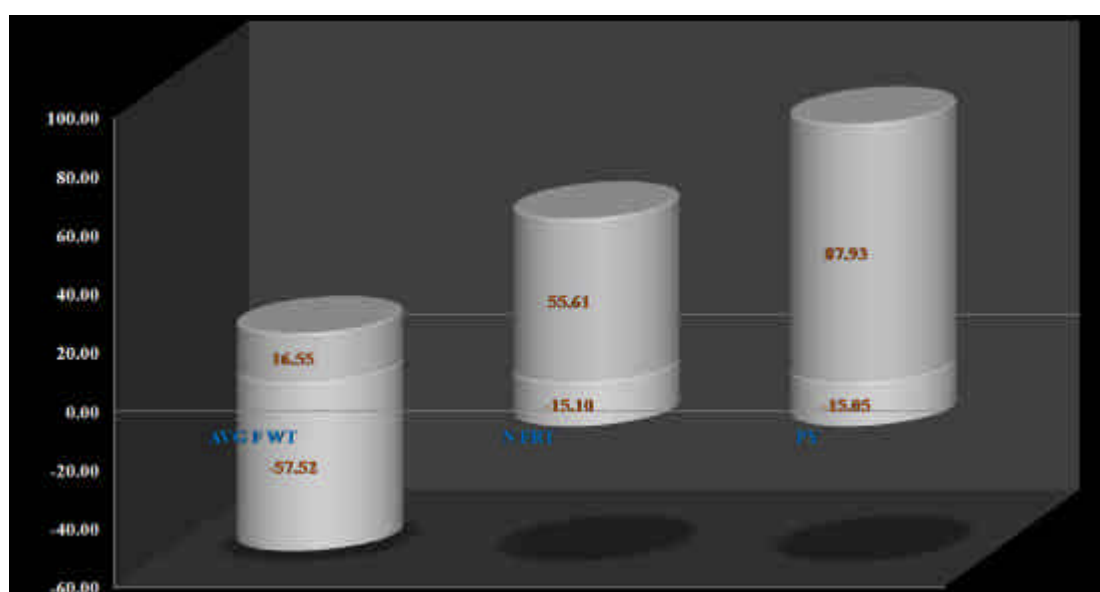


Fig. 9. Range of heterobeltiosis of yield parameters under TyLCV trial

on flowering and fruiting parts (30, 45 and 60 DAT), vector population (45 and 60 DAT), average fruit weight and yield per plant. This shows presence of large variation for the above mentioned characters. These results are in accordance with Yashavantakumar (2008), Kulkarni (2003), Prashanth (2004), Sajjan (2001), Joshi and Thakur (2003), Mahendrakar (2004) Singh *et al.* (2005), Chadha *et al.* (2002) and Rai *et al.* (2003). Significant anova results indicate that further analysis is appropriate.

5.5.2 Analysis of variance for combining ability and genetic components of variation

Analysis of variance for general and specific combining ability showed it was significant for all the morphological, growth, disease index and yield parameters. This indicates the importance of both additive and non-additive genetic variances in the inheritance of the characters.

General combining ability variances were higher compared with specific combining ability variances for all the characters. This indicated the opulence of additive genetic variance in the improvement of these characters. The available additive genetic variance could well be exploited by resorting to simple pure line selection and/or pedigree breeding, whereas the non-additive genetic variance could well be exploited in later generations or by resorting to hybrid breeding. Both the variances could be exploited simultaneously by resorting to population improvement program.

The genetic component variance ratio of gca and sca (V_g/V_s) was less than unity for all the characters except for leaf area at 90 DAT. This indicates the predominance of non-additive gene effects in inheritance of these traits. Since the ratio of additive genetic variance to dominance genetic variance is less than unity, inheritance all the traits may be believed to be by dominance gene action. Dominance variance was more than additive variance and the ration of V_A/V_D was less than unity. Hence, selection may be practiced in seggregating population and also intermating the selected plants in seggregating population or recurrent selection may be practiced. Higher broad sense heritability compared to narrow sense heritability proves that the variation among genotypes may be largely due to the genotypic variation. So, it can be stated that heterosis breeding along with the selection of superior plants in the later generations is ideal to improve these traits for drought tolerance in tomato.

5.5.3 Combining Ability analysis for drought tolerance

5.5.3.1 Morphological parameters

L 01942 may be considered as good general combiner, TLB 133 and L06052 may be considered as average general combiners for plant height. These parents may be recommended for further breeding program to improve this trait. P2 x P3, P1 x P4, P6 x P8, P4 x P6, P2 x P6 and P1 x P6 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve plant height content.

L 01942 may be considered as good general combiner and L 06052 as average general combiner for number of branches. These parents may be recommended for further breeding program to improve this trait. P1 x P8, P4 x P 8, P1 x P5 and P2 x P6 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve number of branches.

For stem girth, L 06052 may be considered as good general combiner, L 01942 and L 02079 as average general combiner and LA 3913 as poor general combiner. These parents may be recommended for further breeding program to improve this trait. P1, P5, P1 x P8, P3 x P6, P2 x P6, P4 x P8, P3 x P7 and P6 x P8 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve stem girth.

L 01942 may be considered as good general combiner, L 06052 and LA 3913 as average general combiners and TLB 133 as poor general combiner for number of pubescence. These parents may be recommended for further breeding program to improve this trait. Among these hybrids, P6 x P8, P1 x P4, P2 x P3, P4 x P5 and P2 x P8 had high significant positive SCA effects. These may be recommended for heterosis breeding to improve number of pubescence. Channarayappa *et al.* (1992) reported that presence of pubescence on tomato leaves give resistance to herbivory. They have reported that the whiteflies (*B. tabaci*) prefer not to attack on tomato genotypes with more number of pubescence. More number of pubescence is also reported to be a tolerant trait against whitefly (*B. tabaci* and *B. argentifolli*) complex, as well as to aphids, mites and Lapidoptera pests (Resende *et al.*, 2006; Blauth *et al.*, 1998; Lawson *et al.*, 1997).

5.5.3.2 Growth parameters

L 01942 may be considered as good general combiner, L 06052 as average general combiners and TLB 133 as poor general combiner for number of leaves. These parents may be recommended for further breeding program to improve this trait. P2 x P 6, P4 x P 7, P3 x P7, P1 x P5, P1 x P8, P1 x P7, P4 x P8 and P2 x P3 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve number of leaves.

L 01942 may be considered as good general combiner, L 06052 as average general combiners and TLB 133 as poor general combiner for leaf area. These parents may be recommended for further breeding program to improve this trait. P6 x P8, P4 x P5, P1 x P5, P4 x P8, P3 x P7, P3 x P6 and P1 x P8 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve leaf area.

5.5.3.3 Disease index parameters

Out of the eight parents, L 01942 may be considered as good general combiner, TLB 133 and L 06052 as average general combiners for per cent plant survival. These parents may be recommended for further breeding program to improve this trait. P2 x P3, P6 x P8, P4 x P8, P2 x P4, P5 x P7, P1 x P6, P5 x P8, P1 x P3, P4 x P5 and P2 x P6 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve per cent plant survival.

For disease severity index on vegetative parts, significant negative GCA is preferred. L 01942 may be considered as good general combiner, TLB 133 as average general combiner and L 06052 as poor general combiner for this trait. These parents may be recommended for further breeding program to improve this trait. P2 x P3, P2 x P6, P5 x P7, P5 x P8, P2 x P4, P4 x P7 and P4 x P6 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve this trait.

For disease severity index on flowering and fruiting parts, significant negative GCA is preferred. L 01942 may be considered as good general combiner, TLB 133 as average general combiner and L 06052 as poor general combiner for this trait. These

parents may be recommended for further breeding program to improve this trait. Hybrids with most proffered SCA are P2 x P3, P5 x P8, P5 x P7, P2 x P4, P6 x P8 and P4 x P5. These may be recommended for heterosis breeding to improve this trait.

For vector population, significant negative GCA is preferred. L 01942 may be considered as good general combiner and L 06052 as average general combiner for this trait. These parents may be recommended for further breeding program to improve this trait. Hybrids with most proffered SCA are P2 x P3, P4 x P5, P6 x P8, P2 x P4 and P4 x P7. These may be recommended for heterosis breeding to improve this trait.

5.5.3.4 Yield parameters

L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for number of fruits. These parents may be recommended for further breeding program to improve this trait. P2 x P4, P4 x P8, P1 x P8, P5 x P8 and P2 x P6 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve this trait.

Three parents had significant positive GCA for average fruit weight. L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for this trait. These parents may be recommended for further breeding program to improve this trait. P4 x P7, P5 x P6, P4 x P8, P6 x P8, P3 x P4, P1 x P7 and P2 x P3 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve this trait.

Three parents had significant positive GCA for yield per plant. L 01942 may be considered as good general combiner, L 06052 as average general combiner and TLB 133 as poor general combiner for this trait. These parents may be recommended for further breeding program to improve this trait. P2 x P6, P2 x P3, P4 x P5, P4 x P7, P1 x P7 and P1 x P4 may be considered as good specific combiners for this trait. These may be recommended for heterosis breeding to improve this trait.

5.5.4 Gene action for drought tolerance traits using diallel analysis

The additive genetic variance was significant for plant height (60 and 90 DAT), number of branches (45 and 90 DAT), stem girth (45, 60 and 90 DAT), number of pubescence (abaxial and adaxial), number of leaves (45, 60 and 90 DAT), leaf area (45, 60 and 90 DAT), per cent plant survival (30, 45 and 60 DAT), disease severity index on vegetative parts (60 DAT), disease severity index on flowering and fruiting parts (30, 45 and 60 DAT), vector population (45 and 60 DAT), number of fruits per plant, average fruit weight and yield per plant. This indicated that the component of variation due to additive genetic variance was important for these traits. These characters could be improved by resorting to simple selection. These results are in accordance with Yashavantakumar (2008), Sajjan (2001), Rai *et al.* (2003) Bhatt *et al.* (2004), Singh *et al.* (2005) and Asati *et al.* (2007). The estimates of H_1 and H_2 were positive and significant for all the traits except for H_1 in stem girth (60 DAT). It indicated that the dominance variance component of variation of these traits was due to dominant effect and there were unequal frequency of alleles. Further proof for the unequal distribution of the alleles over loci was obtained by the ratio of $H_2/4H_1$, which was in the range of 0.16 to 0.24. Only leaf area at 90 DAT had 0.25 for this ratio. These values are less than the maximum value of 0.25 and this indicates the asymmetry of alleles. If this value is 0.25, it indicates the symmetry of positive and negative alleles and if H_1 is equal to H_2 (gene frequency of 0.5), the increased and decreased alleles are in equal proportion. In the present study, H_1 is not equal to H_2 .

The estimates of $H_2/4H_1$ are very low, which indicate that the positive and negative alleles at the loci exhibiting dominance were not in equal proportion of the parents of interest. However, this estimate did not permit a determination as to which type of alleles occurred more frequently. The unequal distribution of positive and negative alleles indicated the operation of non-allelic interaction *i.e.*, epistasis. As H_1 is not equal to H_2 in the present study, the observed low regression could be the result of gene frequency other than 0.5 instead of epistasis. The theoretical consideration of Coughtrev and Mather (1970) and the computer stimulation of Feyt (1976) also indicated that Hayman (1956) test for detecting epistasis is reliable only if the genes are distributed independently in the parents involved in the diallel cross. These results made to think whether the observed heterosis is due to dominance or over dominance. Similar results were reported by Thakur and Kohli (2005).

The estimates of F (Mean F_r over arrays) were significant and positive for stem girth (45 DAT), number of pubescence (abaxial and adaxial), number of leaves (90 DAT), per cent plant survival (30 DAT) and average fruit weight. It indicated the predominance of dominant alleles in the parent for these traits, in this generation. The estimates of F were positive but non-significant for plant height (45, 60 and 90 DAT), number of branches (45 and 90 DAT), stem girth (90 DAT), number of leaves (45 DAT), leaf area (45 and 60 DAT), per cent plant survival (45 and 60 DAT), disease severity index on vegetative parts (30 and 60 DAT), disease severity index on flowering and fruiting parts (30, 45 and 60 DAT), vector population (30, 45 and 60 DAT), number of fruits per plant and yield per plant. This may indicate that the parents of interest had more recessive alleles for these characters. F estimate was negative for number of branches (60 DAT), stem girth (60 DAT), number of leaves (45 DAT), leaf area (90 DAT) and disease severity index on vegetative parts (45 DAT), implying that both dominance and recessive genes contributed equally to this trait in the parents of present study.

Estimates of dominance effect over loci (h^2) were positive and significant for leaf area (45 DAT) and per cent plant survival (30 DAT). It indicated the dominance effect expressed as the algebraic sum over all loci as heterozygous phases in all the crosses.

Average degree of dominance over all loci $(H_1/D)^{1/2}$, was more than unity for all the morphological, growth, disease index and yield parameters except for leaf area at (90 DAT). This shows the presence of over dominance for all these characters. Similar results were reported by Thakur and Kohli (2005). The negative effects of alleles in parents were compensated by positive alleles in hybrids resulting over dominance. Hence, selection of parents with high positive alleles, dominant genes, manifests dominance in hybrids. The degree of dominance might be caused either due to presence of correlated gene distribution and/or due to unidirectional dominance with plus or minus effects and seemed to be not due to epistasis. It appeared that the additive and dominance components (Hayman, 1954b) may likely to be confounded due to the presence of correlated gene distribution. Therefore, both the assumptions *i.e.*, no epistasis and no correlated gene distribution underlying diallel analysis seemed to be not valid (Jagtap and Kolhe, 1987). Estimate of $(H_1/D)^{1/2}$ for leaf area at 90 DAT was less than unity, indicating presence of partial dominance for this trait.

Estimates of number of dominance and recessive genes in parents (KD/KH) were more than unity for all the characters, except for number of branches (60 DAT) and number of leaves (45 DAT). This indicates presence of more of dominant alleles in parents. More recessive alleles may be present in parents for number of branches (60 DAT) and number of leaves (45 DAT), as the values of KD/KH are less than unity. Estimates of number of genes groups controlling that character and exhibiting dominance (h^2/H_2) were less than unity for all the characters studied. This under estimation may be due to the fact that the dominance effects of the genes affecting these traits are not equal in size and direction.

Narrow sense heritability estimates were high for all the characters except for plant height (60 DAT) and average fruit weight. These characters may be controlled by additive genetic variance. This indicated that the individual genotype can be evaluated readily from their phenotypic expression. Simple selection will be more effective in these sets of materials exhibiting greater additive genetic variability and desirable mean performance.

It is evidenced from the study that both additive and non additive gene effects are involved in the genetic control of the traits. So, both gene effects must be considered while developing superior lines. Tomato is a homozygous self pollinated crop and thus it does not make use of the dominance effect of genes at individual loci. Therefore, crosses involving high GCA estimates are required for selection in advanced generations. It is also evidenced from the study that genotypes must be evaluated under stressed conditions for different traits to design TyLCV tolerant lines.

5.5.5 Heterosis

Heterosis is estimated for 14 characters viz., plant height, number of branches, stem girth, number of pubescence (abaxial and adaxial), number of leaves, leaf area, per cent plant survival, disease severity index on vegetative and fruiting parts, vector population, number of fruit per plant, average fruit weight and yield per plant. Significant heterosis was observed in both positive and negative directions for all the morphological, growth, disease index and yield parameters except for plant height.

This indicates that both additive and non additive gene effects are involved in the genetic control of these traits. No significant positive heterosis observed for plant height. This indicates the predominance of non-additive gene action governing inheritance of this trait. Presence of additive and non-additive gene action was also proved by the diallel results. The observed significant heterosis justify the importance of genetic makeup of the parents involved and the genetic divergence between them. The result also indicates that there is a good scope for improvement of the above mentioned traits by heterosis breeding (Fig. 9). Similar reports were recorded by Fageria *et al.* (2001), Joshi and Thakur (2003), Asati *et al.* (2007), Singh *et al.* (2007), Singh *et al.* (2008), Minuyappa *et al.* (1991), Singh *et al.* (1999), Nainar and Pappiah (2002), Ali *et al.* (2002), Maruthi *et al.* (2003), Joshi and Choudhary (1981) and (Farooq *et al.*, 2005).

5.5 Hybrids with combined tolerance to drought and TyLCV

Present study was aimed at tracing out the genetics of drought and TyLCV tolerance in tomato. Eight parents were selected for the diallel analysis out of which two each were tolerant to TyLCV, susceptible to TyLCV, tolerant and susceptible to drought. By hybridization total 28 hybrids were developed. When these hybrids were evaluated to the drought and TyLCV stress, it was observed that *per se* performance of four hybrids was excellent. The hybrids are L 01942 x L 06231, L 06052 x TLB 133, L 06052 x L 06231 and L 09142 x TLB 133 (Plate 9 to 12). These were tolerant to drought as well as TyLCV. These hybrids shared four common parents viz., P1 (L 01942), P2 (L 06052), P5 (TLB 133) and P6 (L 06231). The parents P1 and P2 were tolerant to TyLCV and P5 and P6 were tolerant to drought. These genotypes were selected from diverse genetic groups. This also might have resulted high heterosis for the tolerant characters. High root length, volume, chlorophyll content, pubescences were helpful for these hybrids to get adapted to the adverse conditions. Combination of these lines proved that introgression of multiple resistances is possible in tomato. Values of some important characters for these selected hybrids are presented in Table 115. Plate 13a to h depicts the root parameters of these hybrids.



Plate 9. L 01942 x TKB 133



Plate 10. L 01942 x L 06231



Plate 11. L 06052 x TLB 133

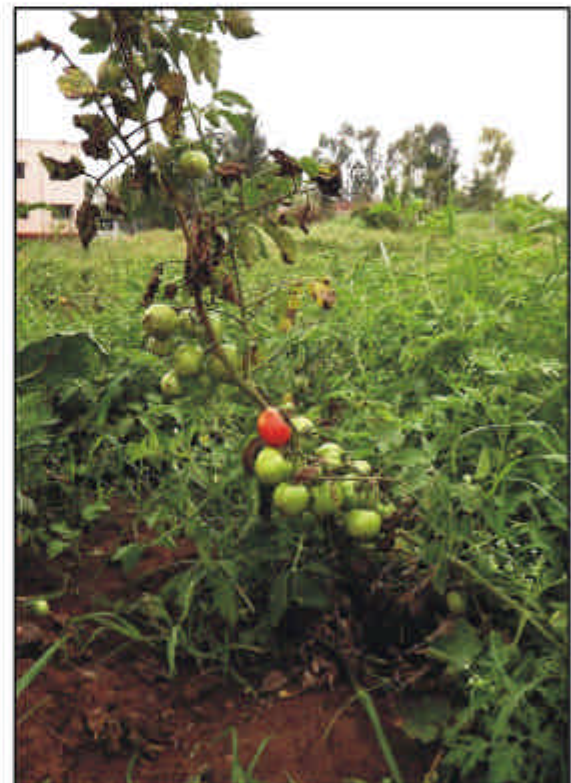


Plate 12. L 06052 x L 06231

Table 115. Details of important characters for the selected hybrids

Characters	Trials	P1xP5	P1xP6	P2xP5	P2xP6
Plant height (cm)	IR 1	54.96	71.93	48.75	49.51
	IR 2	48.11	57.29	35.86	30.09
	Ty	52.43	54.10	50.52	50.36
Number of branches	IR 1	25.65	24.50	20.50	19.93
	IR 2	17.21	15.72	14.93	13.87
	Ty	17.84	21.66	17.84	18.42
Root length (cm)	IR 1	40.81	38.21	40.83	40.25
	IR 2	71.52	67.44	75.94	75.61
Root volume (cc)	IR 1	39.73	32.71	37.90	29.36
	IR 2	48.74	47.03	47.75	44.19
Stomata count	IR 1	8.38	7.76	7.50	7.64
	IR 2	6.75	6.39	6.01	6.04
Number of pubescence	IR 1	393.29	473.63	514.90	474.52
	IR 2	501.76	1588.23	1565.12	2456.75
	Ty	507.28	440.04	431.26	419.84
Per cent plant survival (%)	Ty	93.33	93.10	94.60	93.79
Proline content ($\mu\text{g g}^{-1}$)	IR 1	244.03	318.81	308.61	285.75
	IR 2	410.70	499.89	530.98	457.53
Chlorophyll a ($\mu\text{g}/100\text{g}$)	IR 1	2.45	2.47	2.46	2.08
	IR 2	1.71	1.82	1.81	1.66
Chlorophyll b ($\mu\text{g}/100\text{g}$)	IR 1	0.63	0.65	0.60	0.57
	IR 2	0.51	0.61	0.64	0.62
Total chlorophyll ($\mu\text{g}/100\text{g}$)	IR 1	3.07	3.11	3.05	2.65
	IR 2	2.22	2.43	2.45	2.28
Number of fruits per plant	IR 1	157.60	157.46	181.94	185.28
	IR 2	122.66	141.03	178.23	207.57
	Ty	86.33	107.62	81.01	104.34
Average fruit weight (g)	IR 1	18.19	45.92	24.11	46.45
	IR 2	22.07	46.93	29.13	47.66
	Ty	43.38	27.98	40.76	25.78
Yield per plant (Kg)	IR 1	2.87	7.18	4.39	8.59
	IR 2	2.71	6.51	5.16	9.76
	Ty	3.76	3.01	3.33	2.70

P1 - L 01942; P2 - L 06052; P5 - TLB 133; P6 - L 06231; IR 1 - Normal Irrigation;
 IR 2 - Restricted Irrigation; Ty - TyLCV trial



Plate 13. Root length of a. L 01942 x TLB 133; b. L 01942 x L 06231; c. L 06052 x TLB 133; d. L 06052 x L 06231 and root volume of e. L 01942 x TLB 133; f. L 01942 x L 6231; g. L 06052 x TLB 133 and h. L 06052 x L 06231

5.6 Future line of work

The present work is basic work to combine biotic and abiotic stress tolerance in tomato. In future, the top performing hybrids may be tested in multilocation trials for stability to their tolerance for TyLCV as well as drought. These may also be used in line development program. Lines with high GCA may be used to develop hybrids with different combination of parents. New tools viz., marker assisted selection and QTLs may be developed. Tolerance for TyLCV has to be confirmed whether it is due to tolerance to pest or tolerance to virus.

6. SUMMARY AND CONCLUSIONS

The present research work on Genetics of drought and Tomato Leaf Curl Virus tolerance in tomato (*Solanum lycopersicum* L.) was conducted in experimental field of Department of Crop Improvement and Biotechnology, Kittur Rani Channamma College of Horticulture, Arabhavi, Gokak taluk, Belgaum district, Karnataka. This experiment was conducted during 2011 to 2014.

Hundred tomato genotypes collected from different sources were evaluated for their performance against TyLCV stress. This evaluation was conducted during *rabi* of 2011. No pest or disease control measures were adopted to ensure proper spread of disease in the field. The performance of these tomato genotypes was analyzed for different morphological, growth, disease index and yield parameters. Genotypes varied significantly for all the traits. The difference between GCV and PCV was found to be less indicating less effect of environment on the expression of these traits. GCV was high for most of the characters which indicated that the variation was mostly due to the genetic makeup of the genotypes. Heritability and genetic advance values were also high for all the traits. This point for the effectiveness of simple selection would be good for crop improvement as additive genes govern inheritance. The genotypes were then divided into eight clusters based on Mahalanobis's D^2 analysis.

The genotypes which were used for screening for TyLCV resistance were used for screening for drought tolerance. This experiment was conducted in *Summer* 2012. Genotypes were exposed for two types of irrigation treatments, one with normal irrigation (IR1) and the other with restricted irrigation *i.e.*, once in a week (IR2). Results pertaining to this experiment are presented below. Genotypes varied significantly for all the characters both under stressed as well as non stressed conditions. High GCV and PCV were observed for most of the characters indicating the wealth of genetic variation present among the genotypes. High heritability and genetic advance over mean values point at the feasibility of simple selection of improvement of these traits. The results of the experiment also showed that genotypes for drought tolerance need to be selected under stressed condition. Genotypes were further classified into seven (IR 1) and ten (IR 2) clusters separately for stressed and non stressed conditions based on Mahalanobis's D^2 statistics.

Eight parents were selected from the above two evaluation trials based on their *per se* performances. Genotypes L 01942 (cluster 6) and L 06052 (cluster 7) were selected as tolerant parents and genotype L 02079 (cluster 2) and LA 3913 (cluster 5) were selected as susceptible parents for the further study. Genotype TLB 133 (cluster 3 in IR 1 and IR 2) and L 06231 (cluster 2 in IR 1 and cluster 1 in IR 2) were selected as tolerant parents. Genotype L 02692 (cluster 6 in IR 1 and cluster 8 in IR 2) and BL 1188 (cluster 4 in IR 1 and cluster 2 in IR 2) were selected as susceptible parents.

These selected parents were crossed in diallel fashion (without reciprocals) to develop 28 hybrids. These hybrids were further evaluated along with their parents separately for TyLCV and drought resistance. For drought tolerance, evaluation was done during *Summer* 2013 and for TyLCV tolerance it was done during *rabi* 2013.

Analysis of variance for different morphological, growth, biochemical and yield parameters showed significant difference among the treatments, parents, hybrids and parents vs. hybrids for both IR 1 and IR 2. Analysis of variance for general and specific combining ability showed it was significant for all the morphological, growth, biochemical and yield parameters. This indicates the importance of both additive and non-additive genetic variances in the inheritance of the characters. The estimates of general and specific combining abilities suggested use of heterosis breeding for improvement of the above said traits for drought tolerance. It is evidenced from the study that both additive and non additive gene effects are involved in the genetic control of the traits. So, both gene effects must be considered while developing superior lines.

Analysis of variance for different morphological, growth, disease index and yield parameters showed significant difference among the treatments, parents, hybrids and parents vs. hybrids for most of the characters. Analysis of variance for general and specific combining ability showed it was significant for all the morphological, growth, disease index and yield parameters. This indicates the importance of both additive and non-additive genetic variances in the inheritance of the characters. General and specific combiners were identified for all the characters based on the GCA and SCA estimates. It was learnt from the study of general and specific combining ability that heterosis breeding method can be applied for crop improvement. It was evident from the study that both additive and non additive gene

effects were involved in the genetic control of the traits. So, both gene effects must be considered while developing superior lines. Tomato is a homozygous self pollinated crop and thus it does not make use of the dominance effect of genes at individual loci. Therefore, crosses involving high GCA estimates are required for selection in advanced generations. It is also evidenced from the study that genotypes must be evaluated under stressed conditions for different traits to design TyLCV tolerant lines.

Heterosis was estimated over better parent (heterobeltiosis) under both drought and TyLCV tolerance trials. Many heterotic hybrids were identified for different characters. Estimates of heterosis justified the previous results indicating heterosis breeding to be good tool for crop improvement in tomato.

Out the 28 hybrids, four hybrids were selected, which were tolerant to both drought as well as TyLCV. The hybrids were P1 x P6, P2 x P5, P 2 x P6 and P1 x P5. These hybrids shared four common parents viz., P1 (L 01942), P2 (L 06052), P5 (TLB 133) and P6 (L 06231). The parents P1 and P2 were tolerant to TyLCV and P5 and P6 were tolerant to drought. These genotypes were selected from diverse genetic groups. This also might have resulted high heterosis for the tolerant characters. High root length, volume, chlorophyll content, pubescences were helpful for these hybrids to get adapted to the adverse conditions. Combination of these lines proved that introgression of multiple resistances in possible is tomato.

The present work is basic work to combine biotic and abiotic stress tolerance in tomato. In future, the top performing hybrids may be tested in multilocation trials for stability to their tolerance for TyLCV as well as drought. These may also be used in line development program. Lines with high GCA may be used to develop hybrids with different combination of parents. New tools viz., marker assisted selection and QTLs may be developed. Tolerance for TyLCV has to be confirmed whether it is due to tolerance to pest or tolerance to virus.

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* - *Originals not seen*

Appendix I Meteorological data of Arabhavi during the period of experiment

Month	Rainfall (mm)			Temperature (C ⁰)						Relative Humidity (%)		
				2011		2012		2013				
	2011	2012	2013	Max	Min	Max	Min	Max	Min	2011	2012	2013
January	0.00	0.00	0.00	33.31	12.34	32.70	13.20	29.60	14.70	67.00	58.56	62.20
February	0.00	0.00	0.00	35.96	12.45	33.20	16.80	32.50	16.40	63.42	57.47	56.38
March	5.10	0.00	3.60	37.15	14.56	35.00	19.90	36.50	19.60	57.77	75.22	49.00
April	14.00	164.50	28.00	39.22	17.61	36.50	21.10	37.40	19.80	54.44	61.00	57.52
May	78.00	31.20	-	39.33	18.98	35.50	21.50	-	-	66.11	84.43	-
June	309.60	233.60	-	35.40	18.90	38.30	20.90	-	-	82.44	77.24	-
July	315.70	144.80	-	29.35	18.58	26.00	20.90	-	-	93.33	88.23	-
August	182.30	256.80	-	28.34	18.81	28.10	20.60	-	-	93.11	80.65	-
September	116.30	72.20	-	31.24	18.21	28.50	18.40	-	-	85.33	90.12	-
October	98.70	229.00	-	32.36	16.70	31.30	17.80	-	-	86.77	65.62	-
November	15.00	14.70	-	31.86	12.85	30.20	15.23	-	-	74.00	71.00	-
December	0.00	0.00	-	31.33	11.47	31.50	12.42	-	-	68.77	66.52	-

Appendix II. List of germplasm lines used in the experiment

Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source
1	BL 1187	AVRDC, Taiwan	36	L 02222	AVRDC, Taiwan	71	L 06231	AVRDC, Taiwan
2	BL 1188	"	37	L 02248	"	72	L 06238	"
3	BL 1198	"	38	L 02692	"	73	L 06240	"
4	BL 1199	"	39	L 02709	"	74	L 1023	"
5	BL 1200	"	40	L 02778	"	75	L 1030	"
6	BL 1201	"	41	L 06043	"	76	LA 3923	"
7	LA 3913	"	42	L 06044	"	77	Arka Abha	IIHR, Bengaluru
8	LA 3914	"	43	L 06046	"	78	Arka Alok	"
9	LA 3922	"	44	L 06049	"	79	Arka Meghali	"
10	LA 3923	"	45	L 06052	"	80	Arka Saurabh	"
11	CLN 2116 B	"	46	L 06057	"	81	Arka Vikas	"
12	CLN 2498 E	"	47	L 06058	"	82	Shakti	KAU, Thrissur
13	CLN 2585 A	"	48	L 06106	"	83	Mukti	"
14	CLN 2585 C	"	49	L 06112	"	84	Anagha	"
15	CLN 2585 D	"	50	L 06115	"	85	Nandi	UAS, Bengaluru
16	CLN 2679 E	"	51	L 06119	"	86	PKM 1	TNAU, Coimbatore
17	CLN 2679 F	"	52	L 06122	"	87	SL 120	IIVR, Varanasi

Contd....

Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source	Sl. No.	Genotypes	Source
18	CLN 2714 G	"	53	L 06123	"	88	DMT - 2	UAS, Dharwad
19	CLN 2714 H	"	54	L 06179	"	89	GK - 2	Local Selection
20	CLN 2714 J	"	55	L 06181	"	90	THB 205	UAS, Bengaluru
21	L 01023	"	56	L 06181	"	91	TLB 130	"
22	L 01033	"	57	L 06185	"	92	TLB 133	"
23	L 01049	"	58	L 06188	"	93	M. Palli Tomato	"
24	L 01049	"	59	L 06190	"	94	Patriot	"
25	L 01139	"	60	L 06193	"	95	Podland Pink	"
26	L 01318	"	61	L 06194	"	96	Red Pear	"
27	L 01463	"	62	L 06201	"	97	S. Early	"
28	L 01463	"	63	L 06208	"	98	S. Harry	"
29	L 01464	"	64	L 06218	"	99	Tommy Toe	"
30	L 01696	"	65	L 06219	"	100	W. Cherry	"
31	L 01745	"	66	L 06220	"			
32	L 01869	"	67	L 06221	"			
33	L 01933	"	68	L 06223	"			
34	L 01942	"	69	L 06229	"			
35	L 02079	"	70	L 06230	"			

Appendix III. Mean values of tomato genotypes for plant height, number of branches and stem girth under TyLCV evaluation

Genotypes	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
BL 1187	30.46	58.01	11.23	9.63	13.85	13.94	6.53	6.70	4.43
BL 1188	28.70	63.43	11.90	6.56	13.36	13.25	4.63	11.47	5.50
BL 1198	24.42	68.71	42.47	8.25	12.23	14.03	5.93	15.27	16.03
BL 1199	24.05	32.27	48.20	8.93	13.74	14.53	5.83	14.60	16.33
BL 1200	29.11	63.52	13.43	6.39	10.60	10.49	5.40	14.43	6.80
BL 1201	30.57	63.64	12.87	8.40	12.68	14.54	5.87	7.73	4.07
LA 3913	28.77	65.16	11.53	10.16	11.79	12.71	5.57	12.07	15.40
LA 3914	25.23	63.79	19.60	10.02	15.03	17.85	4.47	12.73	9.77
LA 3922	29.59	65.98	11.63	8.76	15.46	16.12	6.00	14.07	11.47
LA 3923	31.77	43.29	47.10	10.17	13.90	13.34	4.70	14.97	15.67
CLN 2116 B	20.71	43.00	14.63	7.64	14.19	14.46	3.97	10.83	6.13
CLN 2498 E	20.87	37.97	12.30	7.68	12.60	14.56	4.90	12.43	5.30
CLN 2585 A	19.97	37.50	13.87	7.90	13.19	13.15	4.93	10.83	4.93
CLN 2585 C	21.40	37.17	12.57	8.11	14.42	13.96	4.33	11.17	5.20
CLN 2585 D	22.97	38.07	12.07	7.49	12.54	13.30	4.93	11.00	5.47
CLN 2679 E	19.57	39.10	12.30	8.97	12.77	14.37	3.57	11.17	10.53
CLN 2679 F	17.37	39.53	11.60	5.80	11.90	11.63	5.17	13.80	6.33
CLN 2714 G	18.27	40.13	11.60	5.75	12.44	11.20	6.80	14.90	6.23
CLN 2714 H	21.51	36.03	11.23	5.33	12.09	10.99	5.57	14.47	6.67
CLN 2714 J	20.90	39.57	11.67	6.75	10.75	11.94	6.67	14.03	7.10
L 01023	33.82	63.49	47.77	10.08	13.84	14.59	5.87	15.37	16.03
L 01033	28.95	58.23	9.97	11.40	12.96	12.53	6.53	12.13	15.83
L 01049	27.88	63.74	10.67	8.84	13.83	15.79	6.07	15.00	11.83
L 01050	26.14	53.06	14.80	6.37	17.23	18.06	8.80	14.80	14.80
L 01139	30.03	65.58	11.40	7.39	11.88	14.30	6.60	8.47	4.03
L 01318	29.34	65.35	10.73	11.54	11.75	12.52	6.20	11.87	15.77
L 01462	26.09	49.83	20.53	11.38	13.07	18.27	5.33	13.47	11.83
L 01463	27.57	35.73	11.17	5.61	12.73	11.38	6.27	14.67	6.67
L 01464	29.17	53.99	12.87	9.04	13.24	15.34	5.50	8.00	4.00
L 01696	31.22	48.15	11.73	6.69	11.47	14.42	5.60	7.87	4.30
L 01745	30.71	68.11	47.73	9.64	12.80	13.33	6.60	15.50	15.27
L 01869	37.22	63.50	11.73	7.97	14.13	16.15	6.53	14.27	11.97
L 01933	30.01	42.69	47.60	8.95	14.13	14.99	4.50	21.93	14.90
L 01942	31.29	65.31	46.37	9.54	14.17	14.39	4.10	14.80	16.03
L 02079	26.91	53.48	11.00	10.58	11.58	12.42	6.53	10.37	14.67

Contd....

Genotypes	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 02222	26.14	55.26	18.53	9.19	13.91	18.71	4.27	10.93	10.07
L 02248	29.51	42.87	10.60	9.68	14.23	15.85	5.73	13.80	11.73
L 02692	25.43	52.89	11.23	8.28	12.28	14.29	6.10	8.23	3.90
L 02709	25.80	53.43	46.33	9.88	14.54	12.97	6.60	15.23	15.93
L 02778	32.82	57.99	12.63	9.79	15.45	15.36	5.90	14.10	11.97
L 06043	23.88	48.44	47.33	8.14	13.27	14.85	3.80	15.13	14.30
L 06044	24.25	47.63	18.17	9.94	13.24	13.40	8.40	16.03	14.87
L 06046	28.97	57.50	10.07	10.50	14.10	12.48	4.10	13.37	10.27
L 06049	25.99	63.75	18.87	11.70	12.97	14.52	8.57	15.37	14.27
L 06052	25.87	64.07	48.67	10.05	14.31	14.46	6.77	15.27	16.63
L 06057	26.11	53.36	11.37	7.28	13.56	13.72	6.00	8.20	4.53
L 06058	29.67	65.35	18.03	8.36	12.47	14.85	8.43	15.87	14.40
L 06106	25.44	63.52	13.13	9.92	15.41	16.53	6.33	15.03	12.27
L 06112	25.74	64.24	10.30	9.75	11.38	12.43	6.20	12.93	15.30
L 06115	27.05	48.47	10.17	9.69	13.93	12.85	5.23	11.03	15.27
L 06119	17.73	63.29	47.10	10.11	14.38	14.20	5.37	15.17	15.87
L 06122	30.20	68.09	9.73	6.64	11.72	12.44	5.40	13.50	6.80
L 06123	30.16	68.55	17.00	10.69	12.94	13.21	7.80	15.27	13.97
L 06179	22.47	48.94	20.33	10.28	13.38	17.15	4.27	11.07	9.93
L 06181	23.71	47.88	12.93	7.36	12.82	14.84	4.90	11.87	5.17
L 06182	28.11	53.77	12.43	6.25	11.56	12.25	5.67	14.23	6.43
L 06185	27.73	59.61	47.83	10.12	12.87	13.84	6.40	15.63	15.33
L 06188	19.32	53.15	10.30	10.41	12.44	12.37	6.30	12.57	14.37
L 06190	30.40	68.55	12.47	6.94	12.18	12.59	6.70	7.90	4.07
L 06193	29.43	65.08	46.03	10.23	12.88	14.97	4.57	15.43	15.30
L 06194	28.30	53.69	13.80	8.14	13.64	13.67	4.73	10.97	5.37
L 06201	24.33	47.45	48.60	9.39	14.02	13.35	4.77	16.17	15.27
L 06208	28.61	57.90	46.10	8.03	14.09	13.14	5.57	16.30	14.73
L 06218	29.63	65.29	46.63	9.98	12.74	13.75	5.43	16.33	16.00
L 06219	29.15	53.92	20.00	11.74	14.46	16.95	4.63	12.43	9.73
L 06220	30.74	68.20	19.63	10.13	15.61	17.57	6.13	14.53	11.90
L 06221	28.71	64.90	11.27	9.67	13.40	15.77	6.37	14.50	11.73
L 06223	25.05	63.51	18.20	11.14	12.35	12.86	9.00	15.70	13.83
L 06229	29.33	62.91	10.30	10.84	12.66	13.16	4.67	14.67	15.63
L 06230	28.08	57.40	10.73	8.21	14.75	14.84	6.23	14.80	11.67

Contd....

Genotypes	Plant height (cm)			Number of branches			Stem girth (cm)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 06231	23.43	47.43	13.53	6.91	14.70	17.51	9.17	15.10	14.57
L 06238	25.28	53.32	19.83	9.71	14.48	12.63	8.37	15.70	14.00
L 06240	24.89	63.19	14.40	7.68	15.67	15.94	8.43	15.40	15.07
L 1023	25.75	62.79	20.43	10.15	13.33	17.88	5.67	14.20	10.90
L 1030	28.36	65.51	12.43	5.10	10.04	13.12	6.70	14.83	6.60
LA 3924	31.39	64.02	11.20	5.46	11.97	13.32	7.17	14.57	6.13
Arka Abha	31.59	63.23	10.13	8.78	15.03	15.11	5.20	14.23	11.80
Arka Alok	30.99	63.44	19.27	8.83	12.26	13.53	9.47	15.27	13.33
Arka Meghali	32.09	63.06	48.40	10.01	14.53	13.03	4.67	15.53	15.17
Arka Saurabh	31.41	57.63	11.17	10.66	12.59	12.21	6.70	11.73	15.13
Arka Vikas	31.53	58.62	21.17	9.72	14.58	17.08	5.73	14.20	11.63
Shakti	25.43	49.23	14.47	8.91	16.14	17.25	8.33	15.10	15.17
Mukti	26.34	48.11	18.80	9.29	12.14	12.53	9.20	15.87	14.97
Anagha	32.17	58.18	10.57	5.32	12.58	13.55	6.87	13.53	6.50
Nandi	31.77	57.40	47.80	8.43	15.02	14.97	5.30	16.07	15.17
PKM 1	25.05	47.88	10.83	8.61	14.17	16.11	6.23	15.77	11.90
SL 120	25.50	53.41	15.10	8.07	16.13	16.14	8.63	15.10	14.10
DMT - 2	24.09	49.22	17.47	9.63	11.95	13.70	8.23	15.40	14.73
GK - 2	28.39	58.45	14.80	6.75	10.26	11.65	7.70	15.07	13.80
THB 205	26.21	63.45	18.67	9.30	12.10	13.66	8.13	14.83	13.93
TLB 130	29.41	66.54	14.83	5.45	10.47	11.76	7.57	15.10	12.23
TLB 133	26.56	55.37	13.87	6.40	9.99	10.97	8.37	15.23	14.53
M. Palli Tomato	24.70	63.66	15.23	7.69	10.29	12.55	8.53	15.33	14.03
Patriot	30.09	69.28	16.03	6.85	9.16	11.90	7.77	14.77	13.50
Podland Pink	29.45	68.33	16.33	6.79	9.82	10.81	8.63	15.30	13.60
Red Pear	30.49	64.40	16.10	6.27	9.39	12.33	8.20	15.10	13.60
S. Early	27.75	57.04	14.60	7.45	9.69	11.24	7.90	15.70	13.83
S. Harry	25.09	53.48	13.73	6.87	10.49	10.83	8.03	14.67	13.70
Tommy Toe	27.81	53.59	14.87	5.20	10.38	11.69	8.17	15.10	14.60
W. Cherry	27.88	63.40	15.00	5.70	9.34	12.72	7.67	15.90	14.60

Appendix IV. Mean values of tomato genotypes for number of leaves, leaf area and per cent plant survival under TyLCV evaluation

Genotypes	Number of leaves			Leaf area (cm ²)			Per cent Plant Survival (%)				
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
BL 1187	27.08	38.36	21.29	93.19	64.70	17.61	97.00	81.33	35.00	16.67	0.00
BL 1188	36.09	47.50	20.88	115.74	99.99	20.51	89.33	64.33	29.33	13.00	0.00
BL 1198	38.10	44.01	35.97	145.67	191.23	115.25	98.00	68.67	55.33	57.67	46.67
BL 1199	38.45	44.29	32.05	119.62	180.52	34.82	90.00	76.00	59.00	18.00	0.00
BL 1200	34.78	44.03	20.72	110.62	104.95	20.36	79.67	57.00	17.00	7.00	0.00
BL 1201	27.33	38.71	20.65	90.07	66.95	18.48	76.33	66.00	44.33	15.67	0.00
LA 3913	31.67	35.20	21.19	91.87	100.71	21.23	90.00	48.67	26.67	13.67	0.00
LA 3914	30.12	31.30	30.59	73.83	85.56	33.66	86.33	59.33	43.67	42.00	29.67
LA 3922	30.63	30.60	28.54	85.40	84.68	35.24	90.00	51.33	86.67	82.33	72.33
LA 3923	40.06	44.66	39.52	153.19	191.89	126.12	100.00	61.67	55.00	55.33	46.67
CLN 2116 B	28.37	40.38	21.93	90.43	72.32	17.54	89.33	59.67	35.33	8.00	0.00
CLN 2498 E	36.24	43.97	20.62	124.78	94.93	18.83	89.00	61.67	16.67	11.67	0.00
CLN 2585 A	35.25	43.38	19.13	108.74	91.79	19.27	89.67	82.67	39.67	10.00	0.00
CLN 2585 C	37.56	40.48	20.24	117.99	93.15	18.47	70.00	75.00	34.33	9.33	0.00
CLN 2585 D	35.59	42.63	20.56	106.74	97.79	20.91	89.67	74.67	37.33	12.67	0.00
CLN 2679 E	36.15	43.72	21.58	127.64	98.73	22.47	89.33	62.00	36.00	10.00	0.00
CLN 2679 F	33.10	36.05	25.86	117.52	128.05	22.91	60.00	45.67	14.67	2.67	0.00
CLN 2714 G	36.75	41.89	18.75	124.18	93.69	15.78	89.33	71.67	23.33	4.33	0.00
CLN 2714 H	35.91	44.44	20.56	115.67	101.18	20.57	50.00	52.00	35.33	11.67	0.00
CLN 2714 J	35.41	43.54	20.55	114.58	105.03	19.71	90.00	71.67	39.67	10.67	0.00
L 01023	39.67	43.82	30.33	118.09	198.05	34.36	55.00	75.00	55.00	15.00	0.00
L 01033	31.98	35.59	21.91	90.46	106.28	18.43	73.00	52.33	25.33	19.67	0.00
L 01049	28.21	30.95	29.83	72.05	87.55	27.84	90.00	55.00	87.00	82.33	76.33
L 01050	31.96	36.12	32.70	113.02	115.66	37.00	54.67	22.00	81.67	48.00	33.00
L 01139	28.37	37.64	27.17	91.21	65.83	18.00	45.00	67.00	28.33	26.33	0.00
L 01318	32.35	35.15	20.96	89.67	99.35	13.92	34.00	47.00	28.33	19.00	0.00
L 01462	28.74	29.26	32.81	71.32	82.40	39.43	18.00	48.00	48.00	42.33	36.67
L 01463	35.72	42.14	19.80	121.44	97.22	17.92	79.67	52.00	13.33	3.67	0.00
L 01464	25.81	41.11	21.78	84.26	70.47	18.24	90.00	24.00	32.00	21.33	0.00
L 01696	26.46	40.64	21.65	89.64	71.47	17.92	90.00	89.00	33.33	19.00	0.00
L 01745	35.39	44.75	29.72	107.15	189.26	31.19	55.00	44.00	54.33	5.33	0.00
L 01869	28.91	30.43	31.84	73.90	86.98	34.91	95.00	53.33	86.33	83.00	76.67
L 01933	39.19	44.60	30.02	123.95	197.05	34.88	100.00	76.33	57.33	18.00	0.00
L 01942	40.87	42.78	38.77	152.88	185.46	124.90	100.00	71.67	52.33	55.33	43.67
L 02079	30.23	34.77	21.34	82.72	97.47	16.51	81.67	46.00	28.33	21.33	0.00

Contd...

Genotypes	Number of leaves			Leaf area (cm ²)			Plant Survival Percentage (%)				
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
L 02222	31.26	36.50	22.26	90.05	112.06	22.07	91.00	54.33	45.67	40.00	19.67
L 02248	30.20	32.43	27.71	80.32	95.12	27.88	100.00	55.00	86.67	83.00	74.33
L 02692	27.92	37.68	21.38	92.52	66.30	17.28	97.00	85.33	46.00	20.00	0.00
L 02709	40.88	44.57	32.45	123.46	188.80	39.13	55.00	73.67	57.67	19.67	0.00
L 02778	30.78	30.94	31.63	80.15	82.21	39.79	95.00	54.67	88.33	83.00	75.67
L 06043	38.09	44.74	31.13	114.56	187.20	26.68	92.53	71.67	62.67	17.00	0.00
L 06044	30.73	37.18	32.62	104.91	119.14	35.86	92.33	35.00	83.00	54.00	42.00
L 06046	31.61	36.41	20.23	98.67	116.11	17.81	94.67	70.00	46.00	45.33	23.67
L 06049	31.14	36.15	31.86	111.87	113.62	41.87	62.67	45.00	82.67	49.33	40.00
L 06052	38.36	45.70	39.77	147.17	203.78	126.72	56.00	69.67	55.00	56.00	44.00
L 06057	26.36	39.82	21.75	79.20	70.52	19.85	91.00	63.00	54.67	22.00	0.00
L 06058	32.21	36.32	31.19	113.99	116.95	39.58	90.33	47.67	79.33	54.67	41.00
L 06106	30.81	31.73	30.36	74.21	88.57	29.69	45.00	56.67	87.67	84.00	74.00
L 06112	33.02	34.59	19.78	96.92	107.21	17.53	85.67	44.00	19.00	4.67	0.00
L 06115	31.87	36.16	21.41	96.96	99.83	18.75	55.00	36.67	23.67	12.67	0.00
L 06119	38.97	43.80	37.61	150.55	202.75	115.73	67.00	74.00	54.33	53.33	44.33
L 06122	31.00	36.62	25.22	101.32	135.44	21.98	79.67	62.67	6.33	7.33	0.00
L 06123	38.08	34.90	31.59	132.37	110.69	38.74	74.26	52.00	83.00	47.67	38.33
L 06179	28.96	32.11	31.44	68.99	92.73	35.95	88.00	65.67	44.33	45.00	30.67
L 06181	27.95	39.85	21.15	95.34	70.56	15.76	55.00	71.00	30.00	14.67	0.00
L 06182	32.15	36.68	27.23	113.33	130.97	21.77	54.33	52.33	19.33	7.00	0.00
L 06185	39.56	44.74	39.09	148.08	195.36	114.56	90.00	72.00	53.33	17.00	0.00
L 06188	33.35	35.84	21.51	94.20	114.28	14.59	91.67	42.00	22.33	13.00	0.00
L 06190	28.26	38.97	21.62	86.92	67.55	17.58	68.67	34.00	28.67	22.00	0.00
L 06193	40.70	42.57	39.28	159.95	185.50	124.38	70.67	67.00	56.33	53.00	45.67
L 06194	27.42	38.62	21.79	85.96	64.70	16.22	89.67	75.67	23.67	11.00	0.00
L 06201	40.32	44.05	37.12	157.86	190.48	118.80	90.00	71.67	52.67	52.67	46.33
L 06208	38.32	42.84	37.27	149.33	200.88	120.31	92.00	75.33	50.67	9.00	0.00
L 06218	34.88	43.96	31.43	110.53	182.79	31.08	100.00	79.33	60.00	18.33	0.00
L 06219	30.12	35.49	21.33	82.56	108.24	20.32	91.67	65.00	42.00	46.00	30.00
L 06220	30.59	31.41	30.55	80.84	90.41	37.32	100.00	57.33	45.67	46.33	25.67
L 06221	27.88	32.53	29.30	73.42	90.59	36.76	59.67	35.33	87.00	82.67	72.67
L 06223	36.65	32.46	32.04	125.97	108.57	37.77	54.00	14.00	85.67	51.67	43.33
L 06229	31.80	35.32	20.68	93.17	105.28	16.24	95.00	45.67	31.33	7.33	0.00
L 06230	32.02	31.88	31.00	89.82	88.79	29.14	97.00	51.00	88.33	81.67	76.67

Contd.....

Genotypes	Number of leaves			Leaf area (cm ²)			Plant Survival Percentage (%)				
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
L 06231	32.27	36.64	32.68	111.89	118.76	35.46	51.00	46.00	79.00	52.33	40.67
L 06238	31.84	36.48	32.05	112.40	114.43	38.19	57.00	18.00	84.33	49.33	48.00
L 06240	31.35	37.45	31.97	112.56	116.45	33.54	90.00	34.00	85.33	57.00	41.33
L 1023	29.99	32.39	31.50	77.67	89.67	36.94	64.00	58.67	41.67	41.33	27.33
L 1030	31.51	35.50	25.99	114.01	136.19	22.55	79.67	50.67	9.33	3.67	0.00
LA 3924	35.92	44.80	20.59	114.92	95.13	19.89	79.00	45.00	10.33	4.33	0.00
Arka Abha	29.87	31.42	30.99	74.89	91.12	35.14	90.00	57.33	87.33	82.33	78.00
Arka Alok	32.91	35.39	30.73	119.62	120.19	37.44	93.00	43.39	79.00	51.00	40.33
Arka Meghali	38.06	42.17	28.70	122.00	173.61	29.83	100.00	78.33	49.67	18.33	0.00
Arka Saurabh	32.86	34.99	21.84	96.80	106.54	17.48	81.67	47.67	27.00	3.33	0.00
Arka Vikas	30.55	32.81	28.34	80.27	95.54	30.38	93.67	64.67	44.67	44.67	23.00
Shakti	31.24	37.76	30.87	103.92	125.37	36.33	98.67	48.33	82.33	50.00	37.00
Mukti	32.03	36.27	31.97	116.41	121.81	36.42	98.33	94.00	85.00	52.00	41.67
Anagha	36.18	41.86	20.45	108.63	95.22	18.71	79.00	56.33	15.67	4.33	0.00
Nandi	39.17	42.60	40.37	154.42	190.80	132.59	100.00	76.33	63.33	17.00	0.00
PKM 1	27.31	30.69	29.38	66.47	85.26	37.64	100.00	97.33	87.00	82.67	74.33
SL 120	32.17	38.35	32.88	110.06	125.56	39.23	96.67	94.33	84.33	54.33	35.67
DMT - 2	36.83	35.34	31.90	117.75	116.63	35.43	98.33	50.67	80.67	54.67	35.00
GK - 2	35.38	33.89	32.78	118.75	120.85	38.82	97.33	35.33	76.67	49.00	42.00
THB 205	35.76	33.23	30.41	121.23	109.34	35.73	99.33	94.67	85.33	58.33	39.00
TLB 130	35.64	33.05	30.66	112.89	112.87	40.40	98.00	21.67	81.33	49.67	39.33
TLB 133	38.28	33.62	32.39	128.85	107.72	42.68	98.00	94.67	79.67	56.33	42.67
M. Palli Tomato	37.29	32.97	33.11	117.71	102.62	39.83	95.33	75.33	57.33	38.67	13.67
Patriot	37.89	35.78	31.87	124.77	112.59	44.06	94.33	71.67	57.33	41.00	18.67
Podland Pink	37.77	34.80	29.84	125.79	110.55	34.51	94.33	25.67	55.67	40.67	13.67
Red Pear	37.32	33.65	32.23	125.28	115.40	41.66	98.00	51.00	57.33	40.00	13.00
S. Early	36.01	34.33	32.67	118.46	120.16	46.40	95.33	26.00	57.33	37.33	19.33
S. Harry	35.80	35.01	31.65	117.25	107.29	40.99	95.00	78.33	56.33	38.33	18.67
Tommy Toe	35.11	32.15	31.22	116.15	98.30	40.31	95.67	48.33	57.00	41.00	8.67
. Cherry	35.29	34.05	32.98	120.15	116.29	40.49	93.33	73.67	58.33	40.67	15.33

Appendix V. Mean values of tomato genotypes for disease severity index under TyLCV evaluation

Genotypes	Disease Severity Index (Vegetative parts)					Disease Severity Index (Flowering and fruiting parts)				
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
BL 1187	2.00	2.87	3.60	3.47	4.00	90.00	90.00	2.57	3.23	4.00
BL 1188	0.27	1.50	2.20	3.27	4.00	90.00	1.27	3.17	3.50	4.00
BL 1198	4.00	0.00	0.60	0.23	2.50	0.00	2.27	3.17	3.17	3.23
BL 1199	1.73	0.47	1.70	3.10	4.00	0.00	0.37	1.30	2.23	2.67
BL 1200	0.60	1.47	1.47	2.80	4.00	0.53	1.13	3.00	3.17	4.00
BL 1201	0.47	95.00	2.77	3.40	4.00	0.90	1.60	2.53	3.07	4.00
LA 3913	1.20	1.97	2.90	3.33	4.00	0.93	1.83	2.93	3.73	2.67
LA 3914	0.53	2.10	2.20	3.20	3.50	1.17	2.03	3.43	3.40	3.47
LA 3922	1.53	1.17	2.37	3.20	3.50	0.00	3.30	3.37	3.43	3.43
LA 3923	1.00	0.00	0.60	1.53	2.30	0.00	2.47	3.70	3.20	3.33
CLN 2116 B	0.50	1.43	1.60	2.73	4.00	0.37	1.20	2.50	3.27	4.00
CLN 2498 E	4.00	1.40	2.03	3.33	4.00	1.70	1.57	2.50	3.47	4.00
CLN 2585 A	4.00	1.20	1.23	3.53	4.00	1.00	1.73	2.37	3.43	4.00
CLN 2585 C	0.33	1.17	2.17	2.97	4.00	0.83	1.57	2.60	3.47	4.00
CLN 2585 D	0.57	1.27	2.00	3.53	4.00	0.60	1.47	2.97	3.50	4.00
CLN 2679 E	0.70	1.57	1.83	2.73	4.00	0.57	1.30	3.23	3.60	4.00
CLN 2679 F	0.27	1.53	2.67	2.83	4.00	0.40	1.30	2.87	3.30	4.00
CLN 2714 G	0.80	1.33	2.20	3.07	4.00	0.60	1.30	2.93	3.47	4.00
CLN 2714 H	0.20	1.33	1.83	3.77	4.00	0.40	1.20	2.37	3.33	4.00
CLN 2714 J	0.27	1.63	1.97	2.90	4.00	0.37	1.17	2.90	3.20	4.00
L 01023	0.00	0.60	1.63	2.87	4.00	0.00	0.30	1.17	2.47	2.67
L 01033	0.63	1.90	3.03	3.30	4.00	1.20	2.13	2.13	3.57	2.67
L 01049	4.00	1.37	2.27	3.40	3.53	0.00	3.50	3.33	3.70	3.50
L 01050	0.27	1.67	2.13	3.73	3.23	1.60	3.47	3.37	3.37	3.70
L 01139	0.20	1.83	3.40	3.30	4.00	0.47	1.57	2.60	3.20	4.00
L 01318	4.00	1.80	2.93	3.40	4.00	1.27	1.53	2.57	3.40	2.67
L 01462	0.67	1.37	2.30	3.23	3.50	0.57	2.37	3.07	3.60	3.53
L 01463	0.40	1.87	1.60	2.37	4.00	0.53	1.23	3.73	3.27	4.00
L 01464	45.00	2.17	2.73	3.27	4.00	0.63	1.20	2.67	3.37	4.00
L 01696	85.00	2.87	3.47	3.93	4.00	1.17	1.63	2.60	3.20	4.00
L 01745	95.00	0.77	1.53	3.17	4.00	0.00	0.43	1.13	2.23	2.67
L 01869	0.00	1.53	2.17	3.67	3.50	0.00	3.73	3.50	3.53	3.20
L 01933	0.00	0.37	1.67	2.50	4.00	0.00	0.30	1.17	2.40	2.67
L 01942	0.00	0.00	0.00	0.73	2.23	0.00	0.00	0.27	0.40	2.27
L 02079	1.33	1.50	3.23	3.37	4.00	1.27	2.00	2.57	3.57	2.67

Contd...

Genotypes	Disease Severity Index (V)					Disease Severity Index (F)				
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
L 02222	0.87	1.53	3.63	3.57	3.33	1.23	2.00	3.07	3.63	3.53
L 02248	0.00	1.63	2.17	3.60	3.50	0.00	3.43	3.20	3.70	3.27
L 02692	0.13	2.60	2.77	3.53	4.00	0.20	1.67	2.73	3.13	4.00
L 02709	0.00	0.50	1.60	3.20	4.00	0.00	2.03	2.43	3.57	2.67
L 02778	0.00	1.53	2.30	3.10	3.60	0.00	3.03	3.93	3.93	3.43
L 06043	0.00	0.50	1.50	2.63	4.00	0.00	0.70	1.23	2.07	2.67
L 06044	0.87	1.90	2.77	3.27	3.47	0.17	0.77	2.73	3.37	3.07
L 06046	0.67	1.50	2.83	3.43	3.43	0.40	2.07	3.17	3.47	3.67
L 06049	1.47	1.53	2.33	3.33	3.53	0.10	1.20	2.27	3.20	3.53
L 06052	0.00	0.00	0.00	1.13	2.67	0.00	0.00	0.27	0.53	1.77
L 06057	0.40	2.67	2.77	3.23	4.00	0.50	1.63	2.43	3.33	4.00
L 06058	0.67	1.83	2.37	3.47	3.50	0.03	0.83	2.60	3.43	2.97
L 06106	0.00	1.87	2.23	3.37	3.50	0.00	3.63	3.50	3.43	3.60
L 06112	1.17	2.63	2.93	3.27	4.00	1.27	2.03	2.50	3.17	2.67
L 06115	0.93	1.97	2.83	3.50	4.00	1.37	1.83	2.57	3.40	2.67
L 06119	0.00	0.00	0.53	0.87	2.67	0.00	2.13	2.70	3.27	3.50
L 06122	0.53	1.67	2.23	3.03	4.00	0.57	1.20	2.63	3.30	4.00
L 06123	1.23	1.43	2.60	3.27	3.70	1.47	2.83	2.67	2.47	3.10
L 06179	0.93	1.73	2.20	3.27	3.43	0.37	2.10	3.30	3.50	3.37
L 06181	0.67	1.50	1.93	3.03	4.00	1.07	1.53	2.60	3.57	4.00
L 06182	0.40	1.13	1.60	3.20	4.00	0.57	1.17	2.33	3.63	4.00
L 06185	0.00	0.00	0.00	1.30	4.00	0.00	0.00	0.27	0.87	2.67
L 06188	0.87	1.23	3.07	3.50	4.00	1.33	1.90	2.77	3.30	2.67
L 06190	0.70	3.03	3.40	3.37	4.00	0.73	1.43	2.30	3.63	4.00
L 06193	0.00	0.00	0.33	0.70	2.70	0.00	2.30	3.07	3.30	3.37
L 06194	0.53	1.53	1.50	2.53	4.00	0.90	1.40	2.27	3.30	4.00
L 06201	0.00	0.00	0.63	0.87	2.37	0.00	2.23	3.03	3.33	3.53
L 06208	0.00	0.00	0.00	0.57	4.00	0.00	0.00	0.33	1.03	2.67
L 06218	0.00	0.83	1.47	2.27	4.00	0.00	0.53	1.23	2.20	2.67
L 06219	0.30	1.87	2.33	3.30	3.43	0.37	2.13	3.43	3.43	3.10
L 06220	0.77	2.20	2.27	3.30	3.50	0.80	2.57	3.47	3.50	3.40
L 06221	0.00	1.63	2.27	3.53	3.33	0.00	2.73	3.23	3.73	3.67
L 06223	1.57	1.40	2.40	3.77	3.27	1.67	2.57	2.53	3.13	3.03
L 06229	1.27	1.70	2.63	3.57	4.00	1.33	2.23	2.60	3.50	2.67
L 06230	0.00	1.40	2.37	3.33	3.07	0.00	2.90	3.47	3.43	3.53

Contd...

Genotypes	Disease Severity Index (V)					Disease Severity Index (F)				
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT
L 06231	0.57	1.40	2.37	3.20	3.50	0.17	1.00	2.43	3.43	2.80
L 06238	1.07	1.53	2.37	3.40	3.17	0.10	1.33	2.70	3.00	2.87
L 06240	0.40	1.40	2.77	3.83	3.53	0.00	1.27	2.60	3.47	2.60
L 1023	0.67	0.73	2.13	3.23	3.50	0.63	1.70	2.90	3.40	3.77
L 1030	0.40	1.77	2.40	3.23	4.00	0.10	1.17	3.17	3.63	4.00
LA 3924	0.50	1.40	1.97	2.80	4.00	0.50	1.30	3.53	3.37	4.00
Arka Abha	0.00	1.43	2.33	3.27	3.27	0.00	1.70	3.47	3.57	3.13
Arka Alok	1.40	1.17	2.57	3.60	3.40	0.17	0.43	2.37	3.20	3.40
Arka Meghali	0.00	0.47	1.43	2.87	4.00	0.00	0.60	1.23	2.20	2.67
Arka Saurabh	1.17	1.67	3.23	3.40	4.00	1.23	1.73	2.37	3.53	2.67
Arka Vikas	0.63	1.47	2.33	3.33	3.73	1.07	3.30	3.50	3.53	3.53
Shakti	1.17	1.43	2.60	3.40	3.47	0.13	0.80	2.50	2.83	2.73
Mukti	0.70	1.17	2.40	3.40	3.63	1.00	2.77	2.70	3.53	3.60
Anagha	0.50	1.83	2.73	2.73	4.00	0.60	1.23	2.67	3.37	4.00
Nandi	0.00	0.00	0.00	1.30	4.00	0.00	0.63	1.23	2.40	2.67
PKM 1	0.00	1.73	2.23	3.67	3.40	0.00	3.27	3.53	3.43	3.50
SL 120	0.97	1.47	2.53	3.43	3.40	0.20	1.30	2.23	3.10	2.63
DMT - 2	0.83	1.30	2.70	3.57	3.67	0.97	2.30	2.50	3.73	3.47
GK - 2	0.73	1.63	2.60	3.67	3.70	1.07	2.83	2.73	3.23	3.47
THB 205	0.20	1.30	2.47	3.43	3.47	0.80	3.17	2.57	3.07	2.67
TLB 130	0.67	1.60	2.53	3.50	3.70	1.17	3.07	2.40	3.20	3.53
TLB 133	0.67	1.30	2.40	3.83	3.70	1.47	2.60	2.57	2.73	2.77
M. Palli Tomato	0.97	1.37	2.40	3.70	3.50	0.63	1.10	1.77	2.30	2.80
Patriot	1.57	1.77	2.33	3.37	3.47	0.80	0.77	1.60	2.23	3.20
Podland Pink	0.90	1.47	2.43	3.33	3.57	0.27	0.83	1.47	2.40	3.10
Red Pear	0.03	1.77	2.63	3.40	3.40	0.07	1.10	1.50	2.23	3.17
S. Early	1.47	1.43	2.73	3.27	3.43	0.27	0.60	1.60	2.23	3.13
S. Harry	0.97	1.67	2.27	3.37	3.33	0.20	0.40	1.67	2.13	2.90
Tommy Toe	0.53	1.70	2.53	3.57	3.47	0.47	0.77	2.27	2.30	3.40
W. Cherry	0.47	1.47	2.57	3.47	3.67	0.27	1.07	1.70	2.33	3.07

Appendix VI. Mean values of tomato genotypes for vector population and yield parameters under TyLCV evaluation

Genotypes	Vector Population					Number of fruits	Average fruit weight	Yield per plant
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT			
BL 1187	85.00	95.00	20.33	31.50	0.00	42.20	26.21	1.11
BL 1188	90.00	95.00	19.73	30.43	0.00	20.28	58.53	1.19
BL 1198	90.00	4.70	7.33	11.23	17.40	60.09	25.81	1.55
BL 1199	2.23	9.70	17.87	22.63	24.87	49.93	18.40	0.92
BL 1200	2.80	9.00	19.50	30.00	0.00	42.87	27.27	1.17
BL 1201	3.30	10.27	20.83	29.07	0.00	38.75	25.38	0.99
LA 3913	2.60	8.13	17.23	23.60	7.67	30.56	23.20	0.71
LA 3914	1.20	6.73	12.07	19.77	12.20	36.02	27.46	0.99
LA 3922	0.00	1.77	6.40	16.47	6.03	46.44	20.84	0.97
LA 3923	0.00	4.80	9.77	12.87	17.90	41.31	27.64	1.14
CLN 2116 B	3.87	10.60	19.27	27.80	0.00	38.51	24.70	0.95
CLN 2498 E	3.20	11.87	21.67	29.33	0.00	42.14	23.37	0.99
CLN 2585 A	4.20	8.73	20.47	27.90	0.00	22.24	65.47	1.46
CLN 2585 C	3.80	11.77	20.07	27.93	0.00	19.48	65.28	1.28
CLN 2585 D	3.07	11.07	19.73	31.13	0.00	20.71	63.78	1.33
CLN 2679 E	3.97	10.13	20.27	28.37	0.00	21.91	62.87	1.39
CLN 2679 F	3.57	9.53	18.73	29.03	0.00	45.45	28.98	1.32
CLN 2714 G	4.17	10.53	18.83	29.17	0.00	22.34	61.92	1.39
CLN 2714 H	3.23	11.27	20.83	29.70	0.00	17.29	63.20	1.10
CLN 2714 J	4.20	9.87	21.07	31.00	0.00	21.86	59.13	1.29
L 01023	2.07	7.37	16.10	22.60	28.60	51.65	17.16	0.89
L 01033	3.77	7.30	17.27	22.30	7.70	44.71	18.89	0.85
L 01049	0.00	1.50	5.80	16.90	7.73	45.27	24.59	1.11
L 01050	0.13	1.53	11.23	24.33	4.73	53.33	20.99	1.10
L 01139	3.93	9.93	20.00	29.27	0.00	41.56	25.49	1.06
L 01318	5.00	7.17	18.23	24.83	7.33	41.29	20.91	0.87
L 01462	2.10	5.73	10.83	17.97	11.63	44.93	16.25	0.73
L 01463	2.63	10.87	20.30	29.67	0.00	47.63	27.60	1.31
L 01464	3.43	11.27	20.03	27.93	0.00	39.39	27.64	1.08
L 01696	3.10	11.10	18.80	27.67	0.00	38.98	24.73	0.97
L 01745	1.60	10.43	16.60	21.33	26.97	56.69	22.25	1.27
L 01869	0.00	1.70	6.43	17.70	6.70	41.25	21.59	0.89
L 01933	0.60	12.33	17.10	21.90	27.97	63.99	28.01	1.80
L 01942	0.00	4.50	9.73	13.27	15.53	61.81	25.64	1.60
L 02079	2.53	9.93	17.83	22.43	6.73	47.43	15.75	0.75

Contd.....

Genotypes	Vector Population					Number of fruits	Average fruit weight	Yield per plant
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT			
L 02222	1.13	6.00	10.97	17.33	12.70	38.27	23.52	0.89
L 02248	0.00	1.90	7.33	16.53	5.53	47.97	23.59	1.13
L 02692	3.20	11.80	20.90	29.27	0.00	38.76	25.26	0.97
L 02709	3.07	8.00	15.17	23.53	27.07	59.02	18.62	1.11
L 02778	0.00	1.57	7.23	16.80	5.37	58.87	20.38	1.20
L 06043	1.27	12.03	17.40	23.73	26.77	55.82	20.29	1.12
L 06044	0.37	1.83	10.17	25.37	4.07	21.04	50.52	1.06
L 06046	1.00	5.63	9.70	17.47	13.73	36.54	22.48	0.82
L 06049	0.20	2.37	9.77	16.57	4.60	27.83	50.42	1.39
L 06052	0.00	4.67	10.47	12.00	16.13	62.21	25.01	1.57
L 06057	3.40	10.20	19.80	29.53	0.00	40.46	25.40	1.03
L 06058	0.17	1.87	9.70	23.37	4.07	32.41	55.79	1.81
L 06106	0.00	1.77	6.43	16.30	5.60	43.66	21.55	0.93
L 06112	4.47	10.90	16.40	23.40	7.40	41.54	18.33	0.76
L 06115	3.07	10.40	19.50	24.10	6.47	45.51	17.58	0.80
L 06119	0.00	4.70	9.90	12.80	16.83	65.13	17.86	1.16
L 06122	3.03	8.67	18.67	32.10	0.00	47.31	26.53	1.25
L 06123	0.27	1.67	10.00	26.13	5.17	22.44	48.35	1.07
L 06179	1.77	5.80	12.03	17.70	12.77	36.55	25.53	0.92
L 06181	2.93	10.53	18.47	31.00	0.00	45.50	23.98	1.08
L 06182	3.83	10.40	19.13	28.80	0.00	44.91	28.43	1.29
L 06185	1.73	6.90	18.70	22.27	26.87	64.51	22.42	1.47
L 06188	3.70	7.90	14.93	23.23	8.10	45.57	18.67	0.87
L 06190	3.60	9.27	21.53	30.43	0.00	38.66	30.54	1.18
L 06193	0.00	5.30	8.60	11.83	16.50	63.75	27.55	1.76
L 06194	4.23	10.70	20.23	28.77	0.00	40.13	24.29	0.98
L 06201	0.00	4.90	8.87	11.37	14.73	65.64	25.41	1.69
L 06208	3.00	11.03	16.90	21.93	26.60	62.33	21.22	1.32
L 06218	0.87	13.17	16.37	24.17	26.60	57.61	21.85	1.26
L 06219	1.43	6.73	11.67	17.27	12.10	34.52	22.70	0.79
L 06220	1.10	5.77	12.87	18.00	9.23	43.07	23.86	1.04
L 06221	0.00	1.37	5.53	17.27	5.93	43.71	20.15	0.88
L 06223	0.17	1.03	9.83	25.10	6.80	20.06	45.06	0.92
L 06229	0.43	9.80	18.13	23.97	7.80	47.16	13.79	0.65
L 06230	0.00	1.63	4.93	16.83	7.53	43.21	23.94	1.03

Contd.....

Genotypes	Vector Population					Number of fruits	Average fruit weight	Yield per plant
	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT			
L 06231	0.20	1.30	9.07	26.73	5.30	59.29	18.00	1.06
L 06238	0.27	2.00	10.47	22.03	4.43	23.76	45.19	1.07
L 06240	0.17	1.80	9.27	21.67	6.17	25.00	56.50	1.41
L 1023	2.20	6.47	11.17	19.20	13.83	43.30	24.02	1.04
L 1030	3.30	9.80	19.57	28.43	0.00	41.30	26.82	1.11
LA 3924	4.17	10.13	20.10	28.53	0.00	39.99	23.91	0.96
Arka Abha	0.00	2.03	7.83	17.30	5.60	42.73	22.62	0.95
Arka Alok	0.27	2.13	10.10	23.00	5.73	20.55	45.55	0.94
Arka Meghali	1.57	9.50	15.10	21.07	24.00	51.41	20.80	1.07
Arka Saurabh	2.60	7.10	19.80	21.13	7.67	43.24	19.23	0.83
Arka Vikas	1.57	7.03	11.60	18.40	10.37	44.56	19.72	0.88
Shakti	0.37	2.10	9.20	23.83	5.50	26.17	54.27	1.42
Mukti	0.20	1.67	9.40	26.10	6.83	18.76	46.15	0.87
Anagha	4.07	9.27	18.83	29.57	0.00	47.37	26.00	1.23
Nandi	0.50	8.83	14.67	23.37	26.60	59.73	22.27	1.33
PKM 1	0.00	1.53	4.63	16.83	5.50	43.06	22.38	0.98
SL 120	0.17	2.00	8.23	25.87	5.60	29.48	51.30	1.51
DMT - 2	0.07	1.47	8.70	24.23	4.90	20.88	44.27	0.92
GK - 2	0.27	1.07	8.23	23.63	3.97	18.70	53.29	1.00
THB 205	0.17	1.67	9.90	24.87	5.07	22.08	43.72	0.96
TLB 130	0.27	2.10	11.77	19.13	4.13	20.33	48.42	0.99
TLB 133	0.40	1.90	9.47	24.03	4.83	25.29	54.77	1.39
M. Palli Tomato	3.40	7.77	17.47	18.13	6.17	25.58	45.73	1.18
Patriot	3.90	7.60	17.87	16.93	6.67	26.46	47.78	1.26
Podland Pink	2.63	8.10	16.87	19.50	5.90	19.20	38.53	0.74
Red Pear	3.13	8.37	16.47	15.97	5.87	21.65	40.81	0.89
S. Early	4.10	7.90	17.57	17.70	6.10	19.95	40.20	0.79
S. Harry	2.93	7.30	18.07	17.10	6.37	17.78	42.29	0.75
Tommy Toe	3.03	5.90	16.73	16.93	6.60	16.95	41.47	0.70
W. Cherry	3.90	8.40	17.63	16.20	6.63	24.05	41.72	0.99

Appendix VII Mean values of tomato genotypes for plant height and number of branches under two irrigation regimes

Genotypes	Plant height (cm)						Number of branches					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
BL 1187	30.46	58.01	73.47	23.79	47.93	49.55	6.73	17.80	26.40	7.67	10.53	18.33
BL 1188	28.70	63.43	77.99	20.55	47.80	78.47	8.27	17.93	34.93	6.93	9.67	18.27
BL 1198	24.42	68.71	99.17	17.90	43.83	72.69	8.07	18.53	27.40	9.60	12.80	18.27
BL 1199	24.05	32.27	68.40	16.43	23.76	63.22	6.73	15.73	22.20	6.67	10.00	18.00
BL 1200	29.11	63.52	101.27	21.41	32.94	68.43	7.27	17.80	29.53	8.80	11.73	25.80
BL 1201	30.57	63.64	101.85	21.18	33.72	68.62	6.93	17.60	29.73	9.80	12.27	18.13
LA 3913	28.77	65.16	93.55	18.91	49.24	80.54	9.40	21.93	26.93	8.07	9.73	17.93
LA 3914	25.23	63.79	101.59	15.44	33.53	69.23	10.27	21.60	28.47	7.87	12.67	19.00
LA 3922	29.59	65.98	92.75	21.41	33.47	75.47	10.47	22.27	27.93	9.73	11.93	19.47
LA 3923	31.77	43.29	85.07	21.51	48.39	53.93	8.80	20.13	29.67	9.00	9.87	17.13
CLN 2116 B	20.71	43.00	57.60	14.30	27.97	40.33	8.60	21.00	31.00	6.47	11.07	15.87
CLN 2498 E	20.87	37.97	60.23	15.03	26.40	45.43	6.93	16.40	22.67	6.87	9.80	17.73
CLN 2585 A	19.97	37.50	60.67	16.43	29.67	41.53	8.87	18.40	35.27	7.33	10.67	18.27
CLN 2585 C	21.40	37.17	61.13	14.77	28.47	42.80	8.00	18.27	34.87	7.07	10.27	11.80
CLN 2585 D	22.97	38.07	59.90	15.53	25.03	40.13	6.93	17.33	28.00	7.80	9.73	17.13
CLN 2679 E	19.57	39.10	60.67	13.47	29.10	29.20	7.20	15.73	22.40	9.80	11.80	19.27
CLN 2679 F	17.37	39.53	60.70	14.23	27.37	41.53	6.60	17.67	29.53	10.73	12.20	19.33
CLN 2714 G	18.27	40.13	60.83	14.20	26.80	40.47	7.40	17.40	29.80	9.20	12.13	18.20
CLN 2714 H	21.51	36.03	58.03	13.91	26.77	40.53	10.27	22.13	27.20	9.67	11.73	19.93
CLN 2714 J	20.90	39.57	57.80	14.87	28.23	42.93	9.20	22.27	28.60	9.53	11.93	18.60
L 01023	33.82	63.49	100.60	21.89	33.33	46.13	7.07	17.07	29.07	10.13	11.53	18.67
L 01033	28.95	58.23	73.53	29.69	43.87	68.01	6.33	17.67	27.73	8.40	9.93	11.73
L 01049	27.88	63.74	78.01	29.68	43.59	67.97	4.33	14.13	22.93	8.00	6.84	16.80
L 01049	26.14	53.06	74.59	34.80	37.84	54.41	8.00	18.67	34.40	8.27	10.13	18.27
L 01139	30.03	65.58	93.67	18.85	48.33	60.33	8.73	19.53	29.60	8.27	10.13	18.07
L 01318	29.34	65.35	92.73	21.87	34.07	51.63	10.13	21.53	28.87	9.93	9.47	12.15
L 01463	26.09	49.83	68.47	17.10	28.91	48.33	7.53	17.87	27.40	8.13	9.93	17.00
L 01463	27.57	35.73	83.57	21.97	22.51	50.72	10.13	21.80	27.20	10.00	7.80	18.80
L 01464	29.17	53.99	73.45	20.58	34.62	55.99	9.40	19.60	28.07	7.73	9.80	11.62
L 01696	31.22	48.15	68.60	22.18	28.64	48.79	6.87	17.47	27.33	6.67	9.53	15.87
L 01745	30.71	68.11	95.14	23.45	48.08	73.47	9.40	21.33	30.33	6.67	11.00	15.60
L 01869	31.66	63.50	85.23	18.93	48.54	79.77	8.87	20.53	29.20	7.67	6.93	17.67
L 01933	30.01	42.69	93.13	21.42	22.83	76.47	9.93	21.47	28.33	7.80	10.27	17.80
L 01942	31.29	65.31	92.31	24.22	48.10	80.69	9.00	20.87	28.80	8.47	10.07	11.23
L 02079	26.91	53.48	83.22	22.63	33.41	74.11	9.80	21.80	28.27	9.93	11.93	19.53

Contd....

Genotypes	Plant height (cm)						Number of branches					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 02222	26.14	55.26	78.86	23.26	40.01	63.25	6.93	15.33	23.27	8.40	11.60	19.40
L 02248	29.51	42.87	79.09	30.72	31.74	52.06	4.47	15.07	21.73	7.53	6.68	17.07
L 02692	25.43	52.89	72.95	33.73	39.10	58.52	7.93	18.33	35.13	8.00	9.93	11.65
L 02709	25.80	53.43	73.43	33.43	39.16	58.05	7.60	18.60	35.67	7.80	9.60	18.13
L 02778	32.82	57.99	73.69	23.58	43.60	68.12	6.80	17.87	27.73	6.87	9.87	17.20
L 06043	23.88	48.44	69.87	23.49	40.88	42.39	7.93	16.13	22.33	8.33	6.92	11.38
L 06044	24.25	47.63	67.39	23.47	40.75	63.85	7.53	16.13	22.13	9.33	12.20	19.07
L 06046	28.97	57.50	88.52	25.91	45.13	73.09	7.07	17.53	28.87	9.27	11.80	18.33
L 06049	25.99	63.75	100.45	21.94	33.39	45.70	6.67	17.67	30.33	9.73	12.13	12.96
L 06052	25.87	64.07	101.75	21.55	33.55	69.25	7.47	17.40	29.13	9.20	8.49	18.47
L 06057	26.11	53.36	83.50	21.14	33.83	75.87	10.73	21.67	26.20	9.07	11.67	19.13
L 06058	29.67	65.35	93.99	18.59	47.55	53.41	8.93	19.93	29.67	8.73	10.07	17.33
L 06106	25.44	63.52	101.43	22.17	33.44	68.36	10.33	21.53	26.47	10.07	12.07	11.58
L 06112	25.74	64.24	101.24	20.83	33.31	68.35	7.47	17.40	30.20	9.13	8.15	19.00
L 06115	27.05	48.47	67.53	17.80	39.19	42.76	7.27	16.27	22.73	7.33	10.00	18.00
L 06119	17.73	63.29	102.04	15.01	33.59	68.41	10.67	21.93	28.07	9.87	12.07	13.80
L 06122	30.20	68.09	96.88	24.26	48.31	73.51	8.67	20.93	31.53	6.73	10.87	15.40
L 06123	30.16	68.55	95.62	22.95	48.41	73.01	9.60	21.27	31.00	6.60	10.87	15.53
L 06179	22.47	48.94	68.53	23.52	41.17	42.18	6.53	16.00	22.40	8.53	12.07	18.80
L 06181	23.71	47.88	69.33	23.08	40.89	64.01	7.13	15.40	23.00	10.00	12.33	19.07
L 06181	28.11	53.77	83.50	21.75	33.85	75.57	10.27	21.80	28.73	9.80	12.60	19.47
L 06185	27.73	59.61	73.87	31.55	43.23	67.81	7.00	17.60	26.73	8.13	10.47	17.73
L 06188	19.32	53.15	73.04	13.71	33.61	37.23	9.93	19.00	27.40	7.20	10.53	17.40
L 06190	30.40	68.55	96.15	20.25	33.41	55.39	8.60	22.07	31.20	6.00	10.87	15.60
L 06193	29.43	65.08	93.46	21.27	33.15	74.69	9.73	22.07	27.00	9.73	12.40	19.20
L 06194	28.30	53.69	73.46	20.93	33.17	37.79	9.07	19.13	27.40	7.67	10.33	16.47
L 06201	24.33	47.45	68.49	22.58	38.83	63.31	7.00	16.13	22.67	8.80	12.20	18.73
L 06208	28.61	57.90	88.55	25.26	42.79	73.83	6.47	16.87	29.00	9.47	11.40	18.60
L 06218	29.63	65.29	93.61	18.74	48.88	80.66	9.00	20.73	30.20	9.60	10.67	17.93
L 06219	29.15	53.92	72.74	18.02	28.27	48.35	7.33	17.80	27.20	6.73	9.80	15.93
L 06220	30.74	68.20	95.43	23.63	49.25	72.94	9.40	21.00	31.47	7.07	10.93	15.53
L 06221	28.71	64.90	94.03	18.13	48.17	80.45	8.47	20.53	30.53	8.53	9.80	18.00
L 06223	25.05	63.51	102.07	21.50	34.25	68.81	7.00	17.40	29.20	9.60	12.00	19.47
L 06229	29.33	62.91	78.75	31.25	48.31	78.97	4.53	15.13	22.93	7.47	10.40	17.00
L 06230	28.08	57.40	88.47	25.68	43.85	73.35	6.80	18.20	29.67	9.93	12.13	19.40

Contd....

Genotypes	Plant height (cm)						Number of branches					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 06231	23.43	47.43	67.36	24.79	41.39	64.03	6.67	15.93	23.07	9.80	12.20	19.67
L 06238	25.28	53.32	75.07	33.91	38.51	58.15	7.87	19.20	34.87	6.80	9.80	17.60
L 06240	24.89	63.19	101.78	21.53	33.29	68.61	6.73	18.00	29.33	10.07	11.33	19.27
L 1023	25.75	62.79	101.55	22.35	32.70	67.77	7.40	18.00	30.33	11.13	11.87	19.67
L 1030	28.36	65.51	93.75	18.79	48.72	80.44	9.20	19.67	28.47	8.47	10.53	17.80
LA 3923	31.39	64.02	85.27	18.59	48.73	80.83	8.60	18.93	29.33	8.87	10.00	16.93
Arka Abha	31.59	63.23	85.04	25.29	53.03	70.86	8.80	20.13	30.13	9.20	9.47	17.67
Arka Alok	30.99	63.44	85.11	22.51	44.46	67.18	8.33	19.87	29.80	7.07	10.47	16.87
Arka Meghali	32.09	63.06	85.03	24.11	44.45	66.63	9.53	20.27	29.87	7.73	10.40	16.80
Arka Saurabh	31.41	57.63	80.12	23.81	43.46	66.13	9.20	20.40	29.40	6.80	10.13	16.93
Arka Vikas	31.53	58.62	81.03	24.03	43.26	66.55	8.60	19.53	29.87	7.40	10.33	16.47
Shakti	25.43	49.23	68.83	23.30	42.65	66.53	6.73	18.07	27.53	7.60	10.13	17.20
Mukti	26.34	48.11	68.27	21.69	33.71	53.37	7.73	17.27	27.27	7.33	9.80	15.87
Anagha	32.17	58.18	79.27	21.59	33.95	53.64	7.93	17.27	27.20	7.33	9.67	15.93
Nandi	31.77	57.40	80.69	20.68	33.51	53.21	7.67	17.47	27.60	8.20	9.60	17.07
PKM 1	25.05	47.88	68.91	19.08	29.49	47.87	7.13	17.67	27.20	7.60	10.00	17.13
SL 120	25.50	53.41	73.38	32.80	38.81	58.63	7.93	18.53	34.20	7.73	9.87	16.87
DMT - 2	24.09	49.22	68.45	33.03	38.49	58.06	7.27	15.80	23.07	7.73	10.00	16.13
GK - 2	28.39	58.45	73.46	30.07	43.81	67.61	6.13	16.93	27.80	8.13	10.00	17.07
THB 205	26.21	63.45	101.59	21.61	33.09	67.74	7.07	16.67	29.33	8.67	12.00	18.07
TLB 130	29.41	66.54	93.95	18.31	48.83	80.83	8.87	19.67	28.87	9.07	9.93	17.93
TLB 133	26.56	55.37	78.37	25.46	43.23	72.71	6.93	16.07	21.93	9.20	12.27	19.00
M. Palli Tomato	24.70	63.66	100.93	21.93	33.03	67.92	10.33	21.67	29.07	9.00	11.27	19.20
Patriot	30.09	69.28	94.74	24.70	49.81	73.59	9.07	20.60	31.33	6.40	10.60	15.47
Podland Pink	29.45	68.33	94.89	23.72	49.62	73.98	9.20	20.60	31.00	7.13	11.40	15.20
Red Pear	30.49	64.40	92.95	17.78	48.51	81.25	9.33	21.87	28.47	8.53	9.67	17.53
S. Early	27.75	57.04	87.78	28.37	62.33	83.86	6.53	17.27	28.53	9.53	12.33	18.93
S. Harry	25.09	53.48	73.89	32.82	37.96	58.25	8.33	18.53	35.67	7.93	9.53	17.20
Tommy Toe	26.17	53.59	72.93	32.84	38.95	58.63	8.07	18.53	36.07	7.67	10.07	17.47
W. Cherry	27.88	63.40	78.25	30.22	48.82	78.39	4.47	14.73	22.13	8.00	9.60	16.47

Appendix VIII. Mean values of tomato genotypes for stem girth and root parameters under two irrigation regimes

Genotypes	Stem Girth (cm)						Root length (cm)		Root volume (cc)	
	IR 1			IR 2			IR 1	IR 2	IR 1	IR 2
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT				
BL 1187	4.15	6.14	7.85	1.80	1.97	4.85	32.03	48.37	20.40	29.38
BL 1188	4.09	6.09	8.01	1.46	2.95	3.48	28.13	46.87	19.11	27.13
BL 1198	2.93	5.15	7.30	3.22	3.65	4.94	31.87	51.87	23.80	27.45
BL 1199	4.17	5.94	7.83	1.77	2.09	4.81	28.53	50.90	26.04	33.35
BL 1200	2.89	4.76	6.85	2.87	3.93	3.30	21.07	40.63	13.28	22.96
BL 1201	2.81	5.19	7.11	2.09	2.87	5.09	30.07	48.47	23.28	33.93
LA 3913	3.09	4.85	7.11	3.11	3.83	5.11	28.27	44.30	26.94	28.54
LA 3914	3.27	4.82	6.84	3.11	4.07	3.39	26.57	43.90	23.67	24.82
LA 3922	3.05	5.17	6.99	2.92	4.14	5.11	24.53	43.70	21.23	27.13
LA 3923	3.41	4.47	7.57	1.86	3.38	3.25	25.87	44.10	22.00	32.90
CLN 2116 B	3.93	5.34	7.02	2.49	3.39	4.52	25.70	43.20	18.28	26.88
CLN 2498 E	4.15	5.97	7.86	1.46	3.26	5.01	29.63	51.83	21.62	31.17
CLN 2585 A	3.98	6.03	7.97	2.02	3.19	5.01	28.33	46.33	17.64	28.86
CLN 2585 C	3.69	6.06	8.17	1.55	2.96	3.48	27.10	47.43	20.01	27.39
CLN 2585 D	4.29	6.25	7.79	2.06	2.97	5.11	32.03	48.40	23.48	29.06
CLN 2679 E	4.09	6.15	7.99	1.75	3.27	4.94	32.77	50.90	23.54	29.50
CLN 2679 F	2.81	5.04	7.07	2.14	3.85	5.31	28.20	50.97	24.95	33.29
CLN 2714 G	2.87	5.05	6.89	3.01	4.02	4.91	22.53	42.90	13.73	22.00
CLN 2714 H	3.15	4.93	6.87	2.15	4.03	5.05	20.87	42.10	13.92	24.89
CLN 2714 J	2.99	4.89	6.87	3.03	4.13	3.53	25.47	43.43	22.00	33.67
L 01023	2.99	4.99	7.03	2.13	3.89	4.91	22.63	39.60	14.43	24.63
L 01033	3.79	6.08	8.20	1.66	2.90	3.43	30.17	50.27	23.03	28.09
L 01049	3.89	6.26	7.79	1.99	2.86	4.96	31.83	48.17	23.67	28.48
L 01049	3.91	5.78	7.92	1.73	3.00	3.29	26.67	44.87	16.36	27.52
L 01139	3.59	4.50	7.53	2.91	4.23	5.37	26.43	39.90	23.03	31.11
L 01318	2.95	5.06	6.93	2.03	4.13	3.58	24.67	43.67	20.53	32.20
L 01463	3.53	4.64	7.39	2.46	3.49	4.49	25.90	44.57	23.22	26.11
L 01463	3.07	5.12	6.98	1.95	3.87	3.47	25.63	39.97	21.29	27.90
L 01464	3.49	4.54	7.43	2.53	3.47	4.59	25.70	42.90	24.31	31.17
L 01696	3.43	4.55	7.56	2.42	3.59	4.59	26.63	41.30	24.76	29.50
L 01745	4.08	5.24	7.15	1.79	3.44	4.60	27.00	42.53	27.32	31.24
L 01869	3.44	4.59	7.57	2.47	2.49	4.43	30.03	45.23	23.80	32.20
L 01933	2.90	5.07	7.05	1.90	4.07	5.06	26.60	42.40	18.34	33.80
L 01942	3.32	4.57	7.52	3.07	4.17	3.44	24.67	41.93	20.14	27.13
L 02079	3.03	5.02	6.88	2.21	3.06	5.03	29.07	42.43	23.73	26.88

Contd....

Genotypes	Stem Girth (cm)						Root length (cm)		Root volume (cc)	
	IR 1			IR 2			IR 1	IR 2	IR 1	IR 2
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT				
L 02222	3.15	5.21	7.09	1.25	2.78	3.36	28.13	49.53	25.14	31.17
L 02248	4.11	5.64	7.95	1.50	3.05	4.88	31.63	51.03	23.03	28.09
L 02692	4.25	6.13	7.97	2.49	2.97	3.68	27.77	45.23	20.20	27.00
L 02709	3.58	5.87	7.63	2.26	2.93	5.03	26.10	45.80	17.06	27.39
L 02778	3.95	6.11	8.27	1.89	3.01	3.42	31.87	50.00	24.12	25.98
L 06043	3.91	6.38	8.02	2.23	2.03	4.84	29.90	49.40	22.77	29.50
L 06044	3.75	5.79	7.89	2.04	3.01	5.08	29.33	52.67	24.18	29.44
L 06046	3.07	5.21	6.92	2.91	3.81	4.90	31.23	52.50	24.63	30.72
L 06049	2.97	4.88	7.05	2.83	3.12	5.07	22.70	38.97	15.33	23.67
L 06052	2.88	4.99	6.94	3.12	2.72	5.03	22.50	39.93	15.97	24.50
L 06057	2.84	5.24	7.16	3.19	4.09	3.66	29.43	44.03	24.05	27.97
L 06058	3.57	4.56	7.53	2.41	3.44	4.61	26.93	41.33	19.05	27.64
L 06106	3.03	5.08	6.92	2.83	3.93	5.04	21.40	39.93	17.77	24.69
L 06112	3.09	4.89	6.97	3.01	4.02	5.27	23.33	42.27	12.89	25.40
L 06115	4.13	5.81	7.95	1.90	3.32	5.09	28.53	51.50	22.06	34.19
L 06119	3.06	5.09	7.04	2.74	4.00	5.02	26.07	41.10	21.49	31.43
L 06122	3.89	5.10	7.31	2.47	2.39	3.17	25.57	42.90	24.05	27.07
L 06123	3.91	4.98	7.05	2.41	3.50	3.98	25.13	44.43	21.17	24.69
L 06179	3.71	5.85	8.01	1.97	3.32	5.15	27.63	49.37	22.19	29.50
L 06181	4.33	6.09	8.06	1.73	3.34	4.93	30.10	48.97	23.35	31.75
L 06181	2.79	4.92	7.00	2.94	3.98	4.85	26.60	41.13	21.04	29.31
L 06185	4.11	5.77	8.07	2.12	2.98	5.15	31.93	48.60	21.81	28.54
L 06188	3.43	4.61	7.59	2.48	3.50	4.62	26.87	43.30	22.13	24.69
L 06190	4.09	4.89	7.09	2.39	3.38	4.51	26.20	44.07	21.74	32.13
L 06193	3.17	5.15	7.03	3.01	4.14	4.95	27.33	42.90	23.09	30.40
L 06194	3.41	4.47	7.49	2.62	3.58	4.71	23.30	42.33	19.18	27.20
L 06201	3.96	5.86	7.83	1.98	2.87	4.95	31.03	49.10	21.49	32.71
L 06208	2.88	5.12	6.91	3.10	3.86	4.90	28.23	51.13	21.23	31.24
L 06218	3.45	4.38	7.31	2.55	3.43	3.67	24.47	42.60	20.08	28.09
L 06219	3.43	4.44	7.50	2.52	3.50	4.39	26.10	41.50	22.32	30.66
L 06220	4.09	4.91	6.92	2.57	3.53	4.45	24.37	41.63	18.73	30.47
L 06221	3.42	4.40	7.55	3.05	4.15	3.99	26.27	41.23	22.77	34.64
L 06223	2.97	4.97	7.01	3.07	4.24	5.09	24.23	41.00	13.15	22.00
L 06229	3.85	5.89	7.91	1.85	3.02	5.05	31.10	46.87	22.19	25.53
L 06230	3.05	4.90	7.23	3.09	4.07	5.08	30.77	50.60	21.36	31.88

Contd.....

Genotypes	Stem Girth (cm)						Root length (cm)		Root volume (cc)	
	IR 1			IR 2						
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	IR 1	IR 2	IR 1	IR 2
L 06231	4.05	5.87	8.20	1.97	3.05	5.10	29.13	52.83	23.22	34.83
L 06238	3.95	6.24	8.07	1.92	3.12	3.67	27.50	45.27	17.13	24.05
L 06240	2.79	4.98	6.83	3.02	3.93	4.20	20.40	40.27	16.23	24.76
L 1023	3.00	5.18	7.20	2.81	3.93	4.89	21.37	41.13	18.41	25.14
L 1030	3.59	4.43	7.53	2.43	3.36	4.51	23.33	40.77	19.88	30.92
LA 3923	3.48	4.63	7.55	2.53	3.41	3.33	28.70	40.20	23.60	30.66
Arka Abha	3.48	4.35	7.57	2.49	3.51	4.44	25.60	42.73	23.35	27.00
Arka Alok	3.46	4.54	7.39	2.41	3.55	4.44	25.50	41.50	26.04	29.76
Arka Meghali	3.52	4.49	7.48	2.40	3.35	3.96	26.37	42.87	23.22	23.99
Arka Saurabh	3.52	4.55	7.65	2.41	3.47	4.46	24.87	42.57	18.99	30.79
Arka Vikas	3.49	4.61	7.49	2.37	3.35	3.12	27.63	40.43	23.67	29.12
Shakti	3.53	4.57	7.49	2.48	3.56	4.46	28.10	43.43	26.04	29.83
Mukti	3.52	4.47	7.41	2.43	3.57	4.50	28.93	43.53	19.82	32.33
Anagha	3.50	4.37	7.59	2.57	3.53	4.56	27.20	43.40	23.09	29.38
Nandi	3.48	4.53	7.52	2.53	3.53	3.09	25.73	43.70	22.39	30.02
PKM 1	3.43	4.53	7.57	2.53	3.50	4.47	26.40	45.47	21.36	29.18
SL 120	3.88	5.69	7.97	1.93	3.09	5.03	26.23	46.77	16.74	24.89
DMT - 2	4.14	6.08	8.41	2.11	2.83	3.40	29.30	52.80	22.19	33.80
GK - 2	4.07	6.14	7.77	2.02	2.69	4.83	29.50	50.13	22.64	27.20
THB 205	2.85	4.63	6.85	2.83	3.91	4.85	22.23	38.93	15.14	24.69
TLB 130	2.93	5.10	7.03	3.08	4.01	3.51	26.37	41.20	20.85	29.38
TLB 133	2.89	4.73	6.75	3.15	3.99	4.86	28.90	51.27	23.54	31.11
M. Palli Tomato	2.93	5.07	7.11	2.93	3.92	5.11	22.90	41.93	15.91	20.53
Patriot	3.96	5.16	6.99	2.50	3.51	3.26	26.93	40.47	24.18	29.57
Podland Pink	3.94	5.15	6.85	2.58	3.51	4.62	25.90	41.40	20.14	32.46
Red Pear	2.86	5.03	7.09	3.15	4.14	4.98	26.43	42.23	22.90	27.84
S. Early	3.06	4.96	7.08	3.01	4.01	3.58	30.43	50.93	22.83	31.62
S. Harry	4.13	5.94	7.82	1.94	2.79	4.88	26.60	45.90	18.02	26.55
Tommy Toe	3.84	6.11	8.07	1.96	3.05	4.90	29.03	43.17	18.41	27.00
W. Cherry	4.18	6.17	8.07	2.10	3.17	3.39	32.40	47.93	23.80	28.80

Appendix IX. Mean values of tomato genotypes for leaf parameters under two irrigation regimes

Genotypes	Number of leaves						Leaf area (cm2)					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
BL 1187	27.00	47.00	86.67	20.67	51.67	66.33	76.80	153.99	311.08	41.58	129.75	305.02
BL 1188	36.67	61.00	88.00	25.67	35.33	49.00	181.10	337.13	519.21	63.05	166.30	173.71
BL 1198	37.00	52.67	83.00	32.67	47.33	72.67	254.67	412.07	815.67	107.62	295.79	551.55
BL 1199	37.33	51.67	82.67	32.00	30.67	72.33	255.64	407.45	817.11	109.13	301.60	545.50
BL 1200	37.00	56.67	106.00	32.00	43.00	87.00	256.44	471.86	1029.36	156.77	320.46	726.39
BL 1201	38.33	52.33	82.67	24.67	47.33	71.67	268.82	419.27	835.87	157.92	294.72	514.08
LA 3913	33.00	67.67	96.00	29.67	66.67	54.33	187.69	505.22	922.90	160.96	295.86	397.38
LA 3914	37.67	57.67	108.00	33.00	28.33	86.67	253.81	472.03	1092.09	156.78	304.79	744.81
LA 3922	34.33	66.67	96.67	30.00	67.67	82.67	202.09	483.69	914.91	168.56	427.91	592.22
LA 3923	45.00	67.00	99.33	28.33	43.33	64.00	304.05	565.16	970.82	207.58	437.78	777.60
CLN 2116 B	40.00	69.00	84.00	35.33	54.00	70.67	238.63	658.71	1143.48	181.29	371.94	591.76
CLN 2498 E	36.00	51.33	82.00	22.67	46.00	72.00	251.06	405.47	812.34	156.13	291.89	534.72
CLN 2585 A	38.67	62.00	87.67	32.67	31.50	72.67	191.84	338.95	522.29	92.21	153.85	256.52
CLN 2585 C	38.00	61.67	87.33	32.00	45.67	73.00	189.10	321.75	528.02	90.99	154.65	164.61
CLN 2585 D	27.00	47.67	87.67	22.33	52.00	67.00	70.83	157.26	324.43	51.22	119.37	314.83
CLN 2679 E	37.33	51.33	81.33	32.33	46.33	71.00	258.27	398.38	790.98	157.45	296.38	530.31
CLN 2679 F	37.67	51.00	83.00	31.67	46.00	72.67	269.45	407.69	823.97	154.19	298.66	538.08
CLN 2714 G	37.33	57.33	107.67	33.00	41.67	85.67	260.94	492.18	1077.18	159.35	311.27	732.57
CLN 2714 H	38.00	58.00	106.67	33.00	42.00	86.33	269.39	498.89	1045.85	157.02	305.99	709.75
CLN 2714 J	33.67	67.33	97.67	30.33	66.67	82.33	197.35	511.72	921.04	164.26	422.55	594.83
L 01023	37.00	57.67	106.67	33.00	41.00	86.33	260.25	484.80	1067.84	167.84	300.19	496.06
L 01033	26.33	47.67	88.00	22.67	53.00	67.00	83.26	151.51	309.83	49.02	191.86	318.69
L 01049	28.33	53.33	89.67	23.33	52.67	67.00	90.91	186.59	336.56	33.40	189.37	312.90
L 01049	39.00	63.00	86.67	31.33	47.33	72.00	197.82	334.11	508.80	85.08	165.41	260.54
L 01139	34.00	67.00	96.67	31.33	67.33	82.33	198.50	486.05	912.59	170.09	423.24	597.23
L 01318	34.33	67.33	98.00	29.33	68.00	81.00	205.77	506.65	949.53	107.90	433.17	616.09
L 01463	44.00	66.67	100.00	40.00	63.33	92.33	294.51	556.68	959.04	210.06	461.90	791.12
L 01463	35.00	66.67	95.67	29.33	66.67	81.00	212.66	499.21	919.41	152.72	410.02	583.61
L 01464	39.33	70.00	84.67	36.00	53.33	71.33	232.30	657.30	1143.03	191.93	363.66	588.61
L 01696	44.67	66.33	99.33	41.00	63.67	92.33	315.75	551.61	929.20	214.06	459.28	801.43
L 01745	40.33	70.00	83.67	36.33	54.00	71.00	250.21	665.00	1133.87	195.09	363.82	590.68
L 01869	34.67	66.67	96.67	30.33	67.00	83.00	196.46	486.20	927.99	165.27	415.85	615.35
L 01933	34.67	66.67	98.00	30.67	67.00	81.33	199.21	496.24	931.60	166.16	429.28	600.94
L 01942	33.67	66.33	98.00	32.00	68.33	81.00	198.64	498.82	929.60	112.18	445.35	600.11
L 02079	35.33	66.33	95.67	31.00	67.67	83.33	208.79	501.68	919.41	165.93	440.87	617.38

Contd.....

Genotypes	Number of leaves						Leaf area (cm ²)					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 02222	37.67	52.67	82.33	31.33	47.33	49.00	259.26	417.86	834.89	162.65	309.20	549.33
L 02248	29.00	54.33	88.67	22.67	51.67	67.33	100.74	199.54	316.91	51.57	177.03	303.68
L 02692	37.67	61.67	86.67	32.33	31.10	71.67	182.50	327.40	523.96	86.10	158.16	251.46
L 02709	36.67	61.00	87.00	31.67	47.00	71.33	180.51	323.73	517.98	59.29	147.58	229.56
L 02778	26.67	48.33	87.00	22.33	51.67	49.67	78.28	150.58	311.63	47.46	180.78	315.51
L 06043	36.67	50.67	81.67	32.67	46.67	72.00	258.76	404.74	810.45	155.86	201.16	541.62
L 06044	36.67	50.67	83.00	32.67	32.60	73.00	247.63	391.34	815.76	166.51	309.60	540.96
L 06046	36.00	51.67	83.00	31.67	46.67	73.33	249.04	409.34	807.10	102.11	297.98	522.06
L 06049	36.67	57.00	107.67	30.67	40.33	87.00	260.12	480.50	1088.24	152.70	296.87	717.97
L 06052	37.33	51.33	81.00	31.67	30.87	53.67	255.23	408.02	809.44	161.84	185.83	365.04
L 06057	32.33	65.67	96.00	29.00	68.67	81.67	193.90	484.19	911.30	161.50	428.06	592.34
L 06058	34.67	66.33	97.33	30.33	66.00	82.67	199.09	494.66	933.86	166.89	413.39	611.24
L 06106	37.33	57.00	106.67	31.33	27.80	87.67	255.99	476.22	1044.40	155.29	304.13	734.20
L 06112	37.00	57.00	106.00	32.67	42.67	87.00	249.84	474.27	1036.68	102.43	320.60	731.31
L 06115	36.33	51.00	81.33	32.00	31.63	72.67	244.44	400.43	794.95	159.23	301.44	530.89
L 06119	36.00	57.33	106.00	31.33	41.00	85.67	251.83	476.39	1058.21	148.86	307.46	726.64
L 06122	39.67	71.00	83.33	36.33	54.67	72.00	231.62	665.44	1120.97	192.41	244.62	613.71
L 06123	40.67	69.67	84.00	36.33	36.10	73.33	238.82	669.24	1139.51	196.50	365.96	627.25
L 06179	37.67	52.33	82.00	33.00	47.33	71.67	254.32	405.36	821.84	112.90	300.75	538.47
L 06181	37.67	51.00	82.00	31.33	47.33	71.67	255.21	413.70	825.86	152.35	305.92	533.49
L 06181	36.00	56.33	107.67	32.67	41.00	88.33	252.07	476.00	1064.92	155.79	305.91	488.75
L 06185	26.00	48.33	87.00	21.33	35.37	67.33	71.41	159.85	312.43	49.26	129.01	305.57
L 06188	40.00	70.67	84.33	35.00	54.33	72.67	236.20	640.86	1142.62	185.79	367.56	609.97
L 06190	40.67	70.00	84.33	35.67	54.33	73.33	235.26	657.24	1144.44	127.08	375.50	635.69
L 06193	33.00	66.00	97.67	28.67	66.67	81.67	187.75	487.56	931.16	155.99	425.56	601.93
L 06194	39.67	70.00	85.00	37.00	53.67	71.67	236.90	656.53	1148.02	196.47	244.42	602.13
L 06201	37.00	52.67	83.00	32.33	47.00	72.33	265.45	412.39	836.56	160.65	304.68	533.79
L 06208	35.67	51.67	80.33	32.00	47.33	72.67	241.18	407.00	792.10	107.54	291.76	544.75
L 06218	34.00	67.33	96.67	29.00	66.67	82.00	193.48	499.59	901.69	153.57	419.98	602.59
L 06219	44.67	66.00	100.00	41.00	64.33	91.67	309.49	552.39	971.97	227.15	471.63	764.24
L 06220	39.67	70.00	85.00	36.00	54.33	71.33	233.54	650.36	1135.28	193.44	377.02	589.76
L 06221	33.67	68.00	97.67	30.33	67.67	80.67	202.03	517.72	946.66	161.49	444.51	607.61
L 06223	38.00	57.00	106.33	33.00	42.67	87.00	271.27	482.37	1054.70	115.92	317.44	471.97
L 06229	29.67	54.33	91.33	22.33	53.00	67.67	102.76	194.13	337.63	46.81	183.36	211.73
L 06230	38.33	52.33	83.00	30.67	45.33	71.67	272.03	416.46	828.47	149.33	285.71	514.17

Contd.....

Genotypes	Number of leaves						Leaf area (cm2)					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
L 06231	36.33	51.00	82.33	33.67	46.33	71.33	243.80	397.33	830.90	166.31	308.63	521.66
L 06238	38.67	62.67	87.00	32.33	47.00	71.33	193.88	352.33	505.83	98.14	164.28	245.12
L 06240	37.33	56.67	106.67	32.00	42.33	87.33	251.13	489.77	1047.83	98.02	319.96	722.83
L 1023	37.00	52.00	82.33	31.33	46.67	72.00	252.96	407.43	832.33	162.01	304.07	533.67
L 1030	33.67	68.00	97.00	29.33	66.00	80.67	200.57	508.29	922.68	157.46	425.91	593.50
LA 3923	42.67	67.33	99.33	39.67	63.33	91.33	287.86	571.90	944.91	199.71	466.24	788.36
Arka Abha	44.33	66.67	100.33	39.33	62.67	92.33	308.50	550.30	950.88	141.67	449.92	797.74
Arka Alok	45.33	67.00	99.00	40.00	64.33	92.00	319.81	557.37	941.12	218.85	457.89	528.98
Arka Meghali	44.33	66.67	100.67	40.00	64.00	91.67	302.84	561.12	950.92	218.16	469.53	774.43
Arka Saurabh	44.00	67.33	100.00	41.00	65.00	91.67	294.92	571.63	978.24	230.31	478.57	813.48
Arka Vikas	44.00	66.67	98.00	41.00	65.00	90.33	298.90	555.75	940.64	146.85	475.54	776.37
Shakti	44.00	67.00	100.00	38.67	64.00	91.33	294.91	555.27	945.81	208.35	460.87	770.88
Mukti	44.67	68.00	100.00	39.67	64.33	93.00	315.51	565.18	954.67	205.00	469.24	789.35
Anagha	42.67	67.33	99.33	39.33	64.67	91.33	293.12	565.04	942.75	203.63	453.30	791.25
Nandi	44.33	67.00	99.67	40.33	62.33	93.00	302.78	565.68	957.90	141.39	448.23	809.20
PKM 1	44.00	67.33	100.00	39.33	64.67	92.33	304.67	571.23	958.09	210.89	461.18	776.63
SL 120	38.33	61.33	87.67	33.00	47.33	73.00	186.78	317.34	525.46	87.30	153.95	155.42
DMT - 2	37.67	52.33	80.33	32.33	47.67	71.67	265.77	415.25	786.22	159.34	310.90	540.71
GK - 2	28.00	47.33	86.00	21.67	50.67	66.67	83.18	166.39	306.48	31.35	173.70	300.85
THB 205	38.00	56.00	106.00	32.33	42.67	87.00	265.18	468.73	1040.61	168.76	309.71	734.14
TLB 130	33.00	67.00	96.67	30.33	65.67	83.00	187.78	513.21	934.41	163.92	417.55	620.01
TLB 133	38.33	51.67	81.67	32.00	47.00	71.67	262.25	411.71	803.54	161.70	310.02	543.31
M. Palli Tomato	37.00	57.00	107.67	31.33	43.33	87.33	251.60	481.37	1055.53	105.89	328.39	735.39
Patriot	40.00	69.67	85.33	37.00	55.67	71.67	241.17	652.51	1148.80	203.87	368.12	405.47
Podland Pink	41.00	70.00	84.33	36.00	53.67	73.00	247.83	651.18	1154.93	193.73	362.58	606.14
Red Pear	33.67	66.00	96.67	29.67	67.33	82.33	193.58	489.19	947.14	159.76	427.90	608.78
S. Early	38.00	51.33	81.67	31.33	47.33	72.00	253.64	402.63	800.02	151.01	290.13	538.38
S. Harry	38.00	62.00	86.33	32.00	47.67	72.00	186.13	327.86	496.08	90.56	165.65	246.49
Tommy Toe	39.33	62.33	86.33	32.67	47.67	72.67	187.64	339.22	504.42	100.75	154.64	245.38
W. Cherry	30.33	54.33	88.67	21.67	52.00	66.67	97.12	209.32	329.16	48.98	192.50	308.17

Appendix X. Mean values of tomato genotypes for absolute and relative growth rate under two irrigation regimes

Genotypes	Absolute Growth Rate						Relative Growth Rate					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
BL 1187	0.29	0.47	0.56	0.24	0.33	0.45	0.48	0.61	0.59	0.44	0.46	0.50
BL 1188	0.47	0.30	0.59	0.42	0.19	0.47	0.09	0.06	0.01	0.07	0.03	0.02
BL 1198	0.37	0.34	0.86	0.24	0.23	0.76	1.31	0.05	0.02	0.84	0.04	0.03
BL 1199	0.48	0.33	0.80	0.37	0.15	0.67	0.06	0.07	0.01	0.02	0.02	0.02
BL 1200	0.36	0.34	0.30	0.27	0.26	0.24	0.06	0.07	0.02	0.06	0.04	0.02
BL 1201	0.39	0.37	0.83	0.25	0.24	0.78	0.06	0.07	0.27	0.04	0.03	0.19
LA 3913	0.30	0.26	0.77	0.24	0.21	0.64	0.04	0.05	0.01	0.04	0.03	0.01
LA 3914	0.39	0.34	0.24	0.28	0.24	0.16	0.09	0.05	0.01	0.52	0.05	0.01
LA 3922	0.27	0.27	0.25	0.21	0.16	0.25	0.04	0.05	0.02	0.02	0.02	0.03
LA 3923	0.33	0.31	0.25	0.18	0.21	0.31	0.04	0.05	0.02	0.03	0.03	0.03
CLN 2116 B	0.44	0.31	0.24	0.40	0.20	0.25	0.04	0.05	0.69	0.04	0.03	0.55
CLN 2498 E	0.22	0.22	0.85	0.17	0.18	0.77	0.03	0.03	0.45	0.03	0.02	0.39
CLN 2585 A	0.25	0.28	0.80	0.18	0.21	0.70	0.03	0.04	0.02	0.04	0.03	0.03
CLN 2585 C	0.30	0.26	0.72	0.15	0.20	0.65	0.04	0.04	0.01	0.04	0.03	0.04
CLN 2585 D	0.30	0.28	0.83	0.24	0.21	0.71	0.04	0.05	0.90	0.05	0.03	0.80
CLN 2679 E	0.60	0.30	0.74	0.50	0.23	0.65	0.04	0.05	0.01	0.04	0.03	0.02
CLN 2679 F	0.56	0.37	0.67	0.52	0.23	0.55	0.74	0.07	0.01	0.58	0.03	0.02
CLN 2714 G	0.48	0.36	0.32	0.32	0.24	0.28	0.06	0.06	0.01	0.04	0.03	0.02
CLN 2714 H	0.33	0.31	0.77	0.16	0.23	0.63	0.66	0.06	0.02	0.48	0.03	0.04
CLN 2714 J	0.50	0.31	0.84	0.38	0.20	0.75	0.86	0.05	0.01	0.66	0.02	0.05
L 01023	0.54	0.34	0.50	0.48	0.26	0.42	0.05	0.06	1.05	0.05	0.04	0.93
L 01033	0.23	0.29	0.67	0.16	0.18	0.56	0.04	0.05	0.03	0.03	0.03	0.02
L 01049	0.40	0.33	0.86	0.31	0.22	0.73	0.96	0.07	0.01	0.76	0.04	0.02
L 01049	0.36	0.29	0.77	0.23	0.18	0.67	0.93	0.05	0.01	0.63	0.03	0.02
L 01139	0.28	0.33	0.45	0.24	0.21	0.14	0.04	0.05	0.03	0.04	0.03	0.01
L 01318	0.34	0.32	0.74	0.25	0.19	0.66	1.01	0.06	0.02	0.91	0.03	0.02
L 01463	0.26	0.32	0.44	0.15	0.23	0.37	1.29	0.05	0.03	0.63	0.03	0.04
L 01463	0.36	0.33	0.71	0.21	0.21	0.64	1.39	0.05	0.02	0.86	0.03	0.02
L 01464	0.29	0.30	0.32	0.23	0.16	0.22	0.04	0.05	0.02	0.02	0.02	0.03
L 01696	0.60	0.27	0.92	0.42	0.22	0.84	1.42	0.63	1.21	1.08	0.61	1.05
L 01745	0.30	0.32	0.35	0.26	0.20	0.08	0.04	0.49	0.02	0.05	0.17	0.01
L 01869	0.48	0.28	0.13	0.36	0.19	0.15	0.04	0.52	0.01	0.03	0.02	0.01
L 01933	0.42	0.32	0.69	0.35	0.18	0.56	1.53	0.05	1.03	0.97	0.03	0.89
L 01942	0.45	0.35	0.64	0.34	0.22	0.49	1.32	0.23	1.04	1.01	0.09	0.91
L 02079	0.69	0.33	0.46	0.52	0.18	0.38	1.39	0.40	0.02	0.94	0.15	0.04

Contd....

Genotypes	Absolute Growth Rate						Relative Growth Rate					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
L 02222	0.47	0.34	0.77	0.18	0.18	0.64	1.14	0.24	0.01	0.92	0.63	0.02
L 02248	0.54	0.30	0.57	0.48	0.21	0.47	0.93	0.46	0.03	0.71	0.34	0.02
L 02692	0.28	0.32	0.86	0.14	0.19	0.79	1.25	0.42	0.03	0.95	0.28	0.03
L 02709	0.36	0.29	0.66	0.25	0.23	0.60	1.27	0.45	0.01	0.83	0.24	0.02
L 02778	0.29	0.25	0.45	0.19	0.20	0.35	1.10	0.53	0.01	0.82	0.47	0.03
L 06043	0.25	0.29	0.84	0.14	0.18	0.74	1.05	0.47	0.03	0.67	0.36	0.03
L 06044	0.38	0.33	0.84	0.15	0.22	0.74	1.35	0.61	0.01	0.81	0.52	0.03
L 06046	0.56	0.35	0.73	0.41	0.23	0.65	0.92	0.52	0.01	0.68	0.47	0.03
L 06049	0.57	0.37	0.80	0.43	0.25	0.72	0.92	0.44	0.01	0.55	0.31	0.02
L 06052	0.52	0.38	0.71	0.39	0.19	0.64	0.78	0.36	0.01	0.54	0.20	0.02
L 06057	0.36	0.29	0.57	0.25	0.20	0.48	0.84	0.04	0.02	0.61	0.04	0.02
L 06058	0.46	0.29	0.74	0.39	0.23	0.64	0.75	0.06	0.01	0.52	0.03	0.03
L 06106	0.46	0.36	0.66	0.13	0.22	0.56	0.49	0.30	0.02	0.25	0.18	0.04
L 06112	0.49	0.32	0.70	0.19	0.24	0.64	0.55	0.40	0.01	0.26	0.38	0.03
L 06115	0.55	0.28	0.71	0.29	0.23	0.64	0.95	0.04	0.01	0.80	0.03	0.03
L 06119	0.48	0.29	0.66	0.25	0.19	0.60	0.88	0.05	0.01	0.68	0.03	0.01
L 06122	0.53	0.26	0.76	0.39	0.19	0.66	1.21	0.45	0.01	0.73	0.40	0.02
L 06123	0.48	0.30	0.69	0.35	0.19	0.66	1.46	0.05	0.01	0.94	0.03	0.03
L 06179	0.50	0.25	0.65	0.41	0.21	0.55	1.04	0.04	0.01	0.73	0.03	0.02
L 06181	0.61	0.36	0.46	0.48	0.21	0.37	0.98	0.36	0.01	0.74	0.33	0.02
L 06181	0.63	0.34	0.59	0.51	0.20	0.48	0.93	0.42	0.02	0.78	0.40	0.02
L 06185	0.73	0.31	0.33	0.65	0.21	0.25	0.72	0.57	0.02	0.54	0.49	0.03
L 06188	0.41	0.32	0.15	0.11	0.15	0.36	0.55	0.63	0.01	0.41	0.60	0.02
L 06190	0.45	0.37	0.21	0.26	0.21	0.11	0.58	0.57	0.01	0.34	0.51	0.01
L 06193	0.61	0.33	0.34	0.39	0.24	0.31	0.35	0.05	1.00	0.13	0.04	0.89
L 06194	0.38	0.32	0.28	0.23	0.24	0.25	0.60	0.05	0.02	0.29	0.03	0.02
L 06201	0.51	0.37	0.09	0.23	0.24	0.24	1.01	0.57	0.01	0.80	0.42	0.02
L 06208	0.44	0.37	0.25	0.28	0.26	0.21	1.06	0.07	0.01	0.80	0.04	0.02
L 06218	0.39	0.32	0.24	0.21	0.18	0.11	0.94	0.05	0.01	0.72	0.03	0.01
L 06219	0.24	0.28	0.36	0.20	0.18	0.14	0.96	0.53	0.02	0.74	0.48	0.01
L 06220	0.30	0.31	0.35	0.19	0.20	0.22	0.80	0.48	0.02	0.65	0.39	0.02
L 06221	0.69	0.31	0.26	0.44	0.17	0.26	0.05	0.53	0.02	0.03	0.50	0.03
L 06223	0.44	0.36	0.19	0.21	0.22	0.23	0.99	0.49	0.01	0.75	0.45	0.02
L 06229	0.36	0.31	0.20	0.17	0.18	0.20	0.91	0.38	0.01	0.67	0.27	0.02
L 06230	0.64	0.39	0.18	0.55	0.20	0.26	1.12	0.51	0.01	0.84	0.48	0.02

Contd.....

Genotypes	Absolute Growth Rate						Relative Growth Rate					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
L 06231	0.56	0.35	0.09	0.46	0.24	0.22	0.93	0.54	0.00	0.72	0.49	0.02
L 06238	0.50	0.30	0.14	0.40	0.18	0.33	0.95	0.06	0.01	0.72	0.02	0.04
L 06240	0.52	0.36	0.55	0.40	0.19	0.47	1.01	0.07	0.01	0.83	0.02	0.02
L 1023	0.64	0.33	0.46	0.55	0.26	0.33	0.79	0.57	0.01	0.65	0.49	0.03
L 1030	0.32	0.37	0.47	0.21	0.22	0.23	0.85	0.52	0.03	0.65	0.49	0.02
LA 3923	0.26	0.28	0.41	0.13	0.20	0.36	1.02	0.48	0.02	0.85	0.39	0.04
Arka Abha	0.28	0.29	0.38	0.18	0.20	0.27	0.95	0.05	0.02	0.75	0.03	0.03
Arka Alok	0.27	0.30	0.36	0.17	0.19	0.22	1.06	0.05	0.03	0.79	0.03	0.02
Arka Meghali	0.33	0.24	0.34	0.22	0.17	0.29	0.03	0.04	0.01	0.04	0.03	0.01
Arka Saurabh	0.33	0.34	0.48	0.16	0.20	0.40	0.05	0.06	0.02	0.03	0.03	0.03
Arka Vikas	0.22	0.26	0.35	0.18	0.22	0.30	0.02	0.04	0.02	0.04	0.03	0.03
Shakti	0.34	0.33	0.32	0.24	0.24	0.24	0.95	0.38	0.02	0.73	0.34	0.02
Mukti	0.28	0.30	0.35	0.10	0.17	0.31	1.00	0.56	0.02	0.81	0.48	0.04
Anagha	0.33	0.30	0.51	0.17	0.22	0.33	0.05	0.51	0.02	0.03	0.48	0.03
Nandi	0.27	0.32	0.43	0.11	0.20	0.37	0.04	0.06	0.03	0.02	0.02	0.04
PKM 1	0.43	0.29	0.52	0.09	0.19	0.39	0.99	0.59	0.01	0.71	0.43	0.05
SL 120	0.22	0.27	0.36	0.14	0.19	0.28	0.04	0.53	0.03	0.03	0.49	0.03
DMT - 2	0.28	0.27	0.39	0.17	0.20	0.25	0.92	0.05	0.02	0.69	0.03	0.03
GK - 2	0.37	0.32	0.52	0.17	0.21	0.30	0.06	0.06	0.01	0.04	0.04	0.03
THB 205	0.45	0.37	0.43	0.25	0.27	0.32	0.07	0.07	0.01	0.05	0.04	0.03
TLB 130	0.28	0.32	0.39	0.22	0.22	0.24	0.04	0.06	0.03	0.05	0.04	0.02
TLB 133	0.37	0.34	0.30	0.30	0.27	0.21	0.05	0.06	0.02	0.05	0.04	0.02
M. Palli Tomato	0.37	0.35	0.31	0.24	0.22	0.19	0.05	0.06	0.02	0.04	0.03	0.02
Patriot	0.41	0.33	0.38	0.25	0.24	0.24	0.05	0.05	0.01	0.05	0.04	0.02
Podland Pink	0.40	0.27	0.39	0.11	0.14	0.21	0.04	0.04	0.01	0.02	0.02	0.03
Red Pear	0.37	0.34	0.48	0.16	0.22	0.32	0.05	0.06	0.02	0.04	0.03	0.04
S. Early	0.46	0.37	0.37	0.22	0.23	0.23	0.07	0.07	0.01	0.04	0.03	0.02
S. Harry	0.22	0.25	0.38	0.13	0.21	0.36	0.03	0.04	0.02	0.02	0.03	0.04
Tommy Toe	0.37	0.28	0.49	0.08	0.20	0.44	0.05	0.05	0.01	0.02	0.02	0.05
W. Cherry	0.30	0.28	0.25	0.18	0.20	0.24	0.05	0.06	0.02	0.04	0.03	0.03

Appendix XI. Mean values of tomato genotypes for crop growth rate and yield parameters under two irrigation regimes

Genotypes	Crop Growth Rate						Yield Parameters					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	NF	Avg. Frt. Wt.	PY	NF	Avg. Frt. Wt.	PY
BL 1187	0.66	0.54	3.09	0.44	0.37	1.66	135.93	12.49	1.70	105.67	12.45	1.32
BL 1188	0.64	0.56	0.88	0.32	0.36	0.43	135.27	12.55	1.70	104.87	12.42	1.30
BL 1198	0.69	0.63	1.16	0.35	0.42	0.55	134.47	12.40	1.67	134.33	11.27	1.52
BL 1199	0.72	0.61	3.49	0.21	0.28	0.42	134.73	12.76	1.72	136.20	11.19	1.52
BL 1200	0.67	0.63	3.46	0.50	0.48	1.52	133.67	12.48	1.67	135.80	11.26	1.53
BL 1201	0.72	0.68	0.85	0.47	0.44	0.39	134.80	12.79	1.72	134.80	11.01	1.48
LA 3913	0.56	0.47	0.68	0.44	0.39	0.34	105.00	20.80	2.18	89.40	24.40	2.18
LA 3914	0.72	0.63	0.45	0.51	0.44	0.29	114.47	16.13	1.85	95.20	15.91	1.51
LA 3922	0.51	0.49	3.40	0.21	0.30	1.62	106.27	20.74	2.20	90.13	23.84	2.15
LA 3923	0.62	0.57	0.77	0.29	0.39	0.37	165.47	15.05	2.49	154.80	15.76	2.44
CLN 2116 B	0.63	0.57	0.82	0.33	0.37	0.45	31.03	48.63	1.34	23.15	41.10	0.89
CLN 2498 E	0.41	0.40	0.64	0.31	0.33	0.35	23.67	48.87	1.16	21.13	40.87	0.86
CLN 2585 A	0.46	0.51	1.22	0.34	0.39	0.50	25.63	48.43	1.24	21.07	43.83	0.93
CLN 2585 C	0.56	0.49	1.42	0.28	0.37	0.55	16.35	51.67	1.34	11.06	40.83	0.88
CLN 2585 D	0.55	0.52	0.44	0.45	0.39	0.27	24.97	49.53	1.32	21.67	42.87	0.93
CLN 2679 E	0.63	0.56	0.90	0.42	0.42	0.43	26.73	54.47	1.46	20.90	41.83	0.87
CLN 2679 F	0.92	0.69	0.89	0.43	0.42	0.40	24.93	54.17	1.35	18.03	41.80	0.75
CLN 2714 G	0.88	0.67	2.76	0.43	0.44	1.37	26.83	55.00	1.48	19.87	40.80	0.81
CLN 2714 H	0.61	0.58	1.29	0.30	0.43	0.76	25.63	54.10	1.43	20.97	41.83	0.88
CLN 2714 J	0.63	0.57	3.62	0.14	0.38	1.70	23.73	55.23	1.31	18.43	41.13	0.76
L 01023	0.71	0.62	3.28	0.47	0.48	1.66	115.27	15.84	1.83	94.80	16.15	1.53
L 01033	0.43	0.54	2.95	0.30	0.33	1.39	134.40	12.49	1.68	105.20	12.43	1.31
L 01049	0.74	0.60	2.73	0.45	0.41	1.46	134.27	12.51	1.08	105.07	12.27	0.71
L 01049	0.66	0.53	3.65	0.31	0.33	1.42	156.00	11.23	1.75	136.00	11.27	1.53
L 01139	0.51	0.62	2.85	0.44	0.38	1.48	104.73	20.72	2.17	89.67	24.60	2.21
L 01318	0.63	0.59	2.79	0.30	0.34	1.69	105.53	21.00	2.22	90.53	24.05	2.18
L 01463	0.47	0.58	2.99	0.29	0.42	1.60	79.67	52.49	3.30	72.20	60.33	2.74
L 01463	0.66	0.60	2.72	0.36	0.39	1.55	80.10	21.08	2.20	70.10	24.01	2.18
L 01464	0.54	0.56	3.31	0.23	0.29	1.57	85.27	62.56	5.34	71.67	60.78	4.35
L 01696	1.84	0.50	3.67	1.46	0.41	2.68	117.63	52.45	4.17	88.05	57.52	3.72
L 01745	0.91	0.59	3.59	0.83	0.38	1.59	84.27	62.94	5.30	71.67	60.79	4.36
L 01869	0.89	0.51	3.43	0.81	0.35	1.63	164.07	14.99	2.46	156.00	15.97	2.49
L 01933	0.77	0.59	2.86	0.25	0.33	1.69	104.73	20.94	2.19	90.60	24.34	2.20
L 01942	0.83	0.65	2.83	0.78	0.40	1.60	78.73	20.77	2.18	60.67	24.27	2.19
L 02079	1.19	0.61	2.59	1.02	0.34	1.37	104.93	21.03	2.11	91.40	23.77	1.63

Contd....

Genotypes	Crop Growth Rate						Yield Parameters					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	NF	Avg. Frt. Wt.	PY	NF	Avg. Frt. Wt.	PY
L 02222	1.60	0.64	3.27	1.53	0.34	1.74	133.20	12.27	1.63	135.00	11.01	1.49
L 02248	1.60	0.55	3.52	1.47	0.38	1.50	135.87	12.41	1.69	104.27	12.65	1.32
L 02692	1.45	0.60	3.38	1.29	0.36	1.59	100.27	11.00	1.32	57.53	10.75	0.97
L 02709	0.67	0.53	2.77	0.46	0.43	1.18	153.87	10.87	1.67	134.47	10.82	1.45
L 02778	0.55	0.47	2.76	0.34	0.38	1.44	134.47	12.57	1.69	106.07	12.57	1.33
L 06043	0.46	0.53	2.87	0.25	0.34	1.51	118.20	11.27	1.75	94.40	11.00	1.49
L 06044	0.71	0.61	3.31	0.28	0.40	1.69	134.47	12.32	1.66	134.07	11.03	1.48
L 06046	0.77	0.65	3.36	0.32	0.42	1.65	135.53	12.39	1.68	134.93	10.95	1.48
L 06049	0.82	0.68	3.02	0.48	0.46	1.62	114.20	15.93	1.82	93.87	15.91	1.49
L 06052	0.83	0.70	2.57	0.35	0.35	1.45	135.27	12.32	1.67	135.13	10.94	1.48
L 06057	0.54	0.54	2.89	0.34	0.36	1.46	113.53	16.01	1.82	93.67	15.95	1.49
L 06058	0.74	0.54	2.95	0.33	0.42	1.49	105.53	20.91	2.21	90.60	23.96	2.17
L 06106	0.68	0.66	2.85	0.24	0.41	1.42	115.73	15.82	1.83	94.47	15.84	1.50
L 06112	0.75	0.59	2.75	0.40	0.44	1.52	134.33	12.41	1.67	134.53	11.34	1.53
L 06115	0.61	0.53	2.78	0.34	0.42	1.40	135.27	12.55	1.70	134.67	10.90	1.47
L 06119	0.81	0.54	3.43	0.39	0.35	1.76	114.47	15.83	1.81	94.87	15.92	1.51
L 06122	0.68	0.47	2.52	0.34	0.35	1.44	85.07	62.19	5.29	72.40	61.73	4.47
L 06123	0.74	0.55	2.51	0.24	0.35	1.66	85.60	62.33	5.34	70.87	61.13	4.33
L 06179	0.57	0.46	2.66	0.36	0.39	1.29	134.53	12.67	1.70	136.27	11.16	1.52
L 06181	0.78	0.66	3.53	0.33	0.39	1.80	135.87	12.50	1.70	134.93	11.01	1.49
L 06181	0.70	0.63	3.46	0.36	0.37	1.70	116.20	15.97	1.86	95.47	15.67	1.50
L 06185	0.55	0.57	2.55	0.34	0.38	1.22	134.60	12.41	1.67	105.93	12.72	1.35
L 06188	0.75	0.59	3.52	0.20	0.28	1.70	84.53	62.48	5.28	71.47	61.81	4.42
L 06190	0.83	0.68	3.23	0.47	0.39	1.56	86.07	62.09	5.34	71.87	60.41	4.34
L 06193	0.60	0.61	2.82	0.36	0.44	1.47	105.87	21.01	2.22	91.07	24.17	2.20
L 06194	0.71	0.60	3.33	0.43	0.44	1.61	85.13	63.15	5.38	71.87	61.45	4.42
L 06201	0.95	0.69	2.92	0.43	0.44	1.54	133.93	12.53	1.68	135.53	11.00	1.49
L 06208	0.82	0.68	3.03	0.53	0.48	1.65	135.67	12.46	1.69	135.27	11.02	1.49
L 06218	0.72	0.59	3.52	0.39	0.32	1.65	104.87	20.85	2.19	89.13	23.92	2.13
L 06219	1.59	0.51	3.26	1.55	0.33	1.73	79.40	52.01	4.13	72.00	61.19	4.40
L 06220	1.28	0.58	3.06	1.11	0.37	1.62	84.80	62.46	5.30	71.93	61.05	4.39
L 06221	1.07	0.56	3.60	1.03	0.31	1.83	104.27	21.05	2.20	90.27	23.54	2.12
L 06223	0.97	0.66	0.36	0.88	0.41	0.43	135.60	12.67	1.72	135.13	10.89	1.47
L 06229	0.66	0.57	2.84	0.32	0.34	1.42	135.20	12.57	1.70	106.27	12.69	1.35
L 06230	0.92	0.73	2.86	0.32	0.38	1.39	133.80	12.24	1.64	135.13	11.35	1.53

Contd.....

Genotypes	Crop Growth Rate						Yield Parameters					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	NF	Avg. Frt. Wt.	PY	NF	Avg. Frt. Wt.	PY
L 06231	1.05	0.65	2.65	0.94	0.44	1.23	135.87	12.61	1.71	136.73	11.03	1.51
L 06238	0.94	0.56	2.78	0.88	0.33	1.45	154.47	10.89	1.68	135.80	10.92	1.48
L 06240	1.66	0.67	0.22	1.49	0.36	0.35	133.87	12.42	1.66	135.47	11.06	1.50
L 1023	0.78	0.61	3.48	0.43	0.49	1.52	134.20	12.25	1.64	134.60	11.23	1.51
L 1030	0.59	0.68	0.87	0.39	0.40	0.43	166.07	14.93	2.48	154.93	16.13	2.50
LA 3923	0.48	0.52	0.60	0.23	0.38	0.67	165.47	15.21	2.52	155.53	15.85	2.47
Arka Abha	0.52	0.53	0.54	0.33	0.37	0.50	90.73	57.82	5.25	65.67	58.37	3.83
Arka Alok	0.51	0.56	0.68	0.32	0.35	0.41	89.27	57.65	5.15	66.00	57.91	3.82
Arka Meghali	0.61	0.44	3.55	0.40	0.32	1.75	89.73	57.67	5.17	65.87	57.73	3.80
Arka Saurabh	0.61	0.64	0.70	0.30	0.37	0.52	89.20	56.92	5.08	65.40	58.41	3.82
Arka Vikas	0.40	0.49	0.66	0.33	0.40	0.55	90.27	57.34	5.17	65.67	58.71	3.85
Shakti	1.62	0.62	2.70	1.46	0.44	1.35	79.40	52.91	4.20	66.27	57.77	3.83
Mukti	1.74	0.56	2.77	1.39	0.32	1.45	80.33	52.58	4.22	66.07	58.03	3.83
Anagha	1.62	0.55	2.34	1.52	0.41	1.22	80.33	52.81	4.24	65.33	57.35	3.75
Nandi	0.50	0.60	0.79	0.20	0.36	0.68	80.20	53.31	4.28	66.87	57.99	3.88
PKM 1	1.60	0.55	3.22	1.45	0.35	1.65	79.93	52.58	4.20	65.53	57.59	3.77
SL 120	1.71	0.50	2.85	1.60	0.34	1.55	154.40	10.85	1.68	134.67	11.11	1.50
DMT - 2	1.60	0.50	2.56	1.43	0.36	1.35	155.73	11.15	1.74	135.53	10.88	1.47
GK - 2	0.68	0.59	0.42	0.32	0.40	0.55	134.67	12.52	1.69	103.73	12.28	1.27
THB 205	0.84	0.69	0.40	0.46	0.50	0.59	134.40	12.30	1.65	134.53	11.06	1.49
TLB 130	0.52	0.59	0.73	0.40	0.41	0.44	104.93	21.05	2.21	90.80	23.76	2.16
TLB 133	0.68	0.64	0.56	0.55	0.49	0.38	135.00	12.35	1.67	134.20	11.03	1.48
M. Palli Tomato	0.68	0.64	0.58	0.44	0.41	0.35	113.93	16.11	1.84	94.53	15.83	1.50
Patriot	0.77	0.62	0.32	0.46	0.45	0.44	83.87	62.61	5.25	71.47	60.91	4.35
Podland Pink	0.74	0.49	0.18	0.21	0.26	0.38	86.27	61.77	5.33	71.73	60.63	4.35
Red Pear	0.69	0.63	0.53	0.30	0.40	0.59	104.93	20.95	2.20	90.47	24.34	2.20
S. Early	0.86	0.68	0.38	0.42	0.42	0.43	134.13	12.25	1.64	135.27	11.41	1.54
S. Harry	0.40	0.47	0.61	0.24	0.39	0.67	155.73	11.00	1.71	136.20	11.21	1.53
Tommy Toe	0.69	0.51	0.16	0.15	0.37	0.81	155.20	11.02	1.71	135.40	10.85	1.47
W. Cherry	0.55	0.52	0.46	0.34	0.37	0.45	134.33	12.61	1.69	106.07	12.22	1.30

Appendix XII. Mean values of hybrids and parents for plant height and number of branches under two irrigation regimes

Hybrids/ Parents	Plant height (cm)						Number of branches					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	31.39	64.66	99.66	23.97	41.78	75.29	15.78	29.98	46.34	11.82	16.04	22.29
P1xP3	23.35	43.10	64.16	18.75	32.17	55.97	16.61	34.64	43.68	13.84	18.62	16.28
P1xP4	21.28	38.82	56.54	15.39	30.47	49.07	13.70	30.64	41.43	12.84	15.63	20.14
P1xP5	31.84	54.96	80.90	22.26	48.11	72.20	12.33	25.65	38.68	10.10	17.21	21.41
P1xP6	36.42	71.93	100.54	32.48	57.29	93.04	11.62	24.50	36.51	10.21	15.72	22.41
P1xP7	33.39	65.13	91.30	28.74	51.70	74.67	11.50	25.98	40.03	10.69	14.38	22.59
P1xP8	34.72	64.70	88.69	25.76	50.47	73.26	11.15	25.48	39.85	9.59	15.06	18.65
P2xP3	25.65	59.76	96.06	22.91	33.42	72.09	14.31	24.59	33.68	10.07	13.23	20.14
P2xP4	25.25	59.17	90.64	16.72	38.64	68.43	11.12	19.93	30.46	8.55	10.13	17.72
P2xP5	23.98	48.75	76.29	16.79	35.86	58.83	12.48	20.50	35.49	8.29	14.93	15.56
P2xP6	20.83	49.51	75.81	18.33	30.09	56.74	12.09	19.93	34.28	8.77	13.87	18.92
P2xP7	23.23	55.44	85.58	19.86	32.86	58.16	11.54	20.86	37.01	8.95	11.71	13.00
P2xP8	26.89	61.97	86.01	20.23	39.69	57.65	11.25	20.55	37.28	7.80	12.65	21.40
P3xP4	28.20	62.18	94.71	22.47	43.20	81.36	13.84	27.54	33.17	11.97	14.07	20.85
P3xP5	27.34	52.88	81.82	22.54	41.33	72.90	12.76	23.16	31.23	9.52	15.95	19.51
P3xP6	43.12	94.15	137.68	44.06	67.55	126.63	14.67	26.88	34.45	11.64	17.09	25.14
P3xP7	27.41	59.59	90.45	27.48	40.13	76.25	14.72	28.72	38.62	12.28	15.97	21.59
P3xP8	29.30	63.52	90.78	26.31	42.93	74.03	14.77	29.13	40.18	11.47	17.31	23.65
P4xP5	28.84	60.33	88.47	17.03	49.42	76.26	11.46	22.62	33.15	9.89	14.65	22.99
P4xP6	27.72	61.89	88.67	19.04	48.08	77.47	10.92	21.77	31.49	10.11	13.44	21.93
P4xP7	27.03	60.30	86.50	18.08	46.76	71.61	10.56	22.69	33.99	10.33	11.82	26.71
P4xP8	28.56	63.49	87.97	17.55	48.69	71.44	10.79	23.46	36.13	9.76	13.30	19.72
P5xP6	25.42	45.85	66.67	18.51	43.23	62.23	11.58	20.35	34.83	9.04	18.15	17.73
P5xP7	24.98	44.96	65.38	17.93	42.38	57.41	11.58	20.35	34.83	9.04	18.15	19.69
P5xP8	27.53	51.01	69.57	18.34	45.96	58.42	10.59	20.89	37.86	7.92	16.70	22.01
P6xP7	27.97	61.24	82.66	28.38	49.04	70.12	11.06	21.22	37.08	9.93	15.76	26.20
P6xP8	31.04	67.54	83.78	26.08	52.46	67.48	10.62	20.54	36.55	8.76	16.30	19.36
P7xP8	29.44	64.06	81.31	25.69	50.07	59.49	10.53	22.94	42.18	9.55	14.42	28.12
P1	36.64	64.37	93.71	27.39	50.74	81.78	9.54	22.14	30.78	8.57	11.85	24.71
P2	26.15	64.95	105.60	20.56	32.82	68.79	10.15	15.73	27.35	6.34	8.42	27.71
P3	25.16	54.57	86.53	25.26	34.01	75.38	13.08	24.34	26.95	10.08	13.15	27.72
P4	29.58	66.37	96.80	16.99	51.03	81.83	9.63	20.65	26.98	9.42	9.92	24.39
P5	27.04	45.54	68.09	17.13	45.47	62.63	8.78	15.33	26.43	6.22	14.12	29.21
P6	25.85	56.78	76.70	26.83	45.59	74.50	9.31	16.45	27.96	7.87	14.24	21.67
P7	25.13	54.91	74.08	25.08	43.88	56.30	8.37	18.03	32.59	8.19	10.58	19.55
P8	30.25	65.48	76.98	21.96	49.84	53.38	8.16	18.11	34.21	6.45	12.60	22.93

Contd.....

Appendix XIII. Mean values of hybrids and parents for stem girth and root parameters under two irrigation regimes

Hybrids / Parents	Stem Girth (cm)						Root length (cm)		Root volume (cc)	
	IR 1			IR 2			IR 1	IR 2	IR 1	IR 2
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT				
P1xP2	4.61	6.40	9.14	4.23	4.49	5.66	29.74	52.89	25.15	34.83
P1xP3	4.56	5.94	8.19	3.94	4.75	5.15	36.13	57.15	28.59	35.71
P1xP4	4.66	6.47	9.65	4.94	4.85	5.88	36.01	63.43	30.26	31.91
P1xP5	4.57	6.22	9.88	3.79	5.10	5.03	40.81	71.52	39.73	48.74
P1xP6	3.75	5.43	7.81	3.70	4.87	4.81	38.21	67.44	32.71	47.03
P1xP7	4.80	6.72	9.30	4.03	4.21	5.05	38.77	58.26	25.74	34.32
P1xP8	4.45	6.28	8.59	3.32	4.64	4.22	38.81	62.03	25.98	32.23
P2xP3	4.73	6.27	7.81	3.45	3.31	6.19	40.57	68.66	25.77	33.75
P2xP4	4.75	6.65	8.94	4.25	3.35	6.73	36.23	68.23	41.57	43.98
P2xP5	5.11	7.03	10.10	3.54	3.97	6.51	40.83	75.94	37.90	47.75
P2xP6	4.51	6.58	8.45	3.68	4.06	6.64	40.25	75.61	29.36	44.19
P2xP7	4.93	6.95	8.77	3.52	2.85	6.10	40.84	65.47	22.05	30.71
P2xP8	5.60	7.99	9.80	3.31	3.97	6.16	35.98	61.88	28.93	36.75
P3xP4	4.39	5.70	7.29	3.66	3.45	5.72	41.99	71.59	32.70	32.95
P3xP5	4.41	5.62	7.68	2.79	3.74	5.14	45.74	77.75	38.54	45.27
P3xP6	4.49	6.43	7.92	3.59	5.01	6.51	41.36	71.71	33.05	45.92
P3xP7	4.74	6.40	7.69	3.05	2.79	5.16	37.25	55.30	26.00	32.71
P3xP8	4.94	6.78	7.88	2.43	3.82	4.63	37.48	58.50	29.38	34.41
P4xP5	4.68	6.41	9.86	3.66	4.12	5.90	39.10	71.77	46.05	47.31
P4xP6	4.06	6.05	8.06	3.93	4.39	6.26	41.28	76.45	39.68	46.67
P4xP7	4.85	6.87	8.90	3.88	2.92	5.79	41.55	66.28	33.11	34.28
P4xP8	5.47	7.85	9.79	3.44	4.25	5.61	41.54	70.13	36.93	36.50
P5xP6	4.82	7.03	10.00	3.59	5.49	6.67	43.09	79.24	42.03	55.85
P5xP7	5.00	6.95	9.71	3.08	3.46	5.39	42.51	67.49	37.10	45.41
P5xP8	5.72	8.06	10.78	2.74	4.78	5.35	33.85	57.71	37.19	43.05
P6xP7	5.51	8.18	10.17	4.11	4.74	7.12	41.66	69.78	28.77	42.27
P6xP8	6.12	9.05	11.23	4.49	5.03	7.75	41.96	70.20	29.56	43.45
P7xP8	5.78	8.30	9.94	3.17	3.41	5.49	33.72	50.55	25.79	32.01
P1	3.63	5.00	7.80	3.82	4.67	3.90	26.33	43.00	20.79	27.57
P2	3.82	5.33	6.90	2.96	2.47	5.30	22.67	43.67	17.73	25.48
P3	4.23	5.17	6.00	2.80	3.30	5.03	29.33	45.33	22.94	27.39
P4	3.70	5.20	7.38	3.97	2.93	5.40	25.00	46.33	32.87	28.92
P5	4.16	5.60	9.07	2.47	3.90	4.70	30.00	54.67	28.07	32.63
P6	3.25	5.07	6.42	2.87	4.29	5.23	29.00	53.67	20.88	32.26
P7	4.68	6.67	8.13	2.97	2.27	4.83	29.33	41.67	18.79	25.27
P8	4.63	6.73	7.83	1.87	3.57	3.73	28.33	44.67	22.26	25.55

Appendix XIV. Mean values of hybrids and parents for stomatal count, pubescence and number of leave under two irrigation regimes

Hybrids / Parents	IR 1			IR 2			Number of leaves					
	Stomatal count	Pubescence (AB)	Pubescence (AD)	Stomatal count	Pubescence (AB)	Pubescence (AD)	IR 1			IR 2		
							45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT
P1xP2	8.91	290.83	567.14	7.33	1047.75	1716.09	37.79	63.30	93.86	33.52	51.81	72.51
P1xP3	9.88	245.91	553.86	8.49	323.70	1680.91	38.24	71.40	98.96	35.02	65.16	85.86
P1xP4	9.16	234.33	460.77	7.69	313.48	1562.87	45.27	83.67	119.12	39.45	81.69	82.37
P1xP5	8.38	393.29	845.14	6.75	501.76	1993.48	42.58	72.43	108.05	40.11	61.73	92.86
P1xP6	7.76	473.63	957.90	6.39	1588.23	2529.44	47.46	69.66	107.03	39.62	64.22	91.95
P1xP7	11.13	211.14	486.84	9.08	296.89	1879.78	48.20	84.30	120.41	45.97	60.87	99.87
P1xP8	10.00	173.77	391.27	8.31	244.50	1576.12	42.94	76.57	103.93	32.11	55.10	73.72
P2xP3	9.49	263.60	500.35	7.98	1174.13	609.56	44.67	75.78	110.20	40.96	61.43	87.47
P2xP4	8.87	287.33	477.43	7.28	1281.63	575.37	39.74	65.81	99.09	34.69	56.45	62.04
P2xP5	7.50	514.90	1007.39	6.01	1565.12	1120.79	46.65	71.67	113.16	44.05	53.02	89.41
P2xP6	7.64	474.52	868.08	6.04	2456.75	1052.28	44.07	58.76	95.64	36.96	46.71	73.84
P2xP7	10.55	204.36	392.07	8.48	1066.37	509.71	46.00	73.27	110.05	43.62	45.15	83.12
P2xP8	10.15	207.37	381.03	8.30	1119.60	490.47	46.95	76.26	108.08	34.67	45.19	66.98
P3xP4	9.20	171.08	336.48	8.05	217.90	384.29	48.41	92.73	127.87	43.86	91.32	94.70
P3xP5	7.67	276.66	603.92	6.54	340.28	653.33	44.70	79.77	114.19	43.55	69.83	103.16
P3xP6	8.06	370.45	740.80	6.86	1472.82	879.88	36.25	57.48	83.79	31.80	53.82	75.78
P3xP7	10.23	121.81	308.11	8.72	167.32	387.88	51.01	92.37	128.02	50.18	68.60	111.16
P3xP8	10.59	115.18	280.35	9.16	158.19	346.01	49.43	91.18	119.58	37.94	66.15	88.58
P4xP5	8.65	335.96	654.57	7.14	418.69	692.57	46.79	81.11	121.11	43.44	75.42	87.33
P4xP6	8.90	271.99	482.23	7.30	931.56	560.43	56.44	82.65	127.92	46.07	82.77	93.38
P4xP7	10.79	131.31	255.83	8.91	184.00	316.39	42.48	76.46	109.13	39.31	64.16	73.75
P4xP8	11.76	126.48	234.54	9.86	180.07	285.87	43.03	78.51	106.95	31.76	63.96	60.08
P5xP6	5.88	603.57	1214.51	4.44	1783.14	1351.05	42.41	57.87	94.11	37.65	50.09	83.65
P5xP7	8.89	347.45	760.96	6.88	437.36	826.08	40.21	66.00	99.03	40.40	44.39	84.93
P5xP8	8.66	342.53	740.97	6.80	432.25	797.38	40.76	68.14	96.68	32.40	44.17	70.46
P6xP7	9.02	328.13	654.32	6.92	1488.63	802.90	44.44	63.13	97.40	39.70	46.14	83.38
P6xP8	8.77	329.64	657.71	6.71	1494.47	807.30	44.81	63.74	98.29	40.06	46.48	84.11
P7xP8	13.29	53.57	158.18	10.75	94.55	228.84	42.71	73.75	99.95	34.10	39.96	69.41
P1	8.98	258.44	567.20	7.48	351.71	2476.28	38.67	70.00	99.67	34.33	63.00	83.00
P2	8.32	263.05	446.93	6.73	1552.95	558.31	35.00	52.00	82.33	31.00	35.33	56.00
P3	10.34	150.48	351.89	9.19	188.07	411.21	36.00	70.00	93.67	34.33	65.00	85.67
P4	9.54	159.21	251.51	8.10	206.75	276.99	34.67	65.33	93.00	29.67	68.33	52.33
P5	6.34	367.73	779.55	4.82	449.34	813.12	33.67	53.33	84.00	33.67	42.33	74.67
P6	6.86	363.97	690.69	5.13	1745.97	825.27	41.00	48.00	81.00	32.33	45.67	72.00
P7	13.08	50.69	154.24	10.44	86.49	222.96	36.33	61.67	88.33	36.67	34.67	73.00
P8	12.77	37.39	105.05	10.58	69.50	152.18	36.67	64.33	82.67	22.00	33.67	46.33

Appendix XV. Mean values of hybrids and parents for leaf area and AGR under two irrigation regimes

Hybrids / Parents	Leaf area (cm ²)						Absolute Growth Rate					
	IR 1			IR 2			IR 1			IR 2		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
P1xP2	229.32	466.22	923.22	137.91	337.21	499.73	0.60	0.46	0.80	0.43	0.23	0.63
P1xP3	207.20	524.07	977.36	137.81	455.88	618.74	0.70	0.42	0.67	0.55	0.24	0.52
P1xP4	234.18	610.70	1136.50	172.73	452.85	598.80	0.45	0.37	0.88	0.36	0.25	0.71
P1xP5	250.36	524.69	1065.75	164.98	448.24	658.55	0.77	0.49	0.66	0.57	0.34	0.40
P1xP6	278.97	536.73	1067.42	162.27	449.25	679.99	0.70	0.59	0.82	0.57	0.39	0.60
P1xP7	244.27	523.19	930.65	130.12	368.20	517.47	0.52	0.45	0.91	0.36	0.24	0.78
P1xP8	218.01	475.39	847.16	101.95	353.27	442.83	0.52	0.37	0.64	0.44	0.22	0.52
P2xP3	300.84	578.91	1090.34	205.41	374.13	594.31	0.76	0.48	0.80	0.56	0.24	0.63
P2xP4	259.10	498.58	949.95	185.18	258.49	417.13	0.56	0.46	1.06	0.41	0.26	0.84
P2xP5	330.85	539.09	1117.73	222.98	337.73	598.07	0.87	0.58	0.84	0.61	0.35	0.54
P2xP6	309.80	471.43	954.09	188.03	276.47	512.87	0.64	0.55	0.78	0.49	0.33	0.56
P2xP7	287.34	472.00	858.06	164.36	214.06	385.40	0.51	0.45	0.93	0.32	0.21	0.79
P2xP8	292.54	480.55	861.56	149.39	226.61	346.37	0.63	0.46	0.81	0.49	0.23	0.66
P3xP4	270.31	695.50	1229.38	222.24	503.02	686.71	0.54	0.34	0.77	0.44	0.23	0.61
P3xP5	280.12	596.81	1133.37	209.59	489.23	732.23	0.83	0.45	0.55	0.63	0.32	0.30
P3xP6	224.89	452.16	839.54	152.62	365.27	556.88	0.71	0.50	0.63	0.59	0.34	0.43
P3xP7	277.45	595.14	998.34	175.15	403.96	586.67	0.57	0.40	0.80	0.42	0.22	0.68
P3xP8	269.90	580.75	965.12	152.53	406.44	527.18	0.72	0.41	0.67	0.62	0.25	0.54
P4xP5	281.24	599.39	1160.51	223.53	414.71	621.53	0.63	0.42	0.80	0.49	0.34	0.52
P4xP6	340.62	653.10	1243.32	235.94	446.38	699.95	0.47	0.44	0.84	0.41	0.34	0.62
P4xP7	219.78	499.92	852.28	156.53	277.23	387.15	0.33	0.35	0.99	0.24	0.22	0.85
P4xP8	222.86	504.82	851.85	143.69	286.51	353.66	0.47	0.36	0.85	0.44	0.25	0.70
P5xP6	282.19	453.96	942.44	183.91	355.00	607.28	0.78	0.56	0.61	0.61	0.43	0.30
P5xP7	236.93	415.98	780.41	148.22	270.98	443.84	0.67	0.48	0.80	0.46	0.32	0.56
P5xP8	240.09	420.96	779.67	134.63	280.70	408.35	0.74	0.45	0.59	0.60	0.32	0.35
P6xP7	260.28	422.20	768.00	142.74	265.85	453.26	0.49	0.49	0.82	0.37	0.32	0.65
P6xP8	262.12	425.50	773.17	143.65	267.39	455.71	0.49	0.50	0.83	0.37	0.32	0.66
P7xP8	216.54	387.79	598.83	91.36	188.86	246.31	0.51	0.43	0.92	0.41	0.23	0.81
P1	196.27	501.12	979.48	113.17	451.36	598.80	0.50	0.38	0.63	0.38	0.21	0.51
P2	261.00	401.30	810.92	163.13	177.63	352.03	0.53	0.41	0.74	0.36	0.18	0.58
P3	211.84	529.84	931.25	162.91	441.34	616.51	0.66	0.34	0.50	0.53	0.20	0.38
P4	182.56	485.17	862.97	161.53	291.90	384.30	0.24	0.23	0.78	0.22	0.19	0.63
P5	227.03	391.89	831.88	164.72	313.06	520.06	0.56	0.32	0.34	0.41	0.25	0.12
P6	269.52	404.98	821.15	157.68	309.64	546.26	0.37	0.36	0.39	0.33	0.26	0.24
P7	183.89	329.93	517.14	91.14	154.06	244.65	0.31	0.34	0.86	0.17	0.17	0.78
P8	186.20	332.89	506.77	65.69	168.41	178.10	0.48	0.32	0.56	0.46	0.19	0.47

Appendix XVI. Mean values of hybrids and parents for relative and crop growth rate under two irrigation regimes

Hybrids/ Parents	Relative Growth Rate						Crop Growth Rate					
	IR 1			IR 2			IR 1			IR 2		
	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT	45 - 60 DAT	45 - 90 DAT	60 - 90 DAT
P1xP2	1.13	0.31	0.60	0.85	0.15	0.90	0.94	0.78	3.10	0.70	0.48	1.77
P1xP3	1.58	0.40	0.62	1.21	0.14	1.28	1.27	0.80	3.38	1.24	0.50	1.76
P1xP4	0.74	0.15	0.60	0.60	0.08	0.86	0.83	0.67	2.12	0.72	0.50	1.23
P1xP5	1.54	0.61	0.63	1.20	0.47	1.39	1.35	0.93	3.96	1.22	0.63	2.08
P1xP6	1.00	0.22	0.82	0.83	0.10	1.32	1.19	1.05	2.74	1.05	0.77	1.65
P1xP7	1.47	0.37	0.75	1.20	0.21	1.39	1.43	0.85	4.03	1.35	0.50	1.97
P1xP8	0.80	0.17	0.65	0.65	0.07	0.83	0.82	0.70	2.25	0.66	0.42	1.26
P2xP3	1.26	0.46	0.04	0.87	0.19	1.21	1.28	0.84	3.24	1.00	0.51	1.74
P2xP4	0.63	0.28	0.02	0.41	0.15	0.94	0.95	0.79	2.29	0.58	0.55	1.36
P2xP5	1.40	0.73	0.03	0.98	0.54	1.49	1.51	1.07	4.20	1.12	0.70	2.26
P2xP6	0.54	0.27	0.03	0.37	0.14	1.17	1.09	0.98	2.05	0.74	0.71	1.30
P2xP7	1.15	0.46	0.03	0.85	0.27	1.38	1.36	0.81	3.52	1.06	0.46	1.73
P2xP8	0.60	0.28	0.03	0.39	0.14	0.95	1.00	0.87	2.36	0.55	0.50	1.36
P3xP4	0.81	0.27	0.04	0.59	0.10	1.12	1.07	0.65	1.93	0.96	0.49	1.01
P3xP5	1.17	0.49	0.03	0.85	0.30	1.16	1.11	0.61	2.57	1.04	0.41	1.26
P3xP6	0.81	0.29	0.04	0.60	0.11	1.38	1.25	0.89	1.93	1.13	0.67	1.09
P3xP7	1.41	0.47	0.04	1.07	0.23	1.57	1.49	0.70	3.31	1.44	0.41	1.47
P3xP8	0.88	0.30	0.05	0.63	0.10	1.21	1.14	0.75	2.14	0.95	0.43	1.08
P4xP5	0.83	0.49	0.03	0.61	0.42	1.26	1.22	0.81	2.64	1.02	0.63	1.39
P4xP6	0.08	0.08	0.02	0.07	0.05	1.07	0.93	0.82	0.93	0.73	0.70	0.67
P4xP7	0.69	0.26	0.03	0.55	0.18	1.25	1.17	0.63	2.31	1.03	0.43	1.05
P4xP8	0.10	0.07	0.03	0.07	0.04	0.84	0.77	0.66	1.04	0.49	0.45	0.61
P5xP6	0.84	0.52	0.03	0.64	0.43	1.56	1.46	1.09	2.77	1.25	0.83	1.53
P5xP7	1.49	0.73	0.03	1.14	0.58	1.81	1.74	0.91	4.24	1.58	0.59	1.95
P5xP8	0.88	0.52	0.03	0.64	0.43	1.29	1.28	0.89	2.89	1.01	0.57	1.47
P6xP7	0.63	0.26	0.03	0.51	0.17	1.45	1.36	0.88	2.32	1.21	0.63	1.14
P6xP8	0.67	0.28	0.03	0.54	0.18	1.50	1.40	0.90	2.39	1.24	0.64	1.17
P7xP8	0.79	0.30	0.03	0.62	0.20	1.37	1.31	0.73	2.69	1.09	0.39	1.18
P1	1.24	0.22	1.04	1.02	0.09	0.83	0.83	0.68	2.94	0.79	0.43	1.64
P2	0.80	0.35	0.02	0.52	0.18	0.80	0.83	0.70	2.52	0.44	0.42	1.47
P3	1.34	0.41	0.04	0.97	0.14	1.23	1.19	0.61	2.53	1.17	0.38	1.22
P4	0.06	0.04	0.01	0.04	0.04	0.59	0.56	0.44	0.68	0.41	0.39	0.44
P5	0.94	0.56	0.02	0.70	0.48	1.04	1.05	0.64	2.69	0.92	0.45	1.35
P6	0.05	0.06	0.02	0.05	0.03	0.80	0.68	0.65	0.58	0.55	0.53	0.46
P7	1.13	0.41	0.03	0.91	0.28	1.53	1.45	0.62	3.33	1.37	0.34	1.37
P8	0.09	0.07	0.03	0.06	0.03	0.69	0.64	0.58	0.92	0.36	0.31	0.51

Appendix XVII. Mean values of hybrids and parents for biochemical and yield parameters under two irrigation regimes

Hybrids / Parents	Biochemical Parameters								Yield Parameters					
	IR 1				ir 2				IR 1			IR 2		
	Proline content	Chloro phyll a	Chloro phyll b	Total chloro phyll	Proline content	Chloro phyll a	Chloro phyll b	Total chloro phyll	NF	Avg. Frt. Wt.	PY	NF	Avg. Frt. Wt.	PY
P1xP2	209.50	1.55	0.22	1.77	306.13	1.07	0.47	1.54	147.74	14.64	2.17	120.14	18.03	2.13
P1xP3	227.57	1.47	0.21	1.68	318.51	0.73	0.32	1.05	135.86	13.12	1.78	100.52	16.68	1.63
P1xP4	189.36	1.57	0.22	1.79	282.34	1.13	0.54	1.66	162.71	22.14	3.61	112.47	20.36	2.28
P1xP5	244.03	2.45	0.63	3.07	410.70	1.71	0.51	2.22	157.60	18.19	2.87	122.66	22.07	2.71
P1xP6	318.81	2.47	0.65	3.11	499.89	1.82	0.61	2.43	157.46	45.92	7.18	141.03	46.93	6.51
P1xP7	221.65	1.60	0.31	1.90	318.27	0.97	0.53	1.50	163.23	17.47	2.89	96.76	16.58	1.53
P1xP8	162.72	1.28	0.40	1.67	254.54	0.81	0.42	1.24	155.24	21.64	3.40	127.90	17.68	2.17
P2xP3	201.14	1.33	0.16	1.49	285.70	0.75	0.41	1.16	148.17	15.90	2.34	144.98	20.11	2.92
P2xP4	203.83	1.50	0.18	1.68	306.27	1.16	0.63	1.79	174.83	21.06	3.70	154.04	20.07	3.09
P2xP5	308.61	2.46	0.60	3.05	530.98	1.81	0.64	2.45	181.94	24.11	4.39	178.23	29.13	5.16
P2xP6	285.75	2.08	0.57	2.65	457.53	1.66	0.62	2.28	185.28	46.45	8.59	207.57	47.66	9.76
P2xP7	209.68	1.25	0.22	1.47	302.55	0.82	0.55	1.37	177.02	17.11	3.02	136.33	16.88	2.31
P2xP8	176.01	1.30	0.45	1.75	284.17	0.90	0.60	1.50	158.68	22.63	3.60	164.61	18.95	3.14
P3xP4	162.21	1.24	0.14	1.38	233.61	0.72	0.43	1.14	167.54	18.46	3.07	133.55	18.09	2.41
P3xP5	193.32	1.33	0.32	1.65	321.86	0.75	0.25	1.00	184.73	18.83	3.48	168.19	23.55	3.93
P3xP6	238.64	1.86	0.54	2.40	371.15	1.24	0.43	1.68	178.26	45.09	7.96	191.31	46.11	8.71
P3xP7	180.37	1.02	0.19	1.21	248.96	0.39	0.35	0.75	144.79	15.62	2.26	100.23	15.43	1.55
P3xP8	153.52	1.05	0.42	1.47	239.15	0.45	0.39	0.84	152.17	19.24	2.91	147.31	16.33	2.38
P4xP5	226.51	2.28	0.57	2.85	397.18	1.71	0.63	2.34	185.96	26.74	4.95	157.45	25.55	4.03
P4xP6	190.19	2.05	0.56	2.61	306.87	1.67	0.67	2.34	185.03	48.31	8.79	185.86	43.77	8.11
P4xP7	183.26	1.14	0.20	1.34	270.21	0.77	0.56	1.33	165.36	21.58	3.67	101.03	15.57	1.59
P4xP8	154.11	1.15	0.43	1.58	261.81	0.82	0.59	1.42	167.13	27.94	4.80	150.17	18.14	2.71
P5xP6	352.75	2.92	0.97	3.89	628.47	2.25	0.64	2.89	144.78	51.43	7.40	150.36	53.06	7.96
P5xP7	260.78	2.07	0.62	2.69	454.37	1.41	0.55	1.96	174.50	21.87	3.81	124.42	21.74	2.71
P5xP8	231.00	2.05	0.82	2.87	436.61	1.44	0.56	2.00	171.53	27.65	4.74	168.65	23.80	4.01
P6xP7	255.99	1.78	0.59	2.37	407.02	1.32	0.58	1.90	173.08	46.45	8.08	137.98	43.29	5.96
P6xP8	253.59	1.80	0.59	2.39	403.79	1.33	0.59	1.91	162.64	47.74	7.80	132.61	44.19	5.84
P7xP8	149.43	0.99	0.45	1.43	236.36	0.54	0.54	1.09	120.52	22.13	2.64	90.44	13.57	1.19
P1	196.34	1.53	0.24	1.77	284.86	0.99	0.37	1.36	112.60	14.83	1.68	74.33	18.33	1.24
P2	166.65	1.17	0.15	1.32	245.50	0.88	0.46	1.33	133.13	14.42	1.89	138.13	17.67	2.44
P3	153.15	0.92	0.11	1.03	206.76	0.25	0.17	0.42	106.75	11.03	1.18	94.53	14.67	1.40
P4	137.01	1.05	0.11	1.16	212.24	0.84	0.49	1.33	111.77	20.87	2.32	81.33	15.33	1.27
P5	205.54	1.85	0.58	2.43	389.04	1.35	0.35	1.70	142.40	22.00	3.15	132.00	26.33	3.46
P6	211.50	1.58	0.56	2.14	353.98	1.30	0.40	1.70	126.60	68.67	8.56	151.00	67.00	9.93
P7	146.21	0.88	0.23	1.10	206.24	0.45	0.46	0.91	116.00	14.33	1.65	59.67	10.00	0.59
P8	94.58	0.76	0.54	1.30	177.89	0.46	0.44	0.90	118.27	23.67	2.75	122.67	13.33	1.57

Appendix XVIII. Mean values of hybrids and parents for morphological paramteres under TyLCV trail

Hybrids/ Parents	Plant height (cm)			Number of branches			Stem girth (cm)			Pubescence (AB)	Pubescence (AD)
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT		
P1xP2	26.03	63.59	48.15	11.81	16.99	17.60	6.69	19.54	20.69	394.50	771.97
P1xP3	21.99	44.39	32.02	15.85	20.16	18.11	6.06	17.81	19.02	324.65	717.49
P1xP4	22.28	41.57	32.08	13.71	15.96	16.02	7.20	19.61	20.26	306.75	601.26
P1xP5	32.78	52.43	35.21	12.59	17.84	17.82	8.64	20.88	19.76	507.28	1100.76
P1xP6	23.62	54.10	38.40	13.10	21.66	23.69	10.30	22.20	23.97	440.04	911.04
P1xP7	26.26	47.94	34.73	11.26	16.65	18.30	6.95	17.93	13.68	230.43	531.23
P1xP8	24.46	45.65	33.63	10.64	18.62	17.44	6.50	18.78	15.08	222.07	505.23
P2xP3	22.84	46.95	35.49	15.59	20.97	19.44	9.13	20.67	21.52	319.45	607.95
P2xP4	23.51	47.60	37.62	15.40	19.12	19.61	9.83	21.64	21.99	306.75	502.30
P2xP5	25.55	50.52	37.60	11.85	17.84	18.31	10.36	21.39	20.46	431.26	840.54
P2xP6	26.36	50.36	33.32	10.22	18.42	20.61	9.92	17.73	18.61	419.84	773.71
P2xP7	25.57	45.83	34.50	10.83	17.13	19.21	8.37	17.25	13.79	231.92	438.27
P2xP8	25.59	47.13	36.09	10.53	19.55	18.75	9.42	21.01	16.88	223.45	410.40
P3xP4	15.15	13.73	9.93	13.07	14.55	12.88	8.52	18.22	18.48	182.06	328.34
P3xP5	20.88	19.32	10.57	11.01	14.60	13.00	9.67	18.70	17.14	322.66	699.76
P3xP6	18.57	21.54	10.18	10.41	16.09	15.92	10.68	17.42	18.49	296.42	604.83
P3xP7	16.91	15.88	9.90	11.69	16.24	16.16	8.35	16.56	12.49	128.70	311.69
P3xP8	17.88	16.44	10.66	10.62	16.82	14.03	7.94	17.35	13.27	116.83	272.96
P4xP5	24.80	18.49	12.87	11.64	13.53	13.33	10.19	19.54	17.75	261.40	491.92
P4xP6	23.01	21.62	12.59	11.55	16.15	17.60	11.23	18.43	18.96	296.66	532.70
P4xP7	20.02	14.25	11.52	12.08	15.40	17.01	8.57	16.31	11.40	130.75	239.07
P4xP8	22.30	15.62	12.95	10.48	15.32	14.07	7.96	16.82	12.69	121.91	211.69
P5xP6	29.63	30.18	12.44	7.68	14.48	16.15	11.21	17.16	16.39	453.88	941.36
P5xP7	37.73	30.96	15.71	10.45	16.18	17.40	9.56	16.90	11.07	351.40	782.58
P5xP8	37.60	30.64	15.81	10.26	18.84	17.32	9.51	18.34	12.68	341.38	751.39
P6xP7	31.18	35.96	14.06	9.94	19.46	23.13	12.79	18.96	14.85	327.66	676.92
P6xP8	30.77	35.68	13.86	9.74	19.14	22.74	12.62	18.65	14.77	322.50	660.63
P7xP8	24.84	19.03	12.45	8.40	16.58	17.01	7.10	13.46	5.78	55.76	163.52
P1	25.83	64.23	47.73	10.95	14.91	15.17	3.67	15.77	17.13	260.80	574.21
P2	24.80	59.17	45.93	9.51	14.49	15.27	7.47	17.13	17.73	259.79	444.63
P3	15.80	16.90	10.47	12.01	14.58	11.82	6.10	13.57	14.23	159.04	353.51
P4	17.83	11.70	11.50	11.40	11.38	11.25	6.77	14.07	13.90	166.90	254.33
P5	36.17	29.97	14.53	7.20	10.64	10.43	8.63	15.43	12.87	363.93	782.28
P6	30.30	37.73	13.37	6.92	15.09	17.81	10.07	13.53	14.50	354.77	695.39
P7	24.03	18.73	11.80	7.48	12.40	14.91	6.73	11.70	4.33	53.31	157.67
P8	24.57	18.27	12.73	6.16	14.81	12.73	5.73	12.33	6.23	36.70	106.14

Appendix XIX. Mean values of hybrids and parents for growth and disease index parameters under TyLCV trail

Hybrids/ Parents	Number of leaves			Leaf area (cm ²)			Plant Survival Percentage (%)			Disease Severity Index (V)		
	45 DAT	60 DAT	90 DAT	45 DAT	60 DAT	90 DAT	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT
P1xP2	52.69	58.79	49.65	172.41	232.96	150.04	99.52	93.16	88.76	0.05	0.06	0.14
P1xP3	50.02	48.86	37.61	147.98	179.89	117.83	97.80	91.88	88.60	0.25	0.42	0.90
P1xP4	49.58	50.10	37.14	151.66	182.21	88.05	98.31	90.71	86.01	0.36	0.59	0.75
P1xP5	53.61	50.22	47.61	183.36	193.90	104.59	99.16	93.33	88.03	0.05	0.20	0.32
P1xP6	59.88	59.37	55.01	201.66	231.71	123.14	98.76	93.10	88.90	0.09	0.32	0.58
P1xP7	46.14	54.34	39.30	151.57	160.66	122.98	99.61	96.21	89.92	0.03	0.36	0.39
P1xP8	52.93	60.35	37.69	157.53	175.56	90.11	94.86	86.51	71.05	0.10	0.60	0.91
P2xP3	51.73	55.76	41.74	149.87	197.09	125.63	93.99	79.44	72.97	0.37	0.62	1.39
P2xP4	52.81	58.96	43.08	152.01	200.72	105.64	95.99	79.95	71.33	0.42	0.69	0.93
P2xP5	53.09	56.02	49.89	201.45	231.73	125.51	99.36	94.60	91.17	0.07	0.24	0.42
P2xP6	50.67	54.62	48.97	163.50	197.68	100.76	99.09	93.79	90.61	0.07	0.24	0.46
P2xP7	44.43	57.39	40.08	148.89	169.92	125.61	98.51	90.25	71.85	0.08	1.29	1.45
P2xP8	53.44	65.98	40.59	162.74	195.53	99.65	94.74	86.19	71.21	0.10	0.58	0.92
P3xP4	43.89	42.81	26.72	107.39	119.11	50.53	80.78	29.33	4.73	1.44	2.44	4.15
P3xP5	47.58	42.55	36.97	130.53	123.31	60.27	89.55	64.55	51.60	0.55	1.08	2.23
P3xP6	47.56	45.30	38.42	127.35	131.08	59.34	88.49	62.91	51.14	0.63	1.26	2.64
P3xP7	40.42	45.55	27.67	108.30	101.30	80.53	86.61	56.15	32.31	0.72	2.37	3.82
P3xP8	49.21	55.23	27.88	111.83	111.48	50.45	83.38	52.90	27.97	0.70	1.74	3.33
P4xP5	47.40	44.17	35.64	135.19	129.84	37.74	92.09	61.88	45.06	0.84	1.53	2.02
P4xP6	49.14	48.26	38.97	127.07	130.97	34.02	91.86	61.59	45.16	0.84	1.51	2.05
P4xP7	40.67	49.00	28.36	108.72	98.58	52.90	91.72	59.39	28.15	0.84	2.56	3.04
P4xP8	47.63	54.95	26.80	113.42	112.09	24.42	85.81	49.93	16.10	0.89	2.09	2.87
P5xP6	42.81	39.13	39.23	158.04	144.11	48.08	98.90	94.20	90.56	0.11	0.45	0.78
P5xP7	43.68	47.31	36.96	142.87	113.23	68.11	98.34	89.98	70.82	0.10	1.47	1.70
P5xP8	49.46	52.13	35.44	147.23	126.50	39.34	93.38	83.00	64.00	0.14	0.91	1.40
P6xP7	45.21	50.22	40.54	148.21	130.79	65.84	98.04	89.29	68.76	0.12	1.74	2.02
P6xP8	46.23	53.24	40.79	139.24	121.33	64.52	98.46	91.73	76.80	0.09	1.18	1.42
P7xP8	38.96	51.77	25.20	116.97	91.88	57.12	90.41	70.97	24.76	0.22	2.74	3.38
P1	43.37	44.02	38.78	150.53	193.03	126.97	99.67	87.67	76.00	0.13	0.17	0.20
P2	39.07	47.07	38.47	140.60	199.57	126.08	98.67	85.00	77.33	0.17	0.20	0.57
P3	35.13	33.02	21.54	87.33	98.12	63.84	82.00	44.67	29.00	0.97	1.67	3.63
P4	33.34	33.55	20.17	92.16	101.02	21.93	88.67	46.33	23.67	1.20	2.00	2.57
P5	38.84	33.61	34.28	134.65	113.96	42.26	97.33	82.00	68.33	0.30	1.43	2.27
P6	36.46	35.07	34.62	122.05	118.24	36.11	96.33	83.67	75.33	0.33	1.33	2.43
P7	26.73	37.63	21.16	93.92	65.66	71.31	97.13	83.33	45.00	0.13	2.80	3.03
P8	37.54	47.50	19.90	108.56	95.51	20.91	85.00	64.67	23.33	0.23	1.63	2.50

Appendix XX. Mean values of hybrids and parents for disease index and yield parameters under TyLCV trail

Hybrids/ Parents	Disease Severity Index (F)			Vector Population			Number of fruits	Average fruit weight	Yield per plant
	30 DAT	45 DAT	60 DAT	30 DAT	45 DAT	60 DAT			
P1xP2	0.03	0.02	0.08	0.13	1.05	2.73	118.39	32.46	3.82
P1xP3	0.34	0.46	0.62	1.43	2.53	5.40	88.73	28.55	2.54
P1xP4	0.25	0.48	0.83	2.73	3.40	7.18	78.99	27.74	2.19
P1xP5	0.06	0.09	0.14	0.12	0.67	1.99	86.33	43.38	3.76
P1xP6	0.05	0.15	0.22	0.21	0.75	2.86	107.62	27.98	3.01
P1xP7	0.10	0.53	0.97	1.48	6.43	10.47	85.74	28.31	2.41
P1xP8	0.13	0.48	1.17	0.41	3.06	8.12	76.97	43.22	3.35
P2xP3	0.51	0.69	0.93	2.28	3.73	8.07	98.43	25.59	2.53
P2xP4	0.34	0.67	1.14	3.09	3.74	8.07	85.62	25.89	2.23
P2xP5	0.06	0.10	0.16	0.19	0.79	2.51	81.01	40.76	3.33
P2xP6	0.04	0.14	0.21	0.25	0.69	2.90	104.34	25.78	2.70
P2xP7	0.17	0.90	1.63	1.85	7.72	12.73	86.48	26.43	2.28
P2xP8	0.19	0.70	1.70	0.64	4.33	11.75	76.62	45.44	3.51
P3xP4	1.58	2.58	3.79	9.39	11.69	24.05	37.96	20.81	0.79
P3xP5	0.79	1.10	1.43	3.37	5.00	10.69	45.67	46.09	2.12
P3xP6	0.82	1.21	1.56	3.66	5.30	11.74	64.03	22.32	1.44
P3xP7	1.12	2.22	3.30	6.42	15.00	26.50	51.35	20.30	1.04
P3xP8	1.04	1.90	3.22	4.50	10.28	24.21	38.73	40.76	1.58
P4xP5	0.67	1.33	2.18	5.64	6.18	13.18	34.38	38.71	1.34
P4xP6	0.64	1.34	2.18	5.59	6.02	13.42	57.48	26.24	1.52
P4xP7	0.76	2.11	3.60	7.27	13.47	23.87	40.94	24.92	1.01
P4xP8	0.79	1.93	3.72	5.98	9.85	22.89	32.14	41.48	1.34
P5xP6	0.07	0.19	0.25	0.21	0.37	2.07	79.75	43.26	3.49
P5xP7	0.20	0.91	1.57	1.95	7.82	12.81	46.70	34.66	1.63
P5xP8	0.21	0.73	1.65	0.64	4.03	11.19	38.12	68.83	2.67
P6xP7	0.20	1.09	1.89	1.87	7.26	12.34	76.29	23.17	1.77
P6xP8	0.13	0.72	1.22	1.44	5.49	9.58	76.88	25.81	1.99
P7xP8	0.37	1.77	3.58	2.71	12.60	23.92	40.80	56.72	2.31
P1	0.10	0.07	0.30	0.33	4.30	10.37	71.26	27.69	1.95
P2	0.10	0.07	0.33	0.67	3.93	10.97	74.94	25.83	1.94
P3	1.40	1.93	2.50	6.20	9.03	18.60	43.48	17.26	0.75
P4	0.93	1.87	3.10	8.27	8.87	18.23	33.18	23.89	0.80
P5	0.40	0.70	0.93	0.70	1.83	7.33	29.55	56.40	1.70
P6	0.20	0.87	1.13	1.00	1.23	9.27	67.67	21.93	1.50
P7	0.28	1.63	2.90	3.33	13.63	21.23	39.29	24.09	0.94
P8	0.33	1.30	3.10	1.07	7.33	19.83	22.61	61.09	1.39

**GENETICS OF DROUGHT AND TOMATO YELLOW LEAF CURL VIRUS
TOLERANCE IN TOMATO (*Solanum lycopersicum* L.)**

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ABSTRACT

The present research work on Genetics of drought and Tomato Leaf Curl Virus tolerance in tomato (*Solanum lycopersicum* L.) was conducted using 100 tomato genotypes from different sources. These genotypes were evaluated for performance against TyLCV in *Rabi* of 2011. The evaluation for drought tolerance was carried out during *Summer* 2012. Observations on different morphological, growth, disease index, biochemical and yield parameters were recorded. Genotypes varied significantly for all the traits. The result of GCV and PCV indicated that the variation was mostly due to the genetic makeup of the genotypes and the effect of environment was found to be low. The genotypes were grouped in to eight, seven and ten cluster respectively for TyLCV, normal irrigation and restricted irrigation, using Mahalanobis's D^2 statistics.

Eight parents were selected from the above two evaluation trials based on their *per se* performances and crossed in diallel fashion (without reciprocals) to develop 28 hybrids. These hybrids were further evaluated along with their parents separately for TyLCV and drought resistance. For drought tolerance, evaluation was done during *Summer* 2013 and for TyLCV tolerance it was done during *Rabi* 2013.

It is evidenced from the study that both additive and non additive gene effects are involved in the genetic control of the traits. So, both gene effects must be considered while developing superior lines tolerant to drought and TyLCV. Estimates of heterosis justified the previous results indicating heterosis breeding to be good tool for crop improvement in tomato.

Four hybrids having combined resistance to drought and TyLCV were selected from hybrid evaluation trial. This study proved the possibility of introgression of multiple resistances in tomato. The present work is basic work to combine biotic and abiotic stress tolerance in tomato.

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