Genetics of bacterial wilt (*Ralstonia solanacearum*) resistance and some quantitative and qualitative traits in sweet pepper

THESIS

By

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CERTIFICATE – I

This is to certify that the thesis entitled, **"Genetics of bacterial wilt (*Ralstonia solanacearum*) resistance and some quantitative and qualitative traits in sweet pepper''** submitted in partial fulfillment of the requirements for the award of the degree of **Doctor of Philosophy (Agriculture)** in the subject of Vegetable Science of Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Mr. Susheel Sharma** son of **Sh. Saruti Sagar** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been fully acknowledged.

Place: Palampur
Dated: September , 2007

(Yudhvir Singh)
Chairman,
Advisory Committee

CERTIFICATE – II

This is to certify that the thesis entitled, **"Genetics of bacterial wilt (*Ralstonia solanacearum*) resistance and some quantitative and qualitative traits in sweet pepper"** submitted by **Mr. Susheel Sharma** son of **Sh. Saruti Sagar** to the Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfillment of the requirements for the degree of **Doctor of Philosophy (Agriculture)** in the subject of **Vegetable Science** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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Needless to say, errors and omissions are mine.

Place: **Palampur** **(Susheel Sharma)**

Dated: September, 2007.

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ABSTRACT

The present study was aimed to obtain information on the genetics of bacterial wilt resistance, morphological and biochemical traits. In addition, the information was gathered on the association of these traits with bacterial wilt resistance and on the extent of heterosis. Six generations (P_1, P_2, F_1, B_1, B_2 and F_2) of six crosses, evolved by utilizing two resistant (PBC-631 and IHR-546) and two susceptible parents (California Wonder and Yolo Wonder) were evaluated in a Randomized Block Design at the experimental farm of Department of Vegetable Science and Floriculture, CSK HPKV, Palampur and HAREC, Bajaura during summer, 2006. The genetics of bacterial wilt resistance was observed to be dominant in nature with the degree varying from incomplete to complete dominance. The crosses, PBC-631 x CW, PBC-631 x YW and IHR-546 x CW revealed the presence of monogenic dominance in the inheritance of bacterial wilt resistance, which was further confirmed from their test cross ratios (1R:1S). Sufficient genetic variability was generated through hybridization for all the morphological and biochemical traits. The presence of dominance components for yield per plant in all the crosses along-with complementary type of interaction in IHR-546 x YW suggested the exploitation of heterosis for yield per plant. Similarly, positive dominance genic effects recorded in most of the cross combinations for number of fruits per plant further indicated to exploit hybrid vigour. However, negative additive [d] component and positive additive x additive [i] component for average fruit weight in most of the crosses suggested to delay selection for improving this trait. In the present study, the nature and magnitude of gene effect varied with different crosses for most of the quantitative as well as biochemical traits. So, specific breeding strategy has to be adopted for a particular cross to get desired improvement. On the basis of correlation and path analysis studies ascorbic acid content, total sugars, reducing sugars, non-reducing sugars, ortho dihydroxy phenols and polyphenol oxidase activity played an important and crucial role in determining the resistance to bacterial wilt. YW x CW was found to be the most promising and consistent heterotic combination for yield per plant, number of fruits per plant, average fruit yield per plant, number of pickings and plant height, however, this cross was highly susceptible to bacterial wilt. Since, the fruits of most

of F_1s were not bell shaped or blocky as preferred by the consumers, therefore, back-cross breeding programme with commercial cultivars accompanied by selection for bacterial wilt resistance is suggested.

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Countersigned
Head of Department

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CHAPTER I

INTRODUCTION

Among fruit vegetables, sweet pepper is a versatile crop and has a specific identity. It is known by various names such as sweet pepper, capsicum, bell pepper, green pepper, *Shimla mirch*, vegetable paprika, etc. It is native to Mexico with secondary centre of origin in Guatemala (Bukasov, 1930). Sweet pepper fruits are generally blocky, square, thick fleshed, three to four lobed and non-pungent. It is used for salad, stuffing, cooked as a vegetable, pickled, or processed and is appreciated world wide for its flavour, aroma, colour and as an important source of vitamin C and provitamin A (at the red stage). Its fruits (actually inflated berries) are important constituents of many recipes and are available in the market year round with different shapes, sizes and colours. Its consumption has been increasing all over the world with the increase in the fast food industry and having many hidden uses.

In India, bell pepper was first introduced by the Britishers in the 19th century in Shimla hills. The crop is commercially grown in the states of Himachal Pradesh, Jammu and Kashmir, Arunachal Pradesh, Uttarakhand and Darjeeling district of West Bengal during summer months and as an autumn crop in Maharashtra, Karnataka, Tamil Nadu and Bihar with an area of more than 6,000 hectares and production of 50,000 metric tons (Anonymous, 2003).

In Himachal Pradesh, sweet pepper (along with chillies) is grown extensively as a cash crop in mid and low hills covering an area of 2,081 hectares with production of 30,876 metric tons (Anonymous, 2006). Sweet pepper has become money

spinner for the hill farmers of Himachal Pradesh wherein ideal climatic conditions enable its off-season production during the period (June-October), when the crop does not grow well in the adjoining plains on account of unfavourable temperature. Recently, sweet pepper growing is rapidly changing the economy of farmers of the state, who are growing it under polyhouses because of its great demand in fast food industry in metropolitan cities.

Production of capsicum in the state has suffered a great setback on account of a myriad of biotic and abiotic stresses. Among biotic stresses, bacterial wilt has assumed alarming proportions in some specific pockets of low and mid hills of the state. Bacterial wilt is a major disease which seriously affects sweet pepper crop especially during hot and humid weather conditions and has become a limiting factor in its commercial cultivation. The disease was first reported in Kangra valley in 1981 on solanaceous texas, remained sporadic in nature till 1985, and has now become endemic in the Kangra and Mandi districts (Sood and Singh, 1992). Yield losses up to 100 per cent have been reported in wilt prone areas of the world (Wang *et al.,* 1997).

Chemical control of bacterial wilt is not feasible at present and reliance has to be put on the use of resistant varieties. The available varieties of sweet pepper in Himachal are highly susceptible to bacterial wilt. Genotypes reported to be resistant at AVRDC, Taiwan and other states of India either lack in desirable horticultural attributes or succumb at other locations and cannot be recommended as such for commercial cultivation in the state. Thus, the incorporation of resistance into commercially important cultivars remains the best, most economical and enduring alternative.

In order to combine various desirable horticultural traits in capsicum along with resistance to diseases, the most appropriate approach is to adopt the recombinant

breeding. In such an approach, the efficiency of breeding programme will mainly depend upon the genetic architecture of the traits under improvement (Cockerham, 1961). So, it becomes imperative to carry out genetic studies to understand the genetic architecture involved in the manifestation of disease resistance, and yield and its component traits.

It has been known since long that certain biochemical constituents which are present in the host earlier to infection or induced after the invasion of the pathogens act either as toxicants or as inhibitors to multiplication, growth and development of pathogen. The biochemical reactions leading to susceptibility or resistance are mediated by enzymes, phenols, sugars, etc. Thus, it is also of considerable importance to study the role of biochemicals that may be associated with bacterial wilt resistance in capsicum. Further, certain structural features and other morphological characters may also be associated with bacterial wilt resistance.

In the light of the above stated facts, there is an urgent need to evolve stable bacterial wilt resistant varieties/hybrids possessing desirable horticultural traits. Therefore, the present investigation was carried out with the following objectives:

- To gather information on the genetics of bacterial wilt resistance and gene effects for some quantitative and qualitative traits,
- to find out the association of biochemical and morphological aspects with bacterial wilt resistance, and
- to study the extent of heterosis and to identify the heterotic combinations on mean performance basis.

CHAPTER-II

REVIEW OF LITERATURE

The reports available in literature pertaining to various aspects of the present studies have been reviewed under the following heads:

2.1 Genetics of resistance to bacterial wilt

2.2 Genetics of morphological and biochemical traits

2.3 Association of bacterial wilt resistance

2.4 Heterosis

2.1 GENETICS OF RESISTANCE TO BACTERIAL WILT

Bacterial wilt, a serious soil-borne disease, in capsicum caused by *Ralstonia solanacearum* E.F. Smith has become a serious problem in India (Gopalakrishnan and Peter, 1991). Yield losses up to 100 per cent have been reported in wilt prone areas of the world (Wang *et al.,* 1997). In India, the disease is prevalent in Karnataka, Kerala, Maharashtra, Orissa and West Bengal causing heavy losses in yield (Kishun, 1987). It was first observed in Kangra valley in 1981 and gradually spread to other districts like Kullu, Mandi (Sood and Singh, 1993), Solan (Gupta *et al.,* 1998), Bilaspur and Hamirpur (Sood *et al*., 2002). Now, it is an endemic disease in most of the districts and causes 80-100 per cent losses in heavily infested fields. Cultural practices and chemicals, if judiciously used, can reduce disease incidence and severity, but alone are expensive and ineffective. Thus, resistant varieties along with use of chemicals and cultural practices appear to be the most practical and durable solution. Wang *et al.* (1996) suggested that growing of disease resistant varieties is the most effective control of

bacterial wilt. In India, the breeding lines PBC-631 (from AVRDC, Taiwan) and IHR-546 (from IIHR, Bangalore) of *Capsicum annuum* L., were found to be highly resistant to bacterial wilt and have been recommended for inclusion in breeding programmes (Singh and Sood, 2003).

Thakur (1990), while studying the inheritance of disease resistance in *Capsicum annuum* L., used PI 257069 and PI 201234 as the resistant parents and California Wonder and Yolo Wonder as the susceptible parents. He found resistance to be digenic recessive in nature in all the four susceptible x resistant cross-combinations.

Genetic analysis of resistance of sweet pepper to bacterial wilt has recently been performed by Lafortune *et al.* (2005) in the doubled haploid (DH) progeny from a cross between a resistant parental line PM 687 and a susceptible cultivar Yolo Wonder for two consecutive years. Two to five genes with additive effects were estimated to control the resistance, indicating an oligogenic control as observed in tomato sources of resistance. They further stated that the similarity of the genetics of resistance to bacterial wilt in pepper and tomato and linkage with TMV resistance locus warrant the comparative mapping of the resistance quantitative trait loci in the genomes of the two species.

Nelson (1974) while working on tomato concluded that the level of bacterial wilt resistance varied from season to season and was associated with polygenes. Tikoo *et al.* (1974) reported genotype dependent gene action for resistance to bacterial wilt in tomato. IHR 663-12-3 proved to have a single dominant gene for resistance, but a few other genotypes were observed to have recessive genes.

Graham and Yap (1976) in an analysis of the P_1, P_2, F_1, F_2, BC_1 and BC_2 generations (six-generation model) of a cross between resistant (V_4) and a susceptible genotype (Walter) of tomato observed dominance for resistance. Further, in a diallel

study, they reported that resistance was mainly due to additive gene action. Gopinath and Madalageri (1986) in an analysis of bacterial wilt infection data from F_2 and BC_1 involving resistant and susceptible variety of brinjal revealed that resistance was controlled by single resistant gene for which the designation *Rps* was given. Tikoo *et al*. (1986) again reported that resistance to bacterial wilt in tomato was governed by recessive genes in CRA 66 Sel-A and a dominant gene in IHR 663-12-3.

Mahir *et al.* (1992) crossed local varieties of tomato having higher level of resistance with imported susceptible varieties and observed that the resistance was controlled by single dominant gene. Monma and Sakata (1992) in a six-generation study involving two bacterial wilt resistant (D-9 and Hawaii 7998) and a susceptible (TPD-5) line of tomato reported resistance to be partially recessive as there was incomplete dominance towards susceptibility. Peter *et al.* (1992) studied six generations of the cross CL-32-d-01-19GS' (resistant) x Pusa Ruby (susceptible) and reported that the resistance was monogenic and incompletely dominant.

Grimault *et al.* (1995) used Hawaii 7998 (resistant) and Floradel (susceptible) genotypes of tomato for bacterial wilt resistance studies and observed it to be monogenic dominant in nature. Mohamed *et al*. (1997) reported bacterial wilt resistance as partially recessive since they could record incomplete dominance towards susceptibility. Monma *et al.* (1997) observed that the genetic mechanism of bacterial wilt resistance in tomato was complex with a duplicate form of epistasis.

Vidyasagar (1998) in a six-generation study involving two bacterial wilt resistant *viz.,* BWR-5 and BT-18 and a susceptible genotype Solan Gola of tomato observed resistance to be dominant in nature as the plant survival in resistant (R) x susceptible (S) F_1s were above 97 per cent, 103 days after transplanting. The F_2, BCP_1 and BCP_2 data

of the cross BWR-5 x Solan Gola suggested the involvement of two interacting genes possibly dominant and recessive epistasis. However, the same was not true with the F_2 and BCP_2 data of the cross BT-18 x Solan Gola.

Chaudhary and Sharma (1999) crossed bacterial wilt resistant varieties of brinjal (Arka Keshav and Arka Neelkanth) with susceptible variety (Pusa Purple Long) to study the inheritance of disease resistance. Segregation studies of F_2 progenies of both the crosses indicated the presence of single dominant gene controlling resistance to bacterial wilt and they further advocated to incorporate resistance into susceptible varieties through back cross pedigree method.

Oliveira *et al.* (1999) studied the genetic nature of bacterial wilt (*Ralstonia solanacearum*) resistance of tomato in crosses using resistant (Hawaii 7998, Rotam 4 and Yoshimatsu 4-11) and susceptible (L390 and TSW 10) parents in the presence of bacterial isolates of biovars I and III. The resistance was found to be oligogenic or polygenic, depending on the genotype-isolate combination. The resistance index of the F_1 in most crosses was higher than the midparent value suggesting that resistance in tomato is partially dominant, as there was incomplete dominance towards resistance.

Chaudhary (2000) carried out an investigation to determine the mode of inheritance of bacterial wilt (*R. solanacearum*) resistance in brinjal. The variable segregation patterns ranging from monogenic dominant and recessive to inhibitory type in different cross-combinations indicated that resistance to bacterial wilt is conditioned by polygenes. Gopalakrishnan *et al.* (2002) in their inheritance studies involving the F_1, F_2, BC_1, and BC_2 generations of a cross between the resistant variety Soorya and the susceptible variety Pusa Kranti of brinjal revealed monogenic and incompletely dominant inheritance of susceptibility over resistance.

The mode of inheritance of bacterial wilt (*Ralstonia solanacearum*) resistance in four tomato crosses (Hawaii-7998 x Solan Gola, Hawaii-7998 x Roma, BT-18 x Solan Gola and TBL-4 x Solan Gola) was studied by Sharma and Verma (2004). The results of their study clearly indicated the involvement of more than one interacting gene, and the role of additive and dominance components and their interactions in the expression of bacterial wilt resistance in tomato. Whereas, Thakur *et al.* (2004) reported dominance of bacterial wilt susceptibility over resistance in tomato. The F_2 segregation into 3 (S) : 1 (R) ratio indicated the monogenic recessive nature of resistance.

2.2 GENETICS OF MORPHOLOGICAL AND BIOCHEMICAL TRAITS

The information on the genetics of quantitative and qualitative traits is of immense importance to the plant breeder for deciding the breeding strategy to be followed. To understand the type of gene action, various mating designs have been developed by various workers. Commonly used approaches of diallel and line x tester provide information about the population as a whole and do not provide any information about the individual parent/cross. Generation mean study enables the gene action to be analysed cross-wise and provide precise information on additive x additive [i] (fixable), additive x dominance [j] and dominance x dominance [l] (non-fixable) interactions, the relative magnitude of which indicates the future breeding strategy. Studies with regard to estimation of different components of genetic variance through generation means have been carried out by various workers in a variety of crops, but such information is too limited in sweet pepper. Nevertheless, literature on various morphological and biochemical traits based on the studies being carried out through other techniques *viz.,*

diallel, line x tester, triple test cross, etc. in addition to generation means technique in *Capsicum* have been reviewed as under:

Popova *et al.* (1970), while studying the inheritance of several biochemical characteristics in F_1 peppers, observed no heterotic effects for dry matter, sugars, vitamin C (ascorbic acid) and carotene, and reported the inheritance of these characteristics to be intermediate in nature.

Chung *et al*. (1979) in crosses of Yolo Wonder with Tatong and Funong's Tender Twig of capsicum reported over dominance for fruit width, flesh weight and days to first flower in the cross with Tatong and number of branches, stalk length, plant height and days to first flower showed overdominance in the cross with Funong's Tender Twig. Epistasis was significant for all the characters except fruit width in the first cross and total number of flowers in the second cross.

Subramanya and Ozaki (1980) reported that long pedicel was partially dominant over short and polygenic in inheritance. F_2 populations exhibited a continuous range of phenotypes. At least 3 loci determined this trait. Thakur *et al.* (1980) reported that fruit size was influenced by additive gene action, number of days to flowering by dominance, and height, fruit number per plant and total yield by over-dominance in a diallel cross involving six varieties of capsicum. Both additive and non-additive effects influenced early yield.

Milkova (1981) in an analysis of data on plant height, fruit (shape) index, pericarp thickness and pedicel length including yield concluded that these characters were controlled by small number of genes.

Prudek (1981) on the basis of data recorded in the parents, F_1s and F_2s of a five-variety diallel, made recommendations for the production of heterotic hybrid sweet

peppers. He reported that systems of genetic control were not always the same in the F_2 as in the F_1. In the F_1, fruit yield was controlled mainly by overdominance effects in an additive genetic system, though incomplete dominance made a contribution in the F_2. In both generations, incomplete dominance contributed to the control of mean fruit weight and pericarp vigour.

Ahmed *et al.* (1982) studied six generations of two crosses (Elephant Trunk x Perennial and Kalocsai E15 x Perennial). They reported both additive and dominance genetic effects to be important for number of days to fruiting and height, whereas only additive gene effects were important for seed number and fruit weight.

Thakur *et al.* (1987), while studying the genetics of fruit characters (average fruit weight, fruit index and flesh thickness) of sweet pepper through generation mean analysis, reported the governance of both additive and non-additive gene action and received similar indication from epistatic effects. They suggested the utilization of heterosis breeding to be more feasible option for all the traits; however, they also suggested recurrent selection to be equally suitable for improvement of average fruit weight.

Kaul and Sharma (1988) observed predominance of additive genetic variance for the characters *viz.,* fruit length, fruit diameter, number of fruits per plant and fruit yield per plant of bell pepper. Whereas, Miranda *et al*. (1988) reported non-additive gene action to be more important than additive gene action for total yield per plant, early yield and plant height in capsicum. There was a predominance of additive variance for total number of fruits per plant. Overdominance was observed for total yield per plant, early yield and plant height, whereas incomplete dominance was noticed for total number of fruits per plant.

Joshi (1989) studied genetics of yield per plant and five yield-related traits *viz.,* plant height, number of branches per plant, fruit length, fruit circumference and number of fruits per plant in three crosses of HC-210, Ruby King and California Wonder with Elephant Trunk of capsicum. He reported epistasis to be important in all the traits studied, and assumed that breeding methods that exploit non-additive gene action, such as reciprocal recurrent selection, would be rewarding for the improvement of these traits.

Blank and Maluf (1997) evaluated two F_1s of sweet pepper in green house and reported that early flowering, increased plant height, and high yield were controlled by dominant alleles and high fruit weight by recessive alleles.

Murthy and Deshpande (1997), while studying the six generations of four crosses of chilli, observed all the three types of gene action i.e. interaction components to be involved in the inheritance of yield attributes. They reported that this could be due to differences in magnitude of the gene effects and genetic background of the crosses and further suggested the exploitation of heterosis breeding, pedigree breeding and selection of desirable transgressive segregants for varietal improvement.

Bal and Singh (1999) reported preponderance of additive gene effects for fruit length and breadth in chilli. They also reported the duplicate type of gene action in majority of the crosses, which will reduce the net gain occurring from heterozygosity due to cancellation of the dominance and epistatic effects and further suggested to adopt recurrent selection for the improvement of fruit length and breadth.

Echeverri *et al.* (1999) carried out genetic analysis of yield, number of fruits per plant, fruit size (fruit weight, locule weight, and fruit length and width) and days to flowering using hybrids between ten sweet pepper cultivars (LPUNAL, Yolo Wonder, Keystone Resistant Giant, Pimentao Amarelo, Morviones, Avelar, California Wonder,

Roque 8-B, Red Pepper, and L-363-46-672) crossed in a diallel fashion. Dominance gene effects were very important for expression of yield per plant and days to flowering, and less important for fruits per plant, mean fruit weight, and fruit width. Overdominance was observed for days to flowering.

Chaim and Paran (2000) studied the inheritance of ten quantitative traits related to plant and fruit development in an intraspecific cross between a bell-type (*Capsicum annuum* var. *annuum* (Grossum group) cv. Maor) and a small-fruited pungent chilli line (*C. annuum* var. *annuum* (Longum group) cv. Perennial). Most of the genetic variation associated with traits that affect the size of the fruit and its shape was found to be additive in nature.

Patel *et al*. (2006) advocated that green fruit yield of chilli is the outcome of the interplay of various yield contributing components and in general pre-ponderance of inter and intra allelic interaction with marginal influence of additive gene effect was evidenced for green fruit yield and most of the component traits *viz.,* number of fruits per plant, average fruit length, average fruit girth and average fruit weight.

Sood and Kaul (2006a) reported both additive and non-additive genetic systems in 15 F_1s (developed through diallel mating design) of bell pepper and suggested to practice selection in later generations, when the non-additive effects have diminished.

3.3 ASSOCIATION OF BACTERIAL WILT RESISTANCE

The importance of biochemical study of defense reaction in the physiology of disease resistance is widely accepted. On infection many physiological changes take place in the host leading to the resistant or susceptible reaction. It is a well established fact that certain biochemical constituents which are present in the resistant host earlier to

infection or induced after the invasion of the pathogen act either as toxicants or inhibit growth, development and multiplication of pathogen. Changes in amino acids, sugars and phenols due to bacterial infections have been reported by many workers (Chand, 1968; Chand and Walker, 1968)

Bhullar *et al.* (1972) studied the role of phenols in resistance to anthracnose (*Capsicum capsici*) and reported that resistant varieties had a higher amount of phenols than susceptible varieties. Narain and Mohapatra (1973) reported that the degree of resistance to *Colletotrichum capsici* on leaves were positively associated with phenol content of leaves.

Thind *et al.* (1981) observed increased total phenols in resistant chilli genotypes and decreased in susceptible genotypes on infection with *Xanthomonas vesicatoria*. Tyagi and Chauhan (1982) found higher sugar content in the leaves of susceptible varieties than the resistant ones and the increased sugar content in susceptible varieties stimulated the spore germination of *Alternaria solani.* The involvement of phenolic compounds and related enzymes in disease resistance mechanisms have been reported to occur in many other field crops also (Manibhushanrao *et al*., 1988). Singh and Singh (1989) opined that increase in phenol content in resistant varieties was associated with increased activity of enzymes leading to the formation of quinones and other oxidation products and resulted in the reduction of multiplication of pathogens.

Azad (1991) reported maximum percentage of reducing (1.3 %), non-reducing (0.8 %) and total (2.1 %) sugars in susceptible varieties, while minimum percentage of reducing (0.95 %), non-reducing (0.64 %) and total (1.6 %) sugars in resistant varieties of chilli fruits during infection with *Colletotrichum capsici*. Saraswathi and Shivashankar

(1998) reported positive, but non-significant correlation between phenol content and bacterial wilt resistance.

Nawalagatti *et al.* (1999) also observed higher total chlorophyll, phenols and lower sugars in resistant over the susceptible genotypes of chilli studied for their reaction to murda complex. Hegde and Anahosur (2001), while screening chilli genotypes against fruit rot under natural conditions, observed that resistant genotypes exhibited higher capsaicin, ascorbic acid and lower total sugars than susceptible ones.

Gopalakrishnan *et al.* (2002) in inheritance studies involving the F_1, F_2, BC_1, and BC_2 generations of a cross between the resistant variety Soorya and the susceptible variety Pusa Kranti of brinjal revealed that roots of resistant variety Soorya had high contents of total phenol (0.36%) and ortho dihydroxy phenol (0.02%), which could prevent the entry and further multiplication of bacteria in the resistant variety. In contrast, the content of total phenol and ortho dihydroxy phenol in the roots of susceptible variety, Pusa Kranti was 0.22 % and 0.001%, respectively.

Kumar *et al*. (2002) studied biochemical assay of resistance to bacterial wilt in tomato involving total phenols, ortho dihydroxy phenols and ascorbic acid using six bacterial wilt resistant genotypes (*viz*., Sakthi, Mukthi, LE 382-1, LE 214, LE 415 and LE 421) and one susceptible genotype, Pusa Ruby. The total phenol, ortho dihydroxy phenol and ascorbic acid in the bacterial wilt-resistant genotypes were higher than susceptible cultivar Pusa Ruby in roots, shoots and whole plant at various growth stages. The presence of phenols and ascorbic acid at higher concentration in roots and stem at early stages in the field establishment was significant in checking the multiplication of *Ralstonia solanacearum* thereby imparting host resistance.

Sheela and Mathew (2002) reported changes in activities of the enzymes polyphenol oxidase (PPO) and peroxidase in resistant (LE 79-5) and susceptible (Pusa Ruby) genotypes of tomato after infection by *R. solanacearum*. The PPO activity was initially higher in the roots of resistant cultivar LE 79-5, but after infection more activity was noticed in Pusa Ruby. A decrease in PPO activity was noticed in LE 79-5 and an increase in Pusa Ruby after infection by *R. solanacearum*. In stems, the PPO activity increased in both genotypes after infection. Peroxidase activity also increased following infection in both root and stem of LE 79-5 and Pusa Ruby.

2.4 HETEROSIS

> The discovery of heterosis has been recognized as one of the major landmarks in the annals of plant breeding and its utilization in breeding hybrid varieties of both cross-pollinated and self-pollinated crops has amply demonstrated its usefulness. The term heterosis signifies the increased or decreased vigour of the hybrids (obtained by crossing two genetically dissimilar individuals) over the better parent (heterobeltiosis) or over the standard check (standard, economic heterosis) or over average performance of parents (relative/ average heterosis).
>
> In *Capsicum annuum* L., the early findings on heterosis as measured by F_1 values exceeding the mean of parents for characters, such as early maturity, plant height, fruit size and productivity both in terms of fruit and total weight have been reported by many workers (Deshpande, 1933; Pal, 1945; Martin, 1949; Angeli, 1957; Marinkov, 1960; Carlson, 1962 and Popova, 1962).

Betlach (1967) reported heterosis for increased number of fruits per plant and yield per plant, but he couldn't find heterosis for average fruit weight. He also reported no marked differences between parents and F_1 progeny for ascorbic acid, dry matter and total sugar content. Marfutina (1970) observed 8.30-8.95 per cent higher dry matter and 33-48 per cent higher total sugars in F_1s than the standard check. Joshi (1986) reported superiority of Bullnose x HC20 (146.79%), HC209 x Ruby King (22.90%) and Yolo Wonder x Bullnose (23.20%) in total yield over the best variety, HC201. He further stated that heterosis for yield resulted from combined heterosis for plant height, number of

primary branches, fruit size, average fruit weight, early yield and number of fruits per plant.

Thakur (1987), while studying eight parent diallel cross in capsicum, suggested utilization of heterosis to improve yield. Eleven crosses out of 28 exceeded the mid parental value and also the better parent in yield, but only six out yielded the best parent, Russian Yellow.

Kaul and Sharma (1988) in a line (12) x tester (2) analysis recorded 34.0, 33.1 and 25.0 per cent heterosis in Sweet Banana x California Wonder, Osh Region x California Wonder and HC201 x California Wonder, respectively, over the better parent for fruit yield per plant.

Echeverri *et al.* (1998) evaluated hybrids between ten sweet pepper cultivars and reported the highest relative heterosis and heterobeltiosis (155.87 and 138.69%) for fruit yield per plant where parent LPUNAL was involved.

Ahmed and Hurra (2000) derived information on heterosis from data on ten quantitative traits recorded in 11 parents (8 lines and 3 testers) and their 24 F_1 hybrids grown at Srinagar during 1997. They suggested that the hybrids KSPS-461 x Oskash, KSPS-461 x KSPS-2, KSPS-461 x California Wonder, KSPS-13 x California Wonder and HC-201 x KSPS-2 revealing the most significant desirable heterosis for yield and yield-contributing characters can be successfully exploited under temperate growing conditions in India.

Chaim and Paran (2000) reported heterosis and transgressive segregation for days to first ripened fruit, plant height and pedicel length in an intraspecific cross between a bell-type and a small-fruited pungent chilli line.

Mamedov and Pyshnaja (2001) studied heterosis in 15 F_1 hybrids (derived from six parental) of sweet pepper for yield and yield components. The number of crosses that exhibited significant desirable heterosis over better parent were 15 for early yield, 15

for total yield, 7 for fruit weight, 12 for fruit number per plant, 9 for fruit length, 4 for fruit girth and 8 for pericarp thickness.

> Pandey *et al*. (2002) evaluated heterosis for fruit yield per plant, fruit number per plant, and ascorbic acid content in sweet pepper. The highest average heterosis was recorded for fruit yield. Yolo Wonder x CW-51 exhibited the highest heterosis over the best parent (51.78%), significant positive heterosis for fruit number (98.45%) and ascorbic acid content (14.21%).

Gomide *et al.* (2003) also observed heterosis among experimental hybrids for total yield and mean fruit weight. Heterosis values relative to the standard cultivar Magali-R-F1 ranged from 7.50 to 49.89 per cent for early yield; 0.45 to 28.55 per cent for total yield; and 3.07 to 47.37 per cent for mean fruit weight.

Sood and Kaul (2006b) also reported heterosis for earliness, average fruit weight, number of fruits per plant and yield in intraspecific crosses of bell pepper and attributed the appearance of heterosis for fruit yield to increased number of fruits, fruit weight, harvest duration and the combined heterosis of other contributing traits.

CHAPTER III

MATERIALS AND METHODS

The present investigations were carried out at the Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during Feb-August 2004 - 2006 and at the Experimental Farm of Hill Agricultural Research and Extension Centre (HAREC), Bajaura during February-August, 2006. The details of material used and methods employed for the present investigations are discussed in detail below:

3.1 EXPERIMENTAL SITE

3.1.1 Palampur

The Experimental Vegetable Farm of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur is located at an elevation of about 1290.8m above mean sea level with $32^0$06′ North latitude and $76^0$32′ East longitude, representing mid hill zone (Zone 2.2) of Himachal Pradesh and has a sub-temperate climate with high rainfall (2500mm). The soil of this zone is silty clay loam with acidic reaction.

3.1.2 Bajaura

The Experimental Farm of HAREC, Bajaura is situated at an elevation of about 1090 m above mean sea level with $31^0$08′ North latitude and 77^0 East longitude. Bajaura falls under mid-hills, sub-humid zone (Zone 2.1) of the state and is endowed with mild summers and cool winters with low monsoon rains (975mm). The soil of the location is sandy loam with acidic to neutral in reaction along with high water table.

The weather data (February-August, 2007) of Palampur and Bajaura collected from the Meteorological Observatory, Department of Agronomy, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur are presented in Appendix-I and II, respectively.

3.2 EXPERIMENTAL MATERIAL

Four parents, including two resistant (PBC-631 and IHR-546) and two susceptible (California Wonder and Yolo Wonder) to bacterial wilt disease, were involved in a crossing programme to generate the experimental material. The important characteristics of the parents involved in crossing plan along with their sources of procurement are given below:

Table 3.1: Characteristics of the parents involved

S. No.	Parents	Fruit shape, size and colour	Source
1.	PBC-631	Paprika type, long and light green	AVRDC, Taiwan
2.	IHR-546	Triangular, medium and dark green	IIHR, Bangalore
3.	California Wonder (CW)	Blocky, large and green	IARI, Katrain
4.	Yolo Wonder (YW)	Blocky, large and green	IARI, Katrain

3.2.1 Crossing programme

To ascertain the genetics of bacterial wilt resistance and various morphological and biochemical traits, six generations *viz.,* P_1, P_2, F_1, F_2, B_1 and B_2 of six crosses were developed by utilizing the four diverse parents. Details of F_1 hybrid combinations are given below:

S. No.	Hybrid combination (Cross)
1.	PBC-631 x California Wonder

2. PBC-631 x Yolo Wonder

3. IHR-546 x California Wonder

4. IHR-546 x Yolo Wonder

5. Yolo Wonder x California Wonder

6. IHR-546 x PBC-631

The F_1 seed of the above crosses was produced at Palampur in the polyhouse during summer-rainy season, 2004. F_1s were then selfed and backcrossed with both the parents (P_1 and P_2) to get F_2, B_1 and B_2 seeds, respectively at Palampur in the polyhouse during summer-rainy season in 2005. Simultaneously, crosses were also attempted in the second year to generate F_1s to have sufficient seed for final evaluation.

3.4 RECORDING OF DATA

3.4.1 Genetics of bacterial wilt resistance

The observations were recorded on bacterial wilt incidence at weekly intervals. Ooze test was carried to ensure the death of plants due to bacterial wilt. All the plants showing wilting symptoms were subjected to ooze test up to final count {90 days after transplanting (DAT)}. The plant survival data as on 90 DAT were utilized to ascertain the genetics of bacterial wilt disease. Plant survival (%) was calculated as:

$$\text{Plant survival (\%)} = \frac{\text{Number of healthy plants in the last recording}}{\text{Number of plants established}} \times 100$$

3.4.2 Genetics of morphological traits

The data were recorded on randomly tagged 5 plants per replication in the non-segregating generations (P_1, P_2 and F_1), 20 plants per replication in the back cross

generations (B_1 and B_2) and 40 plants per replication in the segregating generation (F_2) on the following traits:

1) Days to 50 per cent flowering

Days to 50 per cent flowering were recorded from the date of transplanting to the date when fifty per cent plants in each entry had flowered.

2) Days to first picking

Days to first picking were recorded from the date of transplanting to the date when at least one fruit was harvested.

3) Fruit length (cm)

Fruit length (polar distance) was measured from the stem end to the blossom end.

4) Fruit diameter (cm)

After recording the fruit length, the same fruits were also used for measuring the fruit width at pedicel end, middle of the fruit and near apex. These three observations were then averaged to calculate fruit diameter.

5) Fruit pedicel length (cm)

The same fruits were then used to measure the pedicel length with the help of scale from free end to the other where it was attached with the fruit.

6) Pericarp thickness (cm)

The same fruits were then again used to measure the pericarp thickness with the help of vernier caliper.

7) Number of fruits per plant

Number of fruits picked in all the harvests were counted and finally added to work out the total number of fruits per plant.

8) Fruit yield per plant (kg)

The weight of fruits harvested in each picking was added to calculate the fruit yield per plant.

9) Average fruit weight (g)

Average fruit weight was worked out by dividing the total yield with total number of fruits.

10) Number of pickings

Number of pickings were counted and finally added to calculate the number of pickings per plant.

11) Number of branches per plant

Number of branches arising from the main stem were calculated at the end of final picking.

12) Plant height (cm)

It was also taken at the end of final picking and measured from soil level to the top of the central apical shoot.

3.4.3 Genetics of biochemical traits:

For total soluble solids, ascorbic acid content, peroxidase activity and polyphenol oxidase activity, fresh fruits were used and these characters were expressed on fresh weight basis, whereas total sugars, reducing sugars, non-reducing sugars, total phenols and ortho dihydroxy phenols were expressed on dry weight basis of fruits.

1) Total soluble solids (%)

Total soluble solids (TSS) of the fruits were observed under room temperature with the help of 'ERMA Hand Refractometer' by putting 2-3 drops of juice on prism and the values expressed as per cent of juice (A.O.A.C., 1970).

2) Ascorbic acid content (mg/100g)

The ascorbic acid contents were estimated by 2,6-dichlorophenol Indophenol Visual Titration Method' as described by Ranganna (1979). The standard ascorbic acid solution was prepared by dissolving 100 mg of L-ascorbic acid in 100 ml of metaphosphoric acid (3%). 10 ml of this solution was diluted to 100 ml (100 ppm) with 3 per cent metaphosphoric acid.

The metaphosphoric acid (3%) solution was prepared by dissolving 15g of metaphosphoric acid in 500 ml glass distilled water. The dye was prepared by dissolving 50 mg of sodium salt of 2,6-dichlorophenol indophenol in about 150 ml of hot glass distilled water containing 42 mg of sodium bicarbonate. This was cooled and volume made upto 200 ml. To determine the dye factor, 5 ml each of standard ascorbic acid and metaphosphoric acid (3%) solution were taken in a flask and titrated against the dye to a pink colour which persisted for atleast 15 seconds. Dye factor (mg of ascorbic acid neutralized by one ml of dye) was calculated by using the following formula:

$$\text{Dye factor} = \frac{0.5}{\text{titre}}$$

Here,

0.5 means, 0.5 mg of ascorbic acid in 5 ml of 100 ppm standard ascorbic acid solution.

titre = volume of dye used to neutralize 5 ml of 100 ppm standard ascorbic acid solution along with 5 ml of metaphosphoric acid.

10 g of macerated sample was blended with 3 per cent metaphosphoric acid to make up the volume to 100 ml. Out of this 100 ml solution, 10 ml solution was taken and titrated against 2,6-dichlorophenol indophenol dye. The end point was determined by the appearance of rose pink colour which persisted for at least 15 seconds. The results thus obtained were expressed in terms of mg of ascorbic acid per 100 g of pulp. The ascorbic acid contents were calculated by using the following formula:

$$\text{Ascorbic acid (mg/100g)} = \frac{\text{Titre} \times \text{Dye factor} \times \text{Volume made up}}{\text{Aliquot of extract taken for titration} \times \text{weight of sample taken for estimation}} \times 100$$

Here,

Titre = Volume of dye used to titrate the aliquot of extract of a given sample

3) Total phenols (mg/100g)

Total phenols were determined by Folin-Ciocalteau method by Sadasivam and Manickam (1992).

Materials: 80 per cent ethanol, Folin-Ciocalteau Reagent (FCR), Na_2CO_3 20 per cent, standard (100 mg catechol in 100 ml water)- diluted 10 times for a working standard.

Extraction: Weighed 0.5 g of the sample and ground it with a pestle and mortar in 10 time volume of 80 per cent ethanol. Centrifuged the extract for 20 minutes. Collected the supernatant and re-extracted the residue with five times the volume of 80 per cent ethanol, centrifuged and pooled the supernatants. Evaporated the supernatant to dryness. Dissolved the residue in 5 ml of distilled water.

Procedure: Pipetted out 0.1 ml aliquots of different samples into test tubes and made the volume in each tube to 3 ml with distilled water. Added 0.5 ml of FCR and after three minutes, added 2 ml of 20 per cent Na_2CO_3 solution to each tube. Mixed thoroughly and

placed the tubes in a boiling water bath for exactly one minute, cooled and measured the absorbance at 650 nm against the reagent blank. Prepared a standard curve using different concentrations of catechol. From the standard curve found out the concentrations of total phenols and expressed as mg total phenols per 100 g of sample.

4) Ortho dihydroxy phenols (mg/100g)

Ortho dihydroxy phenols were determined by Arnow's method (Mahadevan and Sridhar, 1986).

Reagents: 80 per cent ethanol, 0.5 N HCl, 1 N NaOH, Arnow's reagent (Dissolved 10 g of sodium nitrite ($NaNO_2$) and 10 g of sodium molybdate ($NaMoO_2$) in 100 ml of water and stored in a brown bottle) and standard (100 mg catechol in 100 ml water)-diluted 10 times for a working standard.

Procedure: Extraction was carried out as in total phenols. Pipetted out 0.1 ml aliquots of different samples into test tubes and made the volume in each tube to 1 ml with water. Added 0.5 N HCl, 1ml of Arnow's reagent, 10 ml of distilled water and 2 ml of 1 N NaOH and mixed thoroughly (pink colour appeared). Maintained the reagent blank without extract and measured the absorbance at 515 nm. Calculated the amount of ortho-dihydric phenols present in the sample using the standard curve prepared from working standard catechol solution at different concentrations and expressed as mg/100 g.

5) Total free amino acids (mg/100g)

Estimation of amino acids was done by ninhydrin method suggested by Jayaraman (1981).

Reagents: Ninhydrin solution (Prepared by dissolving 2 g of ninhydrin in 25 ml of methyl cellusolve, to this solution 25 ml of 0.2M acetate buffer (pH 5.5) was added), 80 per cent ethanol in distilled water and glycine as standard.

Extraction: 0.2 g of powdered sample was extracted with 80 per cent (ethanol in water) solvent. Heated the mixture to 70-80^{0}C during extraction. The cooled extracts were centrifuged and clear extract was concentrated.

Procedure: 0.1 ml of aliquot was taken and the final volume of 4.0 ml was made with distilled water. 1 ml of ninhydrin reagent was added and mixed well. The tubes were kept in boiling water bath for 15 minutes. The tubes were cooled and 1ml of 50 per cent ethanol was added to the tubes. The pink colour developed was measured at 550nm in spectrophotometer. The concentration of total free amino acids was then calculated from the standard curve prepared from glycine (0.9 mg/ml).

6) Total sugars (mg/g)

Total sugars were estimated by the method given by Dubois *et al.* (1956).

Reagents: 80 per cent ethanol, lead acetate, sodium acetate, 5 per cent phenol and 95.5 per cent sulphuric acid.

Extraction: 0.5 g of sample (dried fruit) was macerated in 50 ml of ethanol (80%) and transferred to a conical flask. The contents of the flask were then boiled on boiling water bath up to half of the volume (25 ml). The contents were filtered and filtrate was made to 98 ml with distilled water. 1 ml of saturated lead acetate solution was added to it. To remove the lead ions a pinch of sodium oxalate crystals was added and the volume was made to 100 ml with distilled water.

Procedure: 0.2 ml aliquot was taken in the test tube and 1 ml of 5 per cent phenol (freshly prepared) and 5 ml of 95.5 per cent of concentrated sulphuric acid was added from the top, not from the side of test tube in ice cold solution. The intensity of pink colour was read at 490 nm. The amount of sugars present in the extract was then

calculated using a standard curve from glucose (0.1 mg ml^{-1}).

7) Reducing sugars (mg/g)

Reducing sugars were estimated by the method given by Miller (1972).

Reagents: Dinitrosalicylic acid reagent (DNS reagent) (Prepared by dissolving 1 g dinitrosalicylic acid, 200 mg crystalline phenol and 50 mg sodium sulphite in 100 ml 1 per cent NaOH and stored in 4^0C) and 40 per cent Rochelle salt solution (Potassium sodium tartarate).

Procedure: Extraction was carried out as in total sugars. Pipetted out 0.5 ml of the extract in test tubes and equalized the volume to 3 ml with distilled water in all the tubes. Added 3 ml of DNS reagent. Heated the contents in boiling water bath for 5 minutes. When the contents of the tubes were still warm, added 1ml of 40 per cent Rochelle salt solution. Cooled and read the intensity of dark red colour at 510 nm. Ran a series of standards using glucose (0.1 mg ml^{-1}) and calculated the amount of reducing sugars present in the sample using the standard graph.

8) Non-reducing sugars (mg/g)

Calculated by subtracting reducing sugars from total sugars.

9) Peroxidase activity (change in OD/min/g)

Peroxidase activity was calculated by the method given by Mahadevan and Sridhar (1986).

Reagents: 0.05 M pyrogallol dissolved in phosphate buffer at pH 6.0 and 1 per cent H_2O_2.

Extraction: Took 1 gm of fresh fruit tissue and placed it in pre-cooled pestle and mortar, added chilled phosphate buffer of pH 6.6 and ground it. Squeezed the extracts through 3

layers of muslin cloth to remove the pulp and centrifuged the extracts for 20 minutes at 4^0C. Decanted the supernatant and used the clear extract as enzyme source.

Procedure: Pipetted 3 ml of pyrogallol solution and 0.1 ml of tissue extract into colorimeter tube and adjusted the absorbance to zero at 420 nm in the colorimeter. Added 0.5 ml of H_2O_2 to the tube and inverted the tube immediately to mix the contents and replaced it in the spectrophotometer. Changes in absorbance at every 30 seconds up to 3 minutes were recorded.

10) Polyphenol oxidase activity (change in OD/min/g)

It was also calculated by the method given by Mahadevan and Sridhar (1986).

Reagents: 0.01 M catechol dissolved in phosphate buffer at pH 6.0.

Procedure: Extraction was carried out as in peroxidase. Pipetted 2 ml of the extract and 3 ml of phosphate buffer to a colorimeter tube, mixed the contents by inverting, placed in the spectrophotometer at 495 nm and adjusted the absorbance to zero. Removed the tube and added 1 ml of catechol solution and mixed again. Placed the tube immediately in the spectrophotometer and recorded the changes for every 30 seconds up to 3 minutes.

3.4 STATISTICAL ANALYSIS

Statistical analysis for the characters studied was done at the Department of Statistics, Mathematics and Physics of College of Basic Science, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur by using the Windowstat 8.0 programme of Indostat Services, Hyderabad.

3.4.1 The computation of generation means

Means of various generations were calculated as:

$\overline{X} = \sum x_i / n$

where,

$\overline{X}$ = generation mean,

$\sum x_i$ = grand total,

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

n = number of plants

3.4.2 Estimation of variance of generation means (V_x)

The generation means were subjected to sampling variation which can be estimated by normal statistical procedure. The estimate of variance of generation mean (VX) was obtained by dividing the variance within generation (V_x):

$V\overline{X} = V_x/n$

where,

V_x (variance of the generation mean) = $1/(n-1) [\sum x_i^2 - (\sum x_i)^2 /n]$

x_i = i^{th} observation of a population and

n = number of observations within generation

The value thus obtained was used for further analysis.

3.4.3 Simple scaling tests

To test the adequacy of additive-dominance model following scaling tests given by Mather (1949) and Hayman and Mather (1955) were used:

$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$

$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1}$

$C = 2\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$

$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2}$

The deviation of these scaling tests from zero was tested using the respective standard errors. The deviations from zero of any of these quantities indicated the inadequacy of additive-dominance model. The standard errors of the above scaling tests were calculated as follows:

$$SE(A) = \pm (4VB_1 + VP_1 + VF_1)^{1/2}$$

$$SE(B) = \pm (4VB_2 + VP_2 + VF_1)^{1/2}$$

$$SE(C) = \pm (16VF_2 + VF_1 + VP_1 + VP_2)^{1/2}$$

$$SE(D) = \pm (4VF_2 + VB_1 + VB_2)^{1/2}$$

where,

VB_1, VP_1 etc. are variances of the respective generation means. The deviations of A, B, C and D from zero, were tested using their respective standard errors (C test) as follows:

C(A) = A/SE(A),

C(B) = B/SE(B),

C(C) = C/SE(C), and

C(D) = D/SE(D),

The significance of A, B, C and D tests were tested against the value of 't' tabulated by comparing the values of C(A), C(B), C(C) and C(D) at a degree of freedom which was calculated by summing up the degree of freedom appropriate to the sampling variance of each generation involved in a particular test. The significant deviation of any of the scaling tests A, B, C and D from zero, indicates the failure of additive-dominance model. The significant deviation of A and B tests from zero indicate the presence of [j] type of interaction (additive x dominance), C scaling test reveals the presence of [l] type of interaction (dominance x dominance), and D scaling test indicates the significance of additive x additive [i] type of gene interaction.

3.4.4 Estimation of genic effects

Estimation of various gene effects and test of fitness of appropriate genetic model was done following 'joint scaling test' of Cavalli (1952), as described in detail by Jinks and Jones (1958). Joint scaling test involves estimation of various genetic parameters by using the observed means of different generations. Estimates of these parameters obtained through appropriate weighted least square analysis were used to calculate expected means and were then compared with observed means. The estimation of genic effects and Chi-square test of goodness of fit were carried out first for fitting of a 3-parameter model. In case of three parameter model (additive-dominance model) the following genic effects were estimated:

m = general mean

[d] = additive

[h] = dominance

where, additive-dominance model was a failure, a 6 parameter model was used and following genic effects were estimated:

$m = ½ P_1 + P_2 + 4F_2 – 2B_1 – 2B_2$

$[d] = ½P_1 – ½ P_2$

$[h] = 6B_1 + 6B_2 – 8F_2 – F_1 – (3/2) P_1 – (3/2) P_2$

$[i] = 2B_1 + 2B_2 – 4F_2$

$[j] = 2B_1 – P_1 – 2B_2 + P_2$

$[l] = P_1 + P_2 + 2F_1 + 4F_2 – 4B_1 – 4B_2$

Since the number of estimated parameters are equal to the number of generations used, no degree of freedom was left for testing adequacy of the model. However, standard errors of the parameters were obtained in the usual way as suggested by Mather and Jinks (1982). The standard errors were calculated as follows:

$$SE[m] = \pm (1/4V_{P1} + 1/4V_{P2} + 16V_{F2} + 4VB_1 + 4V_{B2})^{1/2}$$

$$SE[d] = \pm (1/4V_{P1} + 1/4V_{P2})^{1/2}$$

$$SE[h] = \pm (36V_{B1} + 36V_{B2} + 64V_{F2} + V_{F1} + (9/4)V_{P1} + (9/4)V_{P2})^{1/2}$$

$$SE[i] = \pm (4V_{B1} + 4V_{B2} + 16V_{F2})^{1/2}$$

$$SE[j] = \pm (4V_{B1} + V_{P1} + 4V_{B2} + V_{P2})^{1/2}$$

$$SE[l] = \pm (V_{P1} + V_{P2} + 4V_{F1} + 16V_{F2} + 16V_{B1} + 16V_{B2})^{1/2}$$

The significance of [m], [d], [h], [i], [j] and [l] was tested using their respective standard errors (t-test). The significance of these parameters was tested against the table value of 't' at a degree of freedom obtained by summing up the degree of freedom appropriate to the sampling variance of each generation involved in computing a particular parameter.

3.4.5 Analysis of variance

For working out the analysis of variance, the data were analysed by using the following model as suggested by Panse and Sukhatme (1984).

$$y_{ij} = u + g_i + r_j + e_{ij}$$

where,

y_{ij} = phenotypic observation of ith entry in jth replication,

u = general mean,

g_i = effect of ith entry,

r_j = effect of jth replication, and

e_{ij} = error component.

Analysis of variance

Source of variation	df	Mean squares	Expected mean squares
Replications	(r-1)	Mr	$\sigma^2e + g\sigma^2r$
Entries	(g-1)	Mg	$\sigma^2e + r\sigma^2g$
Error	(r-1)(g-1)	Me	σ^2e

where,

r = number of replications,

g = number of entries,

σ^2g = variance due to entries,

σ^2r = variance due to replications, and

σ^2e = error variance

The replications and treatments mean squares were tested against error mean squares by 'F' test for (r-1), (r-1)(g-1) and (g-1), (r-1)(g-1) degrees of freedom at 5% level of significance ($P \leq 0.05$). From this analysis, the following standard errors were calculated where the 'F' test was significant.

Standard error for the treatment mean:

$$SE\ (m) = \pm (Me/r)^{½}$$

Standard error for the difference of treatment mean:

$$SE\ (d) = \pm (2Me/r)^{½}$$

The critical difference (CD) obtained by multiplying SE (d) by the table value of 't' for error degree of freedom at 5% level of significance (P = 0.05).

CD = SE (d) x't' value at error degree of freedom at P = 0.05.

$$\text{Coefficient of variation (CV)\%} = \frac{(Me)^{1/2}}{\text{General mean}} \times 100$$

3.4.6 Estimation of correlation at phenotypic and genotypic levels

For computing phenotypic and genotypic coefficients of correlation, analysis of co-variance was carried out.

Analysis of co-variance

Source of variation	d.f.	Mean sum of square	Expected mean sum of product
Replication	(r–1)	Mr_{xy}	$\sigma e_{xy} + v.\sigma r_{xy}$
Genotypes	(v–1)	Mv_{xy}	$\sigma e_{xy} + r.\sigma v_{xy}$
Error	(r–1)(v–1)	Me_{xy}	σe_{xy}

where,

Error co-variance (σe_{xy}) = Me_{xy}

Genotypic co-variance (σv_{xy}) = $(Mv_{xy}-Me_{xy})/r$

Phenotypic covariance (σp_{xy}) = $\sigma v_{xy} + \sigma e_{xy}$

The phenotypic and genotypic coefficients of correlation were computed following Al-Jibouri *et al.* (1958):

Phenotypic coefficient of correlation (rp_{xy}):

$$rp_{xy} = \frac{\sigma\, p_{xy}}{(\sigma^2 p_x .\, \sigma^2 p_y)^{1/2}}$$

Genotypic coefficient of correlation (rv_{xy}):

$$rv_{xy} = \frac{\sigma v_{xy}}{(\sigma^2 v_x . \sigma^2 v_y)^{1/2}}$$

where,

σp_{xy} = Phenotypic covariance between two traits, x and y

σv_{xy} = Genotypic covariance between two traits, x and y

$\sigma^2 p_x$ and $\sigma^2 p_y$ = Phenotypic variance of traits, x and y, respectively

$\sigma^2 v_x$ and $\sigma^2 v_y$ = Genotypic variance of traits, x and y, respectively

The significance of phenotypic coefficient of correlation was tested against 'r' values as given by Fisher and Yates (1963) at n-2 degree of freedom, where 'n' denotes number of genotypes.

3.4.7 Estimates of direct and indirect effects

Path-coefficient is a standardized partial regression coefficient. It permits the partitioning of coefficients of correlation into direct and indirect effects. The path coefficient analysis of component traits with plant survival were carried out by following Dewey and Lu (1959) as under:

$Py_1 + Py_2.r_{12} + Py_3.r_{13} + \ldots\ldots\ldots\ldots + Py_n.r_{1n} = ry_1$

$Py_1.r_{12} + Py_2 + Py_3.r_{23} + \ldots\ldots\ldots\ldots + Py_n.r_{2n} = ry_2$

$Py_1.r_{13} + Py_2.r_{23} + Py_3 + \ldots\ldots\ldots\ldots + Py_n.r_{3n} = ry_3$

:

:

$Py_1.r_{n1} + Py_2.r_{n2} + Py_3.r_{n3} + \ldots\ldots\ldots\ldots + Py_n = ry_n$

where,

Py_1, Py_2, Py_3 …….. Py_n are the direct path effects of 1, 2, 3, ……., n variables on the dependent variable 'y'.

r_{12}, r_{13}, …….. $r_{(n-1)n}$ are the possible coefficients of correlation between various independent variables and ry_1, ry_2, ry_3, …… ry_n are the correlation coefficients of independent variables with dependent variable 'y'.

The variation in the dependent variable which remained undetermined by including the given variables was assumed to be due to variable(s) not included in the present investigation. The degree of determination (P^2 x R) of such variable(s) on the dependent variable was calculated as follows:

Residual effect (P X R) = $(1 - R^2)^{1/2}$

R^2 = $Py_1ry_1 + Py_2ry_2 + \ldots\ldots\ldots + Py_nry_n$

where, R^2 is the square multiple correlation coefficient and is the amount of variation in yield that can be accounted for by the yield component characters.

3.4.8 Estimation of heterosis

The estimates of heterosis were calculated as the deviation of F_1 mean ($\overline{F_1}$) from the better parent (BP) and $\overline{\text{stan}}$dard check.

1. Heterosis over better parent (BP) (%) = $\dfrac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$

2. Heterosis over the standard check (SC) % = $\dfrac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$

3.4.9 Calculation of standard errors

1) SE for testing heterosis over BP = $\pm\sqrt{2Me/r}$ = SE (H_1)

2) SE for testing heterosis over SC = $\pm\sqrt{2Me/r}$ = SE (H_2)

3.4.10 Test of significance for heterosis

$$1)\ \text{Heterosis over BP} = \frac{\overline{F_1} - \overline{BP}}{SE(H_1)} = \text{`}t_1\text{'}\ \text{calculated value}$$

$$2)\ \text{Heterosis over SC} = \frac{\overline{F_1} - \overline{SC}}{SE(H_2)} = \text{`}t_2\text{'}\ \text{calculated value}$$

The 't' calculated values (t_1, t_2) for heterosis over better parent (BP) and standard check (SC), respectively were compared with 't' tabulated values for error degree of freedom at $P = 0.05$.

CHAPTER IV

RESULTS

The results of the present investigation have been presented character/cross-wise under the following headings:

4.1 Genetics of resistance to bacterial wilt

4.2 Genetics of morphological and biochemical traits

4.3 Association of resistance with biochemical and morphological aspects

4.4 Heterosis

4.1 GENETICS OF RESISTANCE TO BACTERIAL WILT

The experimental results obtained on the bacterial wilt incidence in the parents, F_1s, F_2s and backcrosses (B_1 and B_2) of sweet pepper (*Capsicum annuum* L.) as on 90 days after transplanting (DAT) are given in Table 4.1. The segregation of plants in F_2 and B_2 generations are given in Table 4.2 and Table 4.3, respectively. The resistant parents *viz.,* PBC-631 and IHR-546 had 98.92 and 82.80 per cent plant survival, respectively, whereas the survival percentage of susceptible parents (California Wonder and Yolo Wonder) was zero. The results are presented cross-wise as under:

4.1.1 PBC-631 x CW

In the cross PBC-631 (Resistant) x CW (Susceptible), the survival in F_1 was 96 per cent, whereas 70.71 per cent in F_2. In B_1 (F_1 x PBC-631), the survival percentage was 93.33, but in B_2 (F_1 x CW), it was only 57.14 per cent. The segregation of F_2 population into resistant (239 plants) and susceptible classes (99 plants) was in the ratio of 3(R):1(S) (χ^2-value = 3.32) and B_2 test cross in the ratio of 1(R):1(S) (χ^2-value = 2.43).

Table 4.1: Genetics of bacterial wilt resistance

Cross		Initial plant stand	Resistant (R)	Susceptible (S)	Plant survival (%)
PBC-631 x CW	P_1	35	34	1	97.14
	P_2	19	0	19	0.00
	F_1	25	24	1	96.00
	F_2	338	239	99	70.71
	B_1	135	126	9	93.33
	B_2	119	68	51	57.14
PBC-631 x YW	P_1	33	33	0	100.00
	P_2	19	0	19	0.00
	F_1	25	24	1	96.00
	F_2	286	220	66	76.92
	B_1	89	80	9	89.89
	B_2	132	72	60	54.55
IHR-546 x CW	P_1	35	29	6	82.56
	P_2	21	0	21	0.00
	F_1	23	23	0	100.00
	F_2	220	170	50	77.27
	B_1	98	79	19	80.61
	B_2	129	75	54	58.91
IHR-546 x YW	P_1	24	20	4	83.33
	P_2	21	0	21	0.00
	F_1	25	22	3	88.00
	F_2	324	155	169	47.84
	B_1	134	108	26	80.60
	B_2	132	59	73	44. 07
YW x CW	P_1	25	0	25	0.00
	P_2	29	0	29	0.00
	F_1	26	0	26	0.00
	F_2	170	0	170	0.00
	B_1	149	0	149	0.00

	B_2	117	0	117	0.00
IHR-546 x PBC-631	P_1	34	28	6	82.35
	P_2	27	27	0	100.00
	F_1	13	13	0	100.00
	F_2	133	110	23	82.71
	B_1	78	64	14	82.05
	B_2	63	59	4	93.65

Table 4.2: Segregation of plants in F_2 population

Cross	Number of resistant (R) plants	Number of susceptible (S) plants	Expected ratio (R:S)	χ^2 value (cal)	χ^2 value (tab)	Type of gene action
PBC-631 x CW	239	99	3:1	3.32	3.84	Monogenic dominant
PBC-631 x YW	220	66	3:1	0.56	3.84	Monogenic dominant
IHR-546 x CW	170	50	3:1	0.61	3.84	Monogenic dominant
IHR-546 x YW	155	169	?	-	-	-
YW x CW	0	170	-	-	-	-
IHR-546 x PBC-631	110	23	-	-	-	-

? : did not fit to any genic interaction

Table 4.3: Segregation of plants in B_2 generation

Cross	Number of resistant (R) plants	Number of susceptible (S) plants	Expected ratio (R:S)	χ^2 value (cal)	χ^2 value (tab)
(PBC-631 x CW) x CW	68	51	1:1	2.43	3.84
(PBC-631 x YW) x YW	72	60	1:1	1.09	3.84
(IHR-546 x CW) x CW	75	54	1:1	3.42	3.84
(IHR-546 x YW) x YW	59	73	1:1	?	-
(YW x CW) x CW	0	117	0:1	-	-

(IHR-546 x PBC-631) x PBC-631	59	4	1:0	-	-

? : did not fit to any genic interaction

4.1.2 PBC-631 x YW

In the cross PBC-631 (Resistant) x YW (Susceptible), the survival in F_1 and F_2 were 96 and 76.92 per cent, respectively. In B_1 (F_1 x PBC-631), the survival was 89.89 per cent, whereas in B_2 (F_1 x YW) it was only 54.55 per cent. The segregation of F_2 population into resistant (220 plants) and susceptible (66 plants) classes was in the ratio of 3 (R):1(S) (χ^2-value 0.56) and that of B_2 (test cross) in the ratio of 1(R):1(S) (χ^2-value 1.09).

4.1.3 IHR-546 x CW

In the cross IHR-546 (Resistant) x CW (Susceptible), the survival in F_1 was 100 per cent, whereas in F_2 it was 77.27 per cent. In B_1 (F_1 x IHR-546), the survival was 80.61 per cent, whereas in B_2 (F_1 x CW) it was only 58.91 per cent. The segregation of F_2 population into resistant (170 plants) and susceptible (50 plants) classes was in the ratio of 3 (R):1(S) (χ^2-value 0.61) and that of B_2 (test cross) in the ratio of 1(R):1 (S) (χ^2-value 3.42).

4.1.4 IHR-546 x YW

In the cross IHR-546 (Resistant) x YW (Susceptible), the survival in F_1 and F_2 were 88.00 and 47.84 per cent, respectively. In B_1 (F_1 x IHR-546), the survival percentage was 80.60, but in B_2 (F_1 x CW) it was only 44.07 per cent. The segregation of F_2 population into resistant (155 plants) and susceptible classes (169 plants) did not fit to any of the mono and di-genic ratios.

4.1.5 YW x CW

In the cross involving susceptible varieties *viz.,* YW and CW, all the six generations (P_1, P_2, F_1, B_1, B_2 and F_2) had zero per cent survival.

4.1.6 IHR-546 x PBC-631

In the cross involving resistant parents *viz.,* IHR-546 and PBC-631, plant survival in F_1 and F_2 were 100 and 82.71 per cent, respectively. In B_1 (F_1 x IHR-546) and B_2 (F_1 x PBC-631) the plant survivals were 82.05 and 93.65 per cent, respectively.

4.2 GENETICS OF MORPHOLOGICAL AND BIOCHEMICAL TRAITS

Simple scaling tests (A, B, C and D) as per Mather (1949) and Hayman and Mather (1955) were carried out to test the adequacy of additive-dominance model. Joint scaling test as per Cavalli (1952) was also used to estimate the genic effects by using 3 parameter model and further verifying the same by χ^2 test. In case the 3 parameter model was inadequate as indicated by the significant χ^2 value, six parameter model was used to estimate the various gene effects including non-allelic interactions due to additive x additive [i], additive x dominance [j] and dominance x dominance [l] as per Jinks and Jones (1958) and Mather and Jinks (1982). The results obtained on estimates of scaling test and various genic effects for six crosses studied with respect to various morphological and biochemical characters are documented in Tables 4.4 to 4.25 and are described character-wise here under:

4.2.1 Days to 50 per cent flowering

The estimates of scaling tests and genic effects including interactions for days to 50 per cent flowering are given in Table 4.4. The additive-dominance model was adequate for four crosses *viz.,* PBC-631 x YW, IHR-546 x YW, YW x CW and IHR-546 x PBC-631,

whereas rest of the crosses showed significant values of either A, B, C or D scaling tests and Chi-square values indicating the presence of non-allelic interactions.

The estimates of the genic effects revealed the presence of significantly positive additive genic effects [d] in PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and YW x CW, whereas it was negative in IHR-546 x PBC-631. The dominance genic effects [h] were negatively significant in all the crosses except PBC-631 x CW, which exhibited significant and positive dominance genic effect. Significantly positive additive x additive [i] and negative dominance x dominance [l] genic effects indicated the presence of epistatic effects for this character in the cross PBC-631 x CW, whereas IHR-546 x CW showed negatively and positively significant additive x additive [i] and dominance x dominance [l] genic effects, respectively. Signs of significant [h] and [l] were in opposite direction indicating the duplicate type of gene action in both (PBC-631 x CW and IHR-546 x CW) the crosses.

4.2.2 Days to first picking

The simple scaling tests revealed the inadequacy of additive-dominance model for this trait in all the crosses except PBC-631 x CW and PBC-631 x YW. In the remaining crosses, the significant values either of A, B, C or D and Chi-square indicated the presence of non-allelic interactions (Table 4.5).

The estimates of genic effects revealed the presence of significant positive additive [d] genic effects in PBC-631 x CW and PBC-631 x YW, whereas negative additive genic effect was exhibited in IHR-546 x PBC-631. Significantly negative dominance genic effects [h] for this trait were also observed in PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and IHR-546 x PBC-631. Additive x additive [i] genic effects were

significant and negative in IHR-546 x CW, YW x CW and IHR-546 x PBC-631. Significantly negative additive x dominance effects were observed in IHR-546 x CW and IHR-546 x YW. Dominance x dominance

effects were also significant and negative in IHR-546 x YW and YW x CW, whereas IHR-546 x PBC-631 displayed positive [l] effect along with duplicate type of gene interaction.

4.2.3 Fruit length

The significant values for any one of the A, B, C or D scaling tests in all the crosses except PBC-631 x YW indicated the inadequacy of additive-dominance model (Table 4.6). The inadequacy of this model was also confirmed by significant Chi-square values for all the crosses except PBC-631 x YW.

All the crosses except IHR-546 x YW showed significant values for additive gene effects [d], being positive in PBC-631 x CW and PBC-631 x YW and negative in the remaining three crosses. Dominance gene effects [h] were significantly positive in PBC-631 x YW and IHR-546 x YW only. Significantly positive additive x additive gene effect [i] was observed in IHR-546 x CW, whereas this effect was significant and negative in IHR-546 x PBC-631. Additive x dominance [j] gene effect was negatively significant in IHR-546 x PBC-631. Dominance x dominance gene effects [l] were positively significant for PBC-631 x CW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631, whereas IHR-546 x YW exhibited significant and negative [l] value along with duplicate type of epistasis.

4.2.4 Fruit diameter

All the crosses showed significant values of either A, B, C or D scales indicating the presence of non-allelic interactions. This was further supported by the joint scaling test, which gave significant Chi-square values in all the crosses (Table 4.7).

All the crosses except IHR-546 x PBC-631 showed negative and significant additive genic effects [d]. Significant and negative dominant gene

effects [h] were also observed in all the crosses except PBC-631 x YW. Additive x additive [i] genic effect was significant and positive in PBC-631 x YW, whereas this effect was significant and negative in IHR-546 x PBC-631. Significantly positive additive x dominance [j] genic effects were observed in IHR-546 x CW and IHR-546 x YW. Significant and positive dominance x dominance genic effects [l] were observed in all the crosses. All the crosses except PBC-631 x YW also exhibited duplicate type of non-allelic interaction, as the signs of [h] and [l] were significant and opposite in direction.

4.2.5 Pedicel length

Presence of non-allelic interaction, as evident from the significant values for any of the A, B, C or D scales, was observed in all the crosses (Table 4.8). The Chi-square values were also significant for all the crosses, indicating the inadequacy of additive-dominance model.

Additive gene effects [d] were significantly positive for PBC-631 x CW and PBC-631 x YW, whereas negative for IHR-546 x PBC-631. Dominance genic effects [h] were significant and positive in all the crosses except IHR-546 x PBC-631. Additive x additive [i] genic effects were significant and positive in PBC-631 x CW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631. Additive x dominance gene effects [j] were positively

significant in PBC-631 x CW, IHR-546 x CW, IHR-546 x YW and IHR-546 x PBC-631, whereas PBC-631 x YW displayed significant and negative value of [j]. Dominance x dominance [l] genic effects were observed negatively and positively significant in IHR-546 x CW and IHR-546 x PBC-631, respectively. IHR-546 x CW also showed duplicate type of non-allelic interaction for this trait.

4.2.6 Pericarp thickness

Non-significant values of A, B, C or D scaling tests and χ^2 values revealed that the additive-dominance model was adequate in all the crosses except in PBC-631 x YW and IHR-546 x PBC-631 for pericarp thickness (Table 4.9).

Significant negative additive genic effects [d] were observed in all the crosses except IHR-546 x PBC-631, which displayed significantly positive additive gene effect. Dominance gene effects [h] were positively significant for PBC-631 x CW and IHR-546 x YW, whereas it was significant and negative for PBC-631 x YW. Additive x additive [i] genic effects were significantly negative in PBC-631 x YW and IHR-546 x PBC-631, whereas only PBC-631 x YW exhibited significant and positive dominance x dominance genic effect [l] along with duplicate type of epistasis.

4.2.7 Number of fruits per plant

All the crosses except IHR-546 x PBC-631 gave significant values for either A, B, C or D indicating the presence of non-allelic interactions (Table 4.10). This was further supported by the significant Chi-square values in joint scaling test except for IHR-546 x PBC-631.

The estimates of gene effects showed significant and positive additive genic effects [d] for all the crosses except YW x CW and IHR-546 x PBC-631, however, these crosses displayed negatively significant [d] effects. Similarly, dominance [h] genic effects were significant and positive for all the crosses except PBC-631 x CW and PBC-631 x YW. Significant and negative additive x additive [i] genic effects were observed in PBC-631 x CW and PBC-631 x YW, whereas significant and positive [i] were recorded in YW x CW. Significant and negative additive x dominance [j] genic effects were observed in IHR-546 x CW

and IHR-546 x YW, whereas PBC-631 x CW showed significant and positive [j] effects. Dominance x dominance [l] gene effects were significantly positive in PBC-631 x CW and PBC-631 x YW, whereas significantly negative in IHR-546 x YW. The opposite signs of [h] and [l] in IHR-546 x YW indicated the probable presence of duplicate type of gene action.

4.2.8 Average fruit weight

The additive-dominance model was adequate for YW x CW, whereas rest of the crosses displayed significant values of either A, B, C or D scaling test and χ^2 value indicating the presence of non-allelic interactions (Table 4.11).

Additive genic effects [d] were observed significant and negative for all the crosses except YW x CW and IHR-546 x PBC-631; however, this effect was significantly positive for IHR-546 x PBC-631. Significant and negative dominance [h] genic effect was observed in IHR-546 x YW, whereas it was significant and positive in crosses *viz.,* YW x CW and IHR-546 x PBC-631. Additive x additive [i] genic effects were significant and positive in PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and IHR-546 x PBC-631.

Similarly, additive x dominance [j] genic effects were significantly positive in all the crosses except YW x CW and IHR-546 x PBC-631. Significant and negative dominance x dominance [l] genic effect was observed in PBC-631 x YW, whereas IHR-546 x YW exhibited significant and positive [l] effect along-with duplicate type of interaction.

4.2.9 Yield per plant

All the crosses gave significant values of A, B, C or D scaling tests indicating the inadequacy of additive-dominance model (Table 4.12). This was further confirmed by the significant Chi-square values in joint scaling test.

Significant and negative additive [d] genic effects were observed for all the crosses except IHR-546 x PBC-631, which showed positive and significant additive effect. Dominance [h] values were positively significant in all the crosses except PBC-631 x YW. Additive x additive [i] genic effects were significant in PBC-631 x YW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631 being negative in the former one, while positive in the later crosses. Additive x dominance [j] genic effects were positive and significant only in PBC-631 x CW. Significant and positive dominance x dominance [l] genic effects were observed in PBC-631 x YW and IHR-546 x YW, whereas [l] was negative and significant in IHR-546 x CW and IHR-546 x PBC-631. The later two crosses also had significant [h] and [l] with opposite signs indicating duplicate type of gene action, whereas IHR-546 x YW exhibited complimentary type of epistasis for this trait as evident from the significant positive signs of [h] and [l].

4.2.10 Number of pickings

The fitting of additive-dominance model with respect to IHR-546 x CW, YW x CW and IHR-546 x PBC-631 was confirmed by non-significant values of either A, B, C and D scales and Chi square values in joint scaling test (Table 4.13). Significant values either of A, B, C or D in remaining three crosses revealed the presence of non-allelic interactions.

Additive [d] genic effects were found significant and positive in all the crosses except YW x CW and IHR-546 x PBC-631, whereas dominance [h] genic effects were significantly positive in all the crosses. Additive x additive [i] gene effects were significant and positive in PBC-631 x CW, PBC-631 x YW and IHR-546 x YW.

4.2.11 Number of branches per plant

The non-significant values of A, B, C or D scaling tests and χ^2 values in all the crosses except IHR-546 x CW and IHR-546 x YW indicated the fitting of additive-dominance model, whereas these two crosses showed the presence of non-allelic interactions (Table 4.14).

Additive [d] genic effects were significant and negative for PBC-631 x CW and YW x CW, whereas positive for IHR-546 x YW and IHR-546 x PBC-631. The estimates of dominance [h] genic effects were significant and positive for all the crosses except IHR-546 x CW and YW x CW. Additive x additive [i] genic effects were significant and positive in IHR-546 x YW, similarly, this cross also exhibited significant but negative dominance x dominance [l] genic effect along with duplicate type of gene interaction. Additive x dominance genic effects were displayed only in IHR-546 x CW.

4.2.12 Plant height

The estimates of A, B, C or D scaling tests for plant height and also Chi-square values in joint scaling test were non-significant in IHR-546 x CW, YW x CW and IHR-546 x PBC-631, thus indicating the fitting of additive-dominance model. Non-allelic interactions were revealed in the remaining three crosses (Table 4.15).

Additive genic effects [d] were observed significant and positive in PBC-631 x CW and PBC-631 x YW; however, these effects were significantly negative for IHR-546 x CW, YW x CW and IHR-546 x PBC-631. Significant and positive dominance [h] genic effects were observed in crosses *viz.,* PBC-631 x CW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631. Only IHR-546 x YW exhibited significant and negative additive x additive gene effects [i]. Additive x dominance [j] genic effects were positive and significant in all the crosses that showed

inadequacy for additive-dominance model. Significant and positive dominance x dominance [l] genic effects were observed in PBC-631 x YW and IHR-546 x YW.

4.2.13 Ascorbic acid content

The estimates of scaling tests and genic effects including interactions for ascorbic acid content are given in Table 4.16. The additive-dominance model was adequate only for IHR 546 x PBC-631, whereas rest of the crosses displayed significant values of either A, B, C or D scaling test and χ^2 value indicating the presence of non-allelic interactions.

Additive genic effects [d] were observed to be significant and positive for all the crosses except IHR-546 x PBC-631 where it was significantly negative for this cross. Significant and positive dominance [h] genic effects were observed in IHR-546 x CW, IHR-546 x YW and IHR-546 x PBC-631, whereas PBC-631 x YW exhibited significant and negative [h] values. Additive x additive [i] genic effects were significant and negative

in PBC-631 x CW, PBC-631 x YW and YW x CW, whereas additive x dominance [j] genic effects were significant and negative in IHR-546 x CW, IHR-546 x YW and YW x CW. IHR-546 x YW displayed significant and negative dominance x dominance [l] effect along with duplicate type of epistasis.

4.2.14 Total soluble solids (TSS)

The fitting of additive-dominance model with respect to IHR-546 x CW, YW x CW and IHR-546 x PBC-631 was confirmed by non-significant values of A, B, C and D scales and Chi square values in joint scaling test (Table 4.17). Significant values either of A, B, C or D in remaining three crosses revealed the presence of non-allelic interactions.

Additive [d] genic effects were found significant and negative in all the crosses except YW x CW, whereas dominance [h] genic effects were significantly negative and positive only in PBC-631 x YW and IHR-546 x CW, respectively. Significant and positive additive x additive genic effect [i] was displayed only in PBC-631 x CW. IHR-546 x YW displayed significantly positive additive x dominance [j] gene effects. Dominance x dominance [l] gene effects were significant and positive in PBC-631 x CW and PBC-631 x YW, however, the later cross also exhibited duplicate type of gene interaction as the signs of significant [h] and [l] were in opposite direction.

4.2.15 Total sugars

All the crosses gave significant values of A, B, C or D scaling tests indicating the inadequacy of additive-dominance model (Table 4.18). This was further confirmed by the significant Chi-square values in joint scaling test.

Significant and negative additive [d] genic effects were observed for all the crosses. Dominance [h] values as well as additive x additive [i] genic effects were negatively significant in PBC-631 x CW, IHR-546 x CW and IHR-546 x YW and positively significant only in YW x CW, however, PBC-631 x YW displayed significant and positive dominance genic effect [h] only. Additive x dominance [j] genic effects were significant and negative in PBC-631 x YW, IHR-546 x CW and IHR-546 x PBC-631, whereas these effects were significantly positive only in IHR-546 x YW. Significant and positive dominance x dominance [l] genic effects were observed in PBC-631 x CW and IHR-546 x PBC-631, whereas [l] estimates were significant and negative in PBC-631 x YW and YW x CW. PBC-631 x CW, PBC-631 x YW and YW x CW had significant [h] and [l] values with opposite

signs, indicating the probable presence of duplicate type of gene action in these crosses.

4.2.16 Reducing sugars

All the crosses showed inadequacy of the additive-dominance model as evident from the significant values of either A, B, C or D scales indicating the presence of non-allelic interactions. This was further supported by the joint scaling test which gave significant Chi-square values in all the crosses (Table 4.19).

All the crosses except YW x CW showed significant and negative additive genic effects [d]. Dominance gene effects [h] were significantly negative and positive only in IHR-546 x CW and YW x CW, respectively. Additive x additive [i] genic effects were significant and negative in all the crosses except positively significant only in YW x CW. Significantly negative additive x dominance [j] genic effects were observed in PBC-631 x

CW and IHR-546 x PBC-631, whereas these effects were positive and significant in IHR-546 x YW and YW x CW. Significantly positive dominance x dominance [l] genic effects were observed in IHR-546 x CW and IHR-546 x PBC-631, whereas YW x CW showed significant and negative [l] effect. IHR-546 x CW and YW x CW also exhibited duplicate type of non-allelic interaction as displayed by the significant values and opposite signs of [h] and [l].

4.2.17 Non-reducing sugars

Presence of non-allelic interaction, as evident from the significant values for any of the A, B, C or D scales, was observed in all the crosses (Table 4.20). This was further confirmed by the significant Chi-square value, indicating the inadequacy of additive-dominance model.

Additive gene effects [d] were significantly negative for all the crosses except PBC-631 x YW. Significant negative dominance effects [h] were displayed in PBC-631 x CW and IHR-546 x YW, whereas the estimates of [h] were positive and significant in PBC-631 x YW, IHR-546 x CW and YW x CW.

Additive x additive [i] genic effects were significant and negative in IHR-546 x YW, whereas significantly positive in YW x CW and IHR-546 x PBC-631. Additive x dominance gene effects [j] were positively and negatively significant in PBC-631 x CW and PBC-631 x YW, respectively. Dominance x dominance [l] genic effects were observed to be significant and positive in PBC-631 x CW, IHR-546 x YW and IHR-546 x PBC-631, whereas these effects were significantly negative in IHR-546 x CW and YW x

CW. All the crosses except PBC-631 x YW and IHR-546 x PBC-631 exhibited duplicate type of non-allelic interaction for this trait.

4.2.18 Total phenols

The simple scaling tests (A, B, C and D) revealed the adequacy of additive-dominance model for this trait in three crosses *viz.,* PBC-631 x YW, IHR-546 x CW and YW x CW. In the remaining crosses, the significant values either of A, B, C or D and Chi-square values indicated the presence of non-allelic interactions (Table 4.21).

The estimates of genic effects revealed the presence of significant positive additive [d] genic effects in all the crosses except YW x CW (non-significant) and IHR-546 x PBC-631 (significant and negative). Significantly negative dominant genic effects [h] for this trait were observed in PBC-631 x CW and IHR-546 x PBC-631, whereas the estimate of [h] was significant and positive only in PBC-631 x YW. Additive x additive [i] genic effects were observed to be significant and

negative in PBC-631 x CW, IHR-546 x YW and IHR-546 x PBC-631, whereas significantly positive and negative additive x dominance effects [j] were observed only in PBC-631 x CW and IHR-546 x YW, respectively. IHR-546 x PBC-631 displayed significant and positive dominance x dominance [l] genic effect along with duplicate type of gene interaction.

4.2.19 Ortho dihydroxy phenols

The estimates of scaling tests and genic effects including interactions for ortho dihydroxy phenols are given in Table 4.22. The additive-dominance model was adequate for four crosses *viz.,* IHR-546 x CW, IHR-546 x YW, YW x CW and IHR-546 x PBC-631,

whereas the remaining two crosses showed significant values of either A, B, C or D and Chi square indicating the presence of non-allelic interactions.

The estimates of the genic effects revealed the presence of significantly positive additive genic effects [d] in PBC-631 x CW, PBC-631 x YW and IHR-546 x CW, whereas the estimate of [d] was significant and negative in IHR-546 x PBC-631. The dominance genic effect [h] was negatively significant only in PBC-631 x YW but IHR-546 x CW, IHR-546 x YW and IHR-546 x PBC-631 displayed significant and positive dominance genic effect. Significant and negative additive x additive [i] and dominance x dominance [l] genic effects were present in PBC-631 x YW and PBC-631 x CW, respectively.

4.2.20 Total free amino acids

The fitting of additive-dominance model with respect to PBC-631 x CW, IHR-546 x CW and IHR-546 x PBC-631 was confirmed by non-significant values of either A, B, C and D scales and Chi square values in joint scaling test (Table 4.23).

Significant values in remaining crosses revealed the presence of non-allelic interactions.

Additive [d] genic effects were found significant and positive in all the crosses except YW x CW and IHR-546 x PBC-631 which displayed significant and negative estimates. Dominance [h] genic effects were significantly positive in PBC-631 x CW, PBC-631 x YW and IHR-546 x YW. Additive x additive [i] gene effects were significant and positive in PBC-631 x YW, IHR-546 x YW and YW x CW. Significantly positive additive x dominance [j] genic effects were exhibited by PBC-631 x YW and YW x CW but the estimate of [j] was significantly negative in IHR-546 x YW.

4.2.21 Peroxidase (PO) activity

The significant values of A, B, C or D scaling tests and χ^2 values in all the crosses except PBC-631 x YW indicated the inadequacy of additive-dominance model, thus indicating the presence of non-allelic interactions (Table 4.24).

Additive [d] genic effects were significant and positive in all the crosses. Dominance [h] values were significantly positive and negative in PBC-631 x YW and YW x CW, respectively. Additive x additive [i] genic effects were negative and significant in IHR-546 x CW and IHR-546 x YW, whereas this effect was significant and positive only in IHR-546 x PBC-631. Crosses *viz.,* PBC-631 x CW, IHR-546 x YW and YW x CW exhibited significant and negative estimates of additive x dominance [j] genic effects, whereas these estimates were significantly positive for IHR-546 x CW and IHR-546 x PBC-631. Dominance x dominance [l] genic effects were significant and positive in IHR-546 x CW, IHR-546 x YW, YW x CW and IHR-546 x PBC-631. Signs of significant [h] and [l] were opposite in direction in YW x CW indicating the presence of duplicate type of gene action.

4.2.22 Polyphenol oxidase (PPO) activity

Non-significant values of A, B, C or D scaling tests and χ^2 value revealed that the additive-dominance model was adequate in all the crosses except PBC-631 x YW and IHR-546 x YW for the trait under study (Table 4.25).

Significant and positive additive genic effects [d] were observed in all the crosses except YW x CW. Similarly, dominance gene effects [h] were also positively significant for all the crosses except IHR-546 x PBC-631. Additive x additive [i] and additive x dominance [j] genic effects were significantly positive and negative only in PBC-631 x YW and IHR-546 x YW, respectively.

4.3 ASSOCIATION OF RESISTANCE TO BACTERIAL WILT WITH BIOCHEMICAL AND MORPHOLOGICAL TRAITS

4.3.1 Correlation coefficients

Correlation coefficients among biochemical as well as morphological aspects were worked out at phenotypic and genotypic levels and are presented in Tables 4.26 and 4.27, respectively. For majority of the traits, genotypic correlation values were higher than those at phenotypic levels. The results pertaining to correlation coefficients at phenotypic and genotypic levels with biochemical and morphological traits are presented below:

Biochemical traits

Phenotypic correlation coefficients among biochemical traits showed that plant survival (resistance) was significantly and positively correlated with ascorbic acid content (0.841), total free amino acids (0.717), total phenols (0.643), peroxidase (PO) activity (0.637), ortho dihydroxy (OD) phenols (0.588) and polyphenol oxidase (PPO) activity (0.573), whereas total sugars (-0.543), reducing sugars

(-0.501) and non-reducing sugars (-0.469) exhibited significant and negative correlation coefficients with plant survival (Table 4.26).

The estimates of correlation coefficient of ascorbic acid were significant and positive with total phenols (0.838), ortho dihydroxy phenols (0.806), total free amino acids (0.779) and peroxidase activity (0.497), whereas total sugars (-0.572),

reducing sugars (-0.535) and non-reducing sugars (-0.486) exhibited significant and negative correlation coefficients with ascorbic acid content.

TSS exhibited significant and positive association with total sugars (0.541), reducing sugars (0.512) and non-reducing sugars (0.450), while significant and negative with total phenols only (-0.403).

The inter-relationships of total sugars with reducing sugars (0.923) and non-reducing sugars (0.863) were significant and positive, whereas these were significantly and negatively correlated with peroxidase (PO) activity (-0.702), polyphenol oxidase (PPO) activity (-0.605), total phenols (-0.560) and total free amino acids (-0.406),

Reducing sugars were significantly and positively correlated with non-reducing sugars (0.602), however, these were significantly and negatively correlated with peroxidase activity (-0.661), polyphenol oxidase activity (-0.584), total phenols (-0.539), and total free amino acids (-0.389).

At phenotypic level, non-reducing sugars showed significant and negative correlation with peroxidase activity (-0.588), polyphenol oxidase activity (-0.490) and total phenols (-0.453).

It is evident from the Table 4.26 that total phenols exhibited significant and positive correlation with ortho dihydroxy phenols (0.827), total free amino acids (0.687) and peroxidase activity (0.464). Ortho dihydroxy phenols recorded significant and positive association with total free amino acids (0.652). Peroxidase activity also showed significant and positive correlation with polyphenol oxidase activity (0.792).

Morphological traits

Among morphological traits, plant survival exhibited significant and positive association with number of fruits per plant (0.917), pedicel length (0.731), fruit length (0.688),

number of pickings (0.681) and plant height (0.647), whereas average fruit weight (-0.920), fruit diameter (-0.892) and pericarp thickness (-0.670) displayed negative and significant relationship with plant survival (Table 4.27).

The estimate of correlation coefficient of days to 50 per cent flowering with days to first picking was significant and positive (0.415), whereas these estimates were significant and negative with yield per plant (-0.760), fruit diameter (-0.552), pericarp thickness (-0.548) and average fruit weight (-0.493). Days to first picking exhibited significant and negative association with yield per plant (-0.554) and branches per plant (-0.420).

The inter-relationships of fruit length with plant height (0.912), pedicel length (0.840), number of fruits per plant (0.719) and number of pickings (0.635) were significant and positive, while it was significantly and negatively correlated with pericarp thickness (-0.661), fruit diameter (-0.633) and average fruit weight (-0.572).

Fruit diameter was significantly and positively correlated with average fruit weight (0.957), pericarp thickness (0.782) and yield per plant (0.588), however, it was significantly and negatively associated with number of fruits per plant (-0.814), pedicel length (-0.660), plant height (-0.644) and number of pickings (-0.606).

It is evident from the Table 4.27 that inter-relationship of pedicel length with plant height (0.825), number of fruits per plant (0.689) and number of pickings (0.594) was significant and positive, whereas with pericarp thickness (-0.666) and average fruit weight (-0.585) was significant and negative.

At phenotypic level, the correlation coefficient of pericarp thickness with average fruit weight (0.697) and yield per plant (0.657) was significant and positive, while it was

significantly negative with plant height (-0.698), number of pickings (-0.558) and number of fruits per plant (-0.525).

Number of fruits per plant was significantly and positively correlated with number of pickings (0.711) and plant height (0.694), whereas it was significantly and negatively correlated with average fruit weight (-0.866). Contrary to this, average fruit weight was significant and positively correlated with yield per plant (0.559), but it was significantly and negatively associated with number of pickings (-0.573) and plant height (-0.567). Similarly, number of pickings was significantly and positively associated with plant height (0.662).

At genotypic level, it was observed that the general trend of association among various biochemical and morphological traits was almost similar to that observed at phenotypic level but the values were higher than the corresponding phenotypic correlation coefficients.

4.3.2 Path coefficient analysis

In order to understand the causal factors of the correlations among various biochemical and morphological traits studied, the estimates of direct and indirect effects were computed through path analysis, taking plant survival (resistance to bacterial wilt) as a resultant (dependent) variable in each case. The direct and indirect effects for both biochemical and morphological traits are presented in Tables 4.28 and 4.29, respectively and are described here under:

Biochemical traits

The phenotypic association between plant survival and ascorbic acid content was significant and positive (0.841). Breakup of this association revealed that direct effect of ascorbic acid content was also positive and high (0.687) and indirect effects via majority

of the characters were also positive being maximum in total free amino acids (0.213) followed peroxidase activity (0.167) (Table 4.28). At genotypic level, the major portion of the association between plant survival and ascorbic acid was due to its own positive direct effect (2.058) and indirect effects via ortho dihydroxy phenols (0.539), reducing sugars (0.517) and polyphenol oxidase activity (0.354). The indirect effects via TSS (-0.978), total free amino acids (-0.855), peroxidase activity (-0.474) and total phenols (-0.473), counteracted the positive effects.

The association between plant survival and TSS was negative and non-significant at phenotypic level. Its direct effect was positive (0.111) and indirect effects via most of the characters under study were low in magnitude except ascorbic acid content (-0.258) and peroxidase activity (-0.118). TSS exhibited positive direct effect (1.567) at genotypic level also. Indirect effects via peroxidase activity (0.473), total phenols (0.325) and total free amino acids (0.288) were positive. The negative indirect effects through ascorbic acid content (-1.284), reducing sugars (-0.754), ortho dihydroxy phenols (-0.312), polyphenol

oxidase activity (-0.361) and total sugars (-0.166) affected the total association to greater extent.

The correlation between total sugars and plant survival was negative and significant (-0.543) at phenotypic level, while its direct effect was positive (0.111). The indirect effects via majority of the traits were low, whereas ascorbic acid content (-0.393) and peroxidase activity (-0.235) had fairly high negative indirect effects (Table 4.28). At

genotypic level, this character showed negative direct effect (-0.202). The negative indirect effects through ascorbic acid content (-1.226), reducing sugars (-0.863), polyphenol oxidase activity (-0.627) and ortho dihydroxy phenols (-0.266) contributed the major proportion of association, whereas positive indirect effects through TSS (1.288), peroxidase activity (0.659), total free amino acids (0.446) and total phenols (0.325) counteracted the negative effects to large extent.

The phenotypic association between plant survival and reducing sugars was significant and negative (-0.501), whereas its direct effect was positive and of very low magnitude (0.010). Indirect effects via ascorbic acid content (-0.368) and peroxidase activity (-0.222) were negative, whereas total phenols (0.137) and total sugars (0.103) with positive indirect effects counteracted the negative indirect effects. At genotypic level, direct effect was negative (-0.921) and high in magnitude. Indirect effects via ascorbic acid content (-1.156), polyphenol oxidase activity (-0.606), ortho dihydroxy phenols (-0.243) and total sugars (-0.189) contributed mainly for negative indirect effects, however, TSS (1.283), peroxidase activity (0.632), total free amino acids (0.428) and total phenols (0.321) exhibited positive indirect effects.

Non-reducing sugars had negative direct effect (-0.037) at phenotypic level. Indirect effects via ascorbic acid content (-0.334) and peroxidase activity (-0.197) were negative, whereas total phenols (0.115) had positive indirect effect. At genotypic level, the breaking up of the association showed that the direct effect was negative (-0.099) and low and the major portion of association was through the indirect negative effects via ascorbic acid content (-1.075), reducing sugars (-0.613), polyphenol oxidase activity (-0.528), ortho dihydroxy phenols (-0.243) and total sugars (-0.178). The positive indirect effects via TSS (1.036), peroxidase activity (0.562), total free amino acids

(0.381) and total phenols (0.266) affected the total association to some extent (Table 4.28).

The phenotypic association between plant survival and total phenols was significant and positive (0.643), but the direct effect was negative (-0.254). The maximum positive indirect effect was observed via ascorbic acid content (0.576) followed by total free amino acids (0.188) and peroxidase activity (0.156). At genotypic level also, the direct effect was negative (-0.517). Breakup of association showed that positive indirect effects through ascorbic acid content (1.883), reducing sugars (0.572), ortho dihydroxy phenols (0.512), polyphenol oxidase activity (0.318) and total sugars (0.127) were counteracted by the negative indirect effects via TSS (-0.985), total free amino acids (-0.797) and peroxidase activity (-0.465).

Phenotypic correlation coefficient between plant survival and ortho dihydroxy phenols was significant and positive (0.588) and its direct effect was also positive (0.036), but of lower magnitude. Like total phenols, ascorbic acid content (0.554) followed by total free amino acids (0.178) exhibited maximum positive indirect effects. The negative indirect effect via total phenols (-0.210) affected the total association to some extent (Table 4.28). Ortho dihydroxy phenols exhibited positive direct effect (0.593) for plant survival at genotypic level. The indirect effects through ascorbic acid content (1.871) and reducing sugars (0.378) were positive, whereas the indirect effects via TSS (-0.824), total free amino acids (-0.814), total phenols (-0.446) and peroxidase activity (-0.259) restricted the total association to some extent.

Association between total free amino acids and plant survival was significant and positive (0.717). At phenotypic level its direct effect was also positive (0.274). Major portion of this association was due to indirect effect via ascorbic acid content (0.536),

however, the negative indirect effects via total phenols (-0.174) affected the total association to some extent. At genotypic level, the direct effect was negative and high (-1.062), whereas indirect positive effects via ascorbic acid content (1.655), ortho dihydroxy phenols (0.454), reducing sugars (0.371) and polyphenol oxidase activity (0.233) were found to be major constituents of the total association. Negative indirect effects were observed via TSS (-0.426), total phenols (-0.388) and peroxidase activity (-0.228).

Peroxidase (PO) activity was significantly and positively correlated with plant survival (0.637) and its direct effect was also positive and high (0.335) at phenotypic level. Indirect effects via ascorbic acid content (0.342) and polyphenol oxidase activity (0.105) were positive, whereas negative indirect effect was recorded via total phenols (-0.118). The character exhibited negative direct effect for plant survival at genotypic level (-0.910). The positive indirect effects via ascorbic acid content (1.071), polyphenol oxidase activity (0.814), reducing sugars (0.640), ortho dihydroxy phenols (0.169) and total sugars (0.146) mainly contributed for the total correlation coefficient. Indirect effects via TSS (-0.814), total free amino acids (-0.266) and total phenols (-0.264) were negative.

Phenotypic correlation coefficient of polyphenol oxidase (PPO) activity with plant survival was significant and positive (0.573). The further break-up of the correlation showed that direct effect was also positive (0.133) and indirect effects via peroxidase activity (0.266) and ascorbic acid content (0.258) contributed positively at phenotypic level. It also exhibited positive direct effect (0.895) at genotypic level. Indirect effects via ascorbic acid content (0.814), reducing sugars (0.624) and total sugars (0.141) were positive. The indirect negative effects via peroxidase activity (-0.828), TSS (-0.631), total

free amino acids (-0.276) and total phenols (-0.184) affected the total association to some extent (Table 4.28).

Morphological traits

The direct and indirect effects for morphological traits are presented in Table 4.29. Breakup of the association between days to 50 per cent flowering and plant survival (0.315) revealed that direct effect was negative and low (-0.010). The indirect effect via average fruit weight was positive (0.393), whereas it was negative via yield per plant (-0.155). At genotypic level, direct effect was positive (0.358) and positive indirect effects via pericarp thickness (0.305), average fruit weight (0.235) and number of fruits per plant (0.174) also contributed to the total association. Indirect effects via yield per plant (-0.370), fruit diameter (-0.229) and plant height (-0.119) were found to be negative (Table 4.29).

At phenotypic level, days to first picking had positive and very low magnitude of direct effect (0.003). Indirect effects via most of the traits were of low magnitude except yield per plant (-0.113). Direct effect of days to first picking was also positive at genotypic level (0.129). Indirect effects via days to 50 per cent flowering (0.242) and pericarp thickness (0.170) were positive, whereas negative indirect effects were contributed by yield per plant (-0.255), branches per plant (-0.178) and number of fruits per plant (-0.176).

Fruit length exhibited significant and positive correlation with plant survival (0.688) and its direct effect was also positive but low (0.094) at phenotypic level. Remarkable magnitude of positive indirect effect was recorded via average fruit weight (0.455) followed by pedicel length (0.164), however, negative indirect effect via plant height (-0.182) affected the total association to some extent. At genotypic level also, it

exhibited low positive direct effect (0.098). Indirect effects via number of fruits per plant (0.578), pericarp thickness (0.293), average fruit weight (0.226) and pedicel length (0.221) were positive, whereas negative indirect effects were displayed via plant height (-0.338), number of pickings (-0.251) and fruit diameter (-0.214).

The phenotypic association between plant survival and fruit diameter was significant and negative (-0.892). Direct effect of fruit diameter was positive but of very low magnitude (0.007) and indirect effects via majority of the characters were negative being highest in average fruit weight (-0.762) followed by pedicel length (-0.129), however, positive indirect effects via plant height (0.129) and yield per plant (0.120) affected the total association to some extent. Its direct effect was also positive at genotypic level (0.326). The major portion of the association was due to negative indirect effects via number of fruits per plant (-0.654), pericarp thickness (-0.332), average fruit weight (-0.373), days to 50 per cent flowering (-0.252) and pedicel length (-0.170). However, these effects were counteracted by the positive indirect effects via plant height (0.240), yield per plant (0.233) and number of pickings (0.221).

The correlation between pedicel length and plant survival was significant and positive (0.731) and its direct effect was also positive (0.195) at phenotypic level. Maximum positive indirect effect was displayed via average fruit weight (0.466), but negative indirect effect via plant height (-0.165) counteracted this effect to some extent. The indirect effects via other traits were of low magnitude. At genotypic level also, the direct effect was positive (0.246) and indirect effects via majority of the traits were almost similar to those observed at phenotypic level (Table 4.29).

At phenotypic level, the association between plant survival and pericarp thickness was significant and negative (-0.670) and its direct effect was also negative (-

0.125). Indirect effects via majority of the characters were negative being highest in average fruit weight (-0.555) followed by pedicel length (-0.130). Indirect effects were positive via plant height (0.140) and yield per plant (0.134). The indirect effects via other traits were of low magnitude. At genotypic level, the direct effect was also negative (-0.401). Negative indirect effects were displayed through number of fruits per plant (-0.445), average fruit weight (-0.285), days to 50 per cent flowering (-0.272) and pedicel length (-0.179). Positive indirect effects via plant height (0.272), fruit diameter (0.269), yield per plant (0.268) and number of pickings (0.204) counteracted the negative effects.

The association between plant survival and number of fruits per plant was highly significant and positive (0.917), the direct effect was also positive but of very low magnitude (0.062). The maximum positive indirect effect was contributed via average fruit weight (0.689) followed by pedicel length (0.135). However, at genotypic level, the direct effect was quite high (0.779) and contributed mainly for total association. The indirect effects via average fruit weight (0.335), pericarp thickness (0.229), pedicel length (0.179) and branches per plant (0.138) were positive, whereas these effects were negative via fruit diameter (-0.273), number of pickings (-0.271) and plant height (-0.254).

Phenotypic correlation coefficient between plant survival and average fruit weight was significant and negative (-0.920). Partitioning of the total association revealed that its direct effect was also negative and of higher magnitude (-0.796) and constituted the major proportion of association. The indirect effects via most of other characters were of lower magnitude. At genotypic level, the direct effect was also negative (-0.385) and negative indirect effects via number of fruits per plant (-0.678), pericarp thickness (-0.298), days to 50 per cent flowering (-0.218) and pedicel length (-

0.150) mainly contributed to the negative association. However, positive indirect effects via fruit diameter (0.316), yield per plant (0.220), number of pickings (0.216) and plant height (0.206) counteracted the negative effects at genotypic level (Table 4.29).

The phenotypic association between plant survival and yield per plant was negative (-0.319), while the direct effect was positive (0.204). The maximum negative indirect effect was contributed via average fruit weight (-0.445) and the indirect effects via most of other characters were of lower magnitude. At genotypic level, the direct effect was also positive (0.390) and negative indirect effects via days to 50 per cent flowering (-0.339), pericarp thickness (-0.276) and average fruit weight (-0.217) were the main contributors of negative association, whereas the indirect effect via fruit diameter (0.194) was positive.

Association between number of pickings and plant survival was significant and positive (0.681) at phenotypic level. On the split-up of the total association, positive direct effect of low magnitude (0.084) was observed. The indirect effects via other traits were also of low magnitude except average fruit weight (0.456) and pedicel length (0.116). At genotypic level, the direct effect was negative (-0.289). The major portion of the association was due to positive indirect effects via number of fruits per plant (0.731), average fruit weight (0.287), pericarp thickness (0.284), pedicel length (0.197), branches per plant (0.150) and days to 50 per cent flowering (0.102). These effects were counteracted up-to some extent by the negative indirect effects via plant height (-0.312) and fruit diameter (-0.249).

At phenotypic level, branches per plant had positive and low magnitude of direct effect (0.029). Indirect effects via most of the traits were of low magnitude except average fruit weight (0.158). Direct effect of branches per plant was positive (0.212) at

genotypic level also. Indirect effects via number of fruits per plant (0.505) followed by average fruit weight (0.156) contributed mainly for total association, whereas negative indirect effects via number of number of pickings (-0.205) and days to first picking (-0.109) affected the total association to some extent.

The correlation between plant height and plant survival was significant and positive (0.647), but its direct effect was negative (-0.200) at phenotypic level. The major portion of association was contributed by the indirect effects via average fruit weight (0.451) followed by pedicel length (0.161). At genotypic level, the direct effect was also negative (-0.356). Positive indirect effects via number of fruits per plant (0.556), pericarp thickness (0.307), average fruit weight (0.223), pedicel length (0.219) and days to 50 per cent flowering (0.119) were the major contributors to the total association, however, negative indirect effects via number of pickings (-0.254) and fruit diameter (-0.219) counteracted the positive effects.

4.4 ESTIMATION OF HETEROSIS AND GENERATION MEANS

4.4.1 Heterosis

Estimates of generation means with respect to six crosses studied for various characters are given in Appendices III to XXIV. Perusal of mean values of parents and F_1s revealed the presence of heterosis for various traits under study. In the present study, no single cross could exhibit simultaneously significant desirable heterosis for all the characters. The estimates of extent of heterosis in F_1 generations of six crosses for morphological and biochemical traits are given in Tables 4.30 and 4.31, respectively and their trait-wise description is as under:

4.4.1.1 Days to 50 per cent flowering

Heterosis in the negative direction is desirable for this trait. Heterosis varied from -3.56 (PBC-631 x YW) to -0.33 per cent (PBC-631 x CW) over better parent and -1.63 (YW x CW) to 3.17 per cent (IHR-546 x PBC-631) over standard check. Only one cross (PBC-631 x YW) showed significant negative heterosis over better parent.

4.4.1.2 Days to first picking

Early maturing strains are of immense value in catching early market. Hence for this trait also, the interest of the breeder lies in search of combination having negative heterosis. The range of heterosis over better parent and standard check

varied from -7.72 (IHR-546 x YW) to -1.23 per cent (PBC-631 x YW) and -8.63 (IHR-546 x YW) to -1.18 per cent (PBC-631 x YW), respectively.

All the crosses except PBC-631 x YW displayed significant negative heterosis over better parent as well as standard check.

4.4.1.3 Fruit length

The magnitude of heterosis for this character varied from 8.21 (PBC-631 x YW) to 30.23 per cent (IHR-546 x YW) over better parent and from 12.65 (YW x CW) to 75.30 per cent (IHR-546 x PBC-631) over standard check.

All the crosses exhibited desirable significant heterosis over better parent as well as standard check.

4.4.1.4 Fruit diameter

Heterosis over better parent for this trait ranged from -48.08 (PBC-631 x CW) to 9.70 per cent (IHR-546 x PBC-631), whereas heterosis over standard check ranged from -53.04 (IHR-546 x PBC-631) to 5.27 per cent (YW x CW).

None of the hybrids exhibited desirable significant positive heterosis over better parent as well as over standard check for this trait except IHR-546 x PBC-631, which showed significant positive heterosis (9.70 per cent) over better parent.

4.4.1.5 Pedicel length

A long slender pedicel is desirable to allow for expansion of the developing fruit, especially of large-fruited bell peppers. A short pedicel on a determinate plant results in many deformed fruits. The range of heterosis over better parent and standard check varied from 0.49 (IHR-546 x PBC-631) to 28.52 per cent (IHR-546 x YW) and 5.98 (YW x CW) to 64.94 per cent (PBC-631 x YW), respectively.

Only two crosses (IHR-546 x CW and IHR-546 x YW) showed significant positive heterosis over better parent, whereas all the crosses except YW x CW displayed significant standard heterosis.

4.4.1.6 Pericarp thickness

Heterosis range varied from -14.71 (PBC-631 x YW) to 0.00 per cent (YW x CW) and -27.78 (IHR-546 x PBC-631) to 0.00 per cent (YW x CW) over better parent and standard check, respectively.

None of the crosses was able to display heterosis in desirable direction.

4.4.1.7 Number of fruits per plant

The range of heterosis for this trait varied from 18.70 (YW x CW) to 46.25 per cent (PBC-631 x YW) and 18.70 (YW x CW) to 181.16 per cent (PBC-631 x YW) over better parent and standard check, respectively.

All the crosses exhibited significant heterobeltiosis as well as standard heterosis for this trait.

4.4.1.8 Average fruit weight

Heterosis over better parent for average fruit weight ranged from -57.10 (PBC-631 x YW) to 15.32 per cent (IHR-546 x PBC-631), whereas heterosis over standard check varied from -62.29 (IHR-546 x PBC-631) to 8.19 per cent (YW x CW).

Only two crosses *viz.,* IHR-546 x PBC-631 and YW x CW showed desirable significant heterobeltiosis, whereas only one cross i.e. YW x CW displayed significant standard heterosis for this character.

4.4.1.9 Yield per plant

The magnitude of heterosis for this important character varied from 10.23 (IHR-546 x CW) to 61.70 per cent (IHR-546 x PBC-631) over better parent and from -3.59 (IHR-546 x PBC-631) to 28.63 per cent (YW x CW) over standard check.

All the crosses exhibited significant heterobeltiosis as well as standard heterosis except IHR-546 x PBC-631, which displayed negative standard heterosis for this trait.

4.4.1.10 Number of pickings

Higher the number of pickings more will be the yield, so heterosis in positive direction is desirable for this character. The range of heterosis for this trait was between 3.23 (IHR-546 x CW and IHR-546 x YW) to 10.85 per cent (PBC-631 x YW) and 8.11 (YW x CW) to 29.73 per cent (PBC-631 x YW) over better parent and standard check, respectively.

None of the crosses except PBC-631 x YW was able to display significant positive heterosis over better parent, whereas all the crosses exhibited significant positive standard heterosis for this trait.

4.4.1.11 Branches per plant

Heterobeltiosis for this character ranged from 1.32 (PBC-631 x CW) to 8.56 per cent (PBC-631 x YW) and standard heterosis from 1.32 (PBC-631 x CW) to 9.26 per cent (IHR-546 x PBC-631). Only PBC-631 x YW exhibited positive significant heterobeltiosis for this trait.

4.4.1.12 Plant height

Heterosis range varied from 3.64 (IHR-546 x PBC-631) to 17.56 per cent (IHR-546 x YW) and 4.43 (IHR-546 x CW) to 42.57 per cent (PBC-631 x YW) over better parent and standard check, respectively.

Four crosses over better parent and all the crosses over standard check exhibited significant positive heterosis for this trait.

4.4.1.13 Ascorbic acid content

The magnitude of heterosis for this character varied from -5.57 (IHR-546 x YW) to 1.22 per cent (IHR-546 x PBC-631) over better parent and from 2.67 (YW x CW) to 34.23 per cent (IHR-546 x PBC-631) over standard check.

None of the crosses exhibited desirable significant heterosis over better parent but all the crosses except YW x CW displayed standard heterosis for this trait.

4.4.1.14 Total soluble solids

Heterobeltiosis for this character ranged from -4.42 (IHR-546 x PBC-631) to 3.20 per cent (PBC-631 x CW) and standard heterosis from -10.98 (IHR-546 x PBC-631) to 3.20 (PBC-631 x CW) per cent.

None of the crosses displayed desired significant heterosis over better parent as well as standard check.

4.4.1.15 Total sugars

Heterobeltiosis for this trait ranged from -17.22 (IHR-546 x CW) to 2.46 per cent (IHR-546 x PBC-631), whereas heterosis over standard check ranged from -27.52 (IHR-546 x PBC-631) to 2.38 per cent (YW x CW).

None of the crosses exhibited significant desirable heterosis over better parent as well as over standard check for this trait.

4.4.1.16 Reducing sugars

The magnitude of heterosis for this character varied from -9.44 (IHR-546 x YW) to 14.16 per cent (IHR-546 x PBC-631) over better parent and from -15.38 (IHR-546 x PBC-631) to 15.24 per cent (YW X CW) over standard check.

Three crosses over better parent and only two over standard check (California Wonder) displayed significant desirable heterosis for this trait.

4.4.1.17 Non-reducing sugars

The magnitude of heterosis for non-reducing sugars varied from -38.64 (IHR-546 x CW) to 10.23 per cent (PBC-631 x YW) over better parent and from -47.62 (IHR-546 x PBC-631) to -17.68 per cent (PBC-631 x CW) over standard check.

None of the crosses exhibited significant positive heterobeltiosis as well as standard heterosis except PBC-631 x YW, which displayed significant and positive heterobeltiosis for this trait.

4.4.1.18 Total phenols

The range of heterosis for total phenols was between -14.64 (PBC-631 x CW) to 0.96 per cent (IHR-546 x YW) and -2.15 (YW x CW) to 27.91 per cent (PBC-631 x YW) over better parent and standard check, respectively.

None of the crosses over better parent while all the crosses except YW x CW over standard check exhibited significant positive heterosis for this trait.

4.4.1.19 Ortho dihydroxy phenols

Heterosis over better parent for this trait ranged from -28.35 (PBC-631 x CW) to 6.81 per cent (IHR-546 x CW) whereas heterosis over standard check ranged from 2.48 (YW x CW) to 49.41 per cent (IHR-546 x PBC-631).

None of the crosses showed desirable significant heterobeltiosis whereas all the crosses except YW x CW displayed significant positive standard heterosis for this character.

4.4.1.20 Total free amino acids

The magnitude of heterosis for total free amino acids varied from -10.83 (YW x CW) to -1.47 per cent (IHR-546 x CW) over better parent and from -10.83 (YW x CW) to 14.89 per cent (PBC-631 x CW) over standard check.

None of the crosses exhibited desirable significant heterosis over better parent whereas three crosses displayed positive significant heterosis over standard check for this trait.

4.4.1.21 Peroxidase (PO) activity

Heterobeltiosis for this trait ranged from -8.53 (PBC-631 x CW) to 6.87 per cent (IHR-546 x YW) whereas standard heterosis ranged from 9.86 (YW x CW) to 34.09 per cent (IHR-546 x YW).

Only three crosses over better parent whereas all the crosses over standard check exhibited desirable significant heterosis for this trait.

4.4.1.22 Polyphenol oxidase (PPO) activity

Heterosis for this trait varied from -5.41 (IHR-546 x PBC-631) to 5.30 per cent (YW x CW) over better parent and 7.97 (YW x CW) to 22.46 percent (IHR-546 x CW) over standard check.

None of the crosses showed desirable significant heterobeltiosis whereas all the crosses displayed significant positive standard heterosis for this character.

CHAPTER V

DISCUSSION

The understanding of inheritance of disease and genetic architect of the important economic traits is very essential for formulating a systematic breeding programme for developing resistant variety with desirable horticultural traits. Besides the presence of additive [d] and dominance [h] gene effects, estimation of relative magnitude and type of epistasis is also important to determine the breeding strategy to be used in handling the segregating population for the development of better cultivars. The estimates of only main gene effects and formulating a breeding programme, presuming that epistasis is absent or negligible, will not only be misleading, but will vitiate the estimation of genetic variation. The present investigation was, therefore, undertaken to ascertain the genetics of bacterial wilt resistance, to understand the gene effects ([d], [h], [i], [j], and [l]) governing various morphological and biochemical traits, to assess the association of these parameters with resistance to bacterial wilt, and to study the extent of heterosis involving diverse parents of sweet pepper. The results obtained on these aspects have been discussed in the light of available literature and to suggest an appropriate breeding methodology for the genetic improvement of sweet pepper.

5.1 GENETICS OF BACTERIAL WILT RESISTANCE

Bacterial wilt (a serious soil borne disease) in capsicum has become a devastating problem in India (Gopalakrishnan and Peter, 1991). Yield losses up to 100 per cent have been reported in wilt prone areas of the world (Wang *et al.,* 1997). The disease has also become endemic in Himachal Pradesh, causing losses up to 100 per cent in several

districts of the state (Sood and Singh, 1993; Gupta *et al.,* 1998). Cultural practices and chemicals, if judiciously used, can reduce disease incidence and severity, but alone are expensive and ineffective. The use of resistant varieties is the most simple, effective and widespread method of disease control as well as core of integrated management strategies (Wang *et al.,* 1996). Thus, it becomes imperative to study the genetics of bacterial wilt and the results pertaining to this aspect are discussed here under:

The plant survival in the bacterial wilt resistant parents *viz.,* PBC-631 and IHR-546 were 98.95 and 82.80 per cent, respectively, which indicated 16.32 per cent variation within this group itself. On the other hand, complete susceptibility was observed in the commercial varieties California Wonder (CW) and Yolo Wonder (YW) where not even a single plant could survive till 90 DAT (days after transplanting). The plant survival in the F_1 progenies of PBC-631 x CW and PBC-631 x YW were 96 per cent on account of mortality of one plant in each cross. The F_1 hybrids involving resistant parent IHR-546 with California Wonder and Yolo Wonder had 100 and 88 per cent plant survival, respectively, whereas no plant could survive in the F_1 progenies involving susceptible parents. However, the plant survival was cent per cent in the F_1 involving the resistant parents. This implied that the resistance was dominant in nature and the degree varied from incomplete to complete dominance depending upon not only the resistant, but also the susceptible parents.

The plant survival in F_2, B_1 and B_2 generations of the cross involving resistant parents PBC-631 and IHR-546 were 82.71, 82.05 and 93.65 per cent. Whereas, in F_2, B_1 and B_2 progenies of the cross YW x CW, no plant could survive up to 90 DAT. However, appreciable segregation was observed in F_2 and back cross progenies of resistant x susceptible crosses. In PBC-631 x CW, PBC-631 x YW and IHR-546 x CW the

segregation of F_2s was in the ratio of 3(R):1(S) which suggested monogenic inheritance of resistance in these crosses. This was further confirmed by the test cross ratio of 1(R):1(S) in B_2s in all the three crosses. In the cross IHR-546 x YW, the segregation in F_2 and test cross (B_2) progenies did not fit to mono or di-genic ratios as only 47.84 and 44.07 per cent plants could survive till 90 DAT. Single dominant gene for resistance to bacterial wilt has also been reported in tomato (Tikoo *et al*., 1974; Mahir *et al.,* 1992 and Grimault *et al*., 1995) and brinjal (Chaudhary and Sharma, 1999 and Chaudhary, 2000).

In literature, variable reports on the genetics of bacterial wilt resistance in various solanaceous vegetable crops have been reported. Depending upon the source of resistance and progenies studied in capsicum, the resistance has been reported to be digenic recessive in nature (Thakur, 1990) and controlled by two to five genes with additive effects (Lafortune *et al.,* 2005). The parental lines used in this study were different from those of earlier workers and this variation along with differences in the strains of the pathogen and different environmental conditions of study may perhaps be the reason for the difference in results. Similarly, the resistance has been reported to be poly-genic (Nelson, 1974), monogenic dominant and incompletely dominant (Peter *et al*., 1992), digenic with dominant and recessive epistasis (Vidyasagar, 1998) and partially recessive with incomplete dominance towards susceptibility (Monma and Sakata, 1992 and Monma *et al.,* 1997) in tomato. Chaudhary (2000) has reported variable segregation patterns ranging from monogenic dominant and recessive to inhibitory type in different cross-combinations of brinjal while Gopalakrishnan *et al.* (2002) have revealed monogenic and incompletely dominant inheritance of susceptibility over resistance in brinjal.

In the present investigation, it could be inferred that the bacterial wilt resistant parents used in this study carried gene(s) which were dominant in nature as evident from the resistant F_1s of all the crosses involving susceptible and resistant parents. The plant survival in F_1s ranged from 88 to 100 per cent. However, it was not possible to explain the segregation observed in F_2 and test cross progeny (B_2) of IHR-546 x YW. This might be on account of the fact that bacterial wilt management through host resistance becomes complicated by the wide variability in the pathogen, which is poorly understood in Himachal Pradesh till date (Tripathi, 2004). It shall, therefore, be more appropriate to carry out the genetics of resistance studies under controlled conditions and inoculating the plants with known strain(s) of the pathogen so as to have accurate information. Nonetheless, the present investigation suggests that the resistant sources (PBC-631 and IHR-546) can further be used to develop resistant F_1 hybrids as they expressed complete or near complete dominance in combination with the susceptible commercial varieties California Wonder and Yolo Wonder. Since, the fruits of resistant F_1s were not bell shaped or blocky as preferred by consumers, repeated back crossing with commercial cultivars accompanied by selection for bacterial wilt resistance would be useful to improve the fruit shape. These resistant parents can also be used in recombination breeding to evolve bacterial wilt resistant, high yielding and horticulturally desirable pure line varieties.

5.2 GENETICS OF MORPHOLOGICAL AND BIOCHEMICAL TRAITS

The decision regarding selection of suitable breeding methodology for a purposeful management of genetic variability generated through the hybridization programme would largely depend on the nicking ability and practical utility of the parents in a cross and the genetic architecture of economic traits under consideration (Sprague, 1966). For proper

understanding of gene action governing quantitative and qualitative traits, various mating designs have been developed by various workers. Some of the commonly used approaches like diallel and line x tester do not provide the estimates of non-allelic interactions (epistasis). Generation mean analysis enables the gene action to be analysed crosswise and provides information on non-allelic interactions as well. The present investigations were, therefore, planned to derive information on the nature and magnitude of generation means and gene effects for various quantitative and qualitative traits in sweet pepper. The significant estimates of gene effects and genic interactions are presented in Table 5.1 and the results obtained have been discussed as follows:

Earliness is a highly desirable attribute in capsicum in the sense that the prevailing prices in the market are invariably higher early in the season and thus brings lucrative returns to the farmers. For days to 50 per cent flowering, the non-significant estimates of A, B, C and D scaling tests along with χ^2 values in crosses *viz.,* PBC-631 x YW, IHR-546 x YW, YW x CW and IHR-546 x PBC-631 suggested the absence of non-allelic interactions. Similarly, Chung *et al.* (1979) have also observed epistasis for days to first flower. Also, the dominance gene effects were in desirable (negative) direction in these crosses. These findings substantiate the findings of Echeverri *et al.* (1999). In the cross PBC-631 x CW, the presence of duplicate type of epistasis along with positive dominance and additive x additive genic effects suggested that the selection for early flowering segregants should be carried out in later generations. However, in IHR-546 x CW, the dominance and additive x additive genic effects were in desirable direction coupled with presence of duplicate type of interaction suggesting the

scope of hybrids as well as reciprocal recurrent selection and biparental mating followed by selection in getting desirable segregants in subsequent generations.

For days to first picking, fitting of additive dominance model was displayed in PBC-631 x CW and PBC-631 x YW. All the crosses except IHR-546 x YW and YW x CW displayed dominance gene effects in the desirable direction indicating the effectiveness of heterosis breeding in these crosses. The cross IHR-546 x PBC-631 also showed negative additive x additive genic effects along with duplicate type of gene action suggesting the scope of hybrids as well as reciprocal recurrent selection and biparental mating followed by selection in getting desirable segregants. These results also corroborate the findings of Ahmed *et al.* (1982) and Miranda *et al.* (1988), who have also reported the importance of non-additive gene action for early yield. In IHR-546 x YW and YW x CW, the dominance x dominance interaction was in negative direction, which further indicates the importance of heterosis breeding for getting desirable segregants.

The negative additive x additive gene interaction in IHR-546 x CW and YW x CW revealed the importance of simple pedigree selection.

Additive dominance model was adequate to explain the variation for fruit length in PBC-631 x YW only. Joshi (1989) has also observed epistasis for fruit length. Dominance component was positive in crosses *viz.,* PBC-631 x YW and IHR-546 x YW indicating the usefulness of heterosis breeding. In PBC-631 x CW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631, dominance x dominance component was positive and of higher magnitude, which also suggests the importance of heterosis breeding. In the cross IHR-546 x YW, duplicate type of epistasis was present indicating to defer the selection in the later generations.

Epistasis was present in all the crosses for fruit diameter. All the crosses except PBC-631 x YW had opposite signs of [h] and [l] revealed the presence of duplicate type of gene action. In such situations maximum gain could be obtained by maintaining heterozygosity through mating of selected parents in early segregating generations. In the cross PBC-631 x YW, additive gene effect was negative and additive x additive [i] in positive direction further advocating to defer selection for improving fruit diameter. However, significant Chi-square value in IHR-546 x CW indicated the presence of higher order interactions.

All the crosses showed inter-allelic interactions for pedicel length also. The crosses *viz.,* PBC-631 x CW, PBC-631 x YW, IHR-546 x YW and IHR-546 x PBC-631 showed pronounced dominance gene effects for this trait as evident from their significant dominance or dominance x dominance gene effects signifying the effectiveness of heterosis breeding. However, Milkova (1981) has reported additive gene action for this trait. In PBC-631 x YW, additive x dominance gene effect was negative, whereas

duplicate type of interaction was present in IHR-546 x CW revealing the importance of reciprocal recurrent selection and biparental mating followed by selection. In crosses *viz.,* PBC-631 x CW, YW x CW and IHR-546 x PBC-631, additive gene effects were also present showing the usefulness of simple pedigree selection.

For pericarp thickness, epistasis was present only in two crosses *viz.,* PBC-631 x YW and IHR-546 x PBC-631. Chung *et al.* (1979) and Joshi (1989) have also reported epistasis for this trait. All the crosses recorded the presence of additive gene effects in the undesirable (negative) direction suggesting to defer the selection in the later generations for getting improved pericarp thickness. In PBC-631 x YW, duplicate type of epistasis and in IHR-546 x PBC-631 negative additive x additive gene effects were observed which also indicate the usefulness of delaying the selection to later generations. However, Thakur *et al*. (1987) have reported both additive as well as non-additive gene action for pericarp thickness.

High yield is the basic objective of all the crop improvement programmes. It is of immense importance to develop a genotype, which has a potential to surpass the commercial cultivar(s) otherwise it will achieve little or no success even if it has excellent quality and resistance to various pests. Number of fruits per plant and average fruit weight has direct bearing on yield. For number of fruits per plant, epistasis was observed in all the crosses except IHR-546 x PBC-631. These results are in line with those of Ahmed *et al.* (1982), Joshi (1989) and Chaim and Paran (2000). Dominance and non-additive gene effects were recorded in all the crosses indicating the importance of heterosis breeding for getting increased number of fruits per plant. However, duplicate type of interaction along with dominance gene effects was observed in IHR-546 x YW.

The importance of both additive and dominance gene effects has been reported by Sood and Kaul (2006a).

Additive dominance model was adequate only in YW x CW for average fruit weight indicating the presence of epistasis in rest of the crosses. Significant negative additive gene effects [d] were observed in all the crosses except IHR-546 x PBC-631, but had positive additive x additive gene effects suggesting the scope of improving this trait through delayed selection. However, additive x dominance effects [j] were predominantly positive in all the crosses except YW x CW and IHR-546 x PBC-631. In YW x CW and IHR-546 x PBC-631, dominance gene effects were pronounced along with additive x additive gene effects in the latter cross only advocating the importance of both non-additive as well as additive gene action. These results have corroborated the findings of Thakur *et al.* (1987) and Sood and Kaul (2006a).

A significant contribution of epistasis in controlling the inheritance of yield per plant was observed in all the crosses, which was reflected from the significance of scaling tests. Epistasis for yield has also been reported by Chung *et al*. (1979), Joshi (1989) and Echeverri *et al.* (1999). The results of six parameter model for yield per plant revealed that dominance gene effects [h] were significant in all the crosses except PBC-631 x YW. However, PBC-631 x YW displayed significant dominance x dominance [l] effect of higher magnitude. Complimentary type of gene action, as evident from the positive sign of [h] and [l] components, was noticed in IHR-546 x YW suggesting to exploit heterosis in this cross. Duplicate epistasis was noticed in two crosses namely, IHR-546 x CW and IHR-546 x PBC-631, which was evident from the opposite signs of dominance and dominance x dominance interactions. In view of the presence of duplicate epistasis, the successful breeding method will be the one which can mop up

the genes to form superior gene constellations interacting in a favourable manner. Some forms of recurrent selection namely, diallel selective mating or biparental mating in early segregating generations might prove to be effective alternative approaches (Shekhawat *et al.*, 2006). The predominance of non-additive gene action has also been reported by Miranda *et al.* (1988) and Echeverri *et al.* (1999), whereas Thakur *et al.* (1987) and Sood and Kaul (2006a) reported the importance of both additive as well as non-additive gene action for yield per plant.

The estimates of simple and joint scaling tests suggested the presence of non-allelic interactions for the inheritance of number of pickings in PBC-631 x CW, PBC-631 x YW and IHR-546 x YW, whereas the other three crosses exhibited the fitness of additive–dominance model. The significant and positive additive component [d] in four crosses *viz*., PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and IHR-546 x YW along-with the presence of positive additive x additive gene action in these crosses except IHR-546 x CW showed the presence of increaser alleles and associated pair of genes. These results advocated that the increased manifestation can be achieved through simple selection. Dominance component [h] was equally important in all the crosses except IHR-546 x PBC-631, which also revealed the effectiveness of heterosis breeding.

For number of branches per plant, only IHR-546 x CW and IHR-546 x YW exhibited the presence of non-allelic interaction. Dominance component [h] was found to be significant and positive in PBC-631 x CW, PBC-631 x YW and IHR-546 x PBC-631, which reveals the effectiveness of heterosis breeding for this trait. Duplicate type of epistasis was observed in IHR-546 x YW.

The estimates of simple and joint scaling tests suggested the presence of non-allelic interactions for the inheritance of plant height in PBC-631 x CW, PBC-631 x YW

and IHR-546 x YW. The dominace component [h] was significant for plant height in PBC-631 x CW, IHR-546 x CW, YW x CW and IHR-546 x PBC-631, while the cross combinations PBC-631 x YW and IHR-546 x YW exhibited the presence of additive x dominance and dominance x dominance components, which also indicate the importance of heterosis breeding. These results corroborate the findings of Miranda *et al.* (1988).

A significant contribution of epistasis was observed in controlling the inheritance of ascorbic acid content in all the cross combinations except IHR-546 x PBC-631. In crosses PBC-631 x CW, PBC-631 x YW and YW x CW, the additive component [d] was positive and significant, but the additive x additive [i] gene interactions indicated the presence of decreaser alleles thereby suggesting to delay the selection for desirable recombinants in the later generations. In the cross IHR-546 x CW, additive x dominance [j] was negative, which also suggested to delay selection, whereas IHR-546 x YW revealed duplicate type of gene interaction. IHR-546 x PBC-631 exhibited dominance [h] component suggesting the usefulness of heterosis breeding in this particular cross.

For total soluble solids (TSS), epistasis was present only in PBC-631 x CW, PBC-631 x YW and IHR-546 x YW as evident from the significant estimates of either A, B, C or D scales. All the crosses except YW x CW exhibited the presence of negative additive gene effects, which suggested that selection in early generations will be a futile exercise. In PBC-631 x CW and IHR-546 x CW, dominance and dominance x dominance components were observed, which also revealed the importance of heterosis breeding. However, in the cross PBC-631 x YW, duplicate type of interaction was also present.

Epistasis contributed significantly for controlling the inheritance of total sugars, reducing sugars as well as non-reducing sugars in all the cross combinations, which was

evident from the significance of scaling tests in all the crosses. For total sugars, additive genic effects were negative in all the crosses, which indicated no scope of improvement in early generations. Crosses *viz.,* PBC-631 x CW, PBC-631 x YW and YW x CW exhibited the presence of duplicate type of gene interaction. The presence of duplicate epistasis will decrease variation in F_2 and will also hinder the pace of progress through selection. Therefore, targeting of transgressive segregants in the later generations may be effective for selection of plants with high sugar content. Further, PBC-631 x CW, IHR-546 x CW, IHR-546 x YW and YW x CW exhibited significant Chi-square values indicating the presence of higher order interactions.

For reducing sugars, all the crosses except YW x CW exhibited the negative estimates of both additive as well as additive x additive gene effects. Significant Chi-square value of IHR-546 x CW indicated the presence higher order interactions. In addition, YW x CW displayed the presence of duplicate type of gene action. For non-reducing sugars, cross combinations PBC-631 x CW, IHR-546 x CW, IHR-546 x YW and YW x CW exhibited duplicate type of epistasis signifying to adopt reciprocal recurrent selection and biparental mating followed by selection. However, Chi-square was significant in PBC-631 x CW revealing the presence of higher order interactions.

Three crosses (PBC-631 x CW, IHR-546 x YW and IHR-546 x PBC-631) for total phenols and two (PBC-631 x CW and PBC-631 x YW) for ortho dihydroxy phenols exhibited the presence of non-allelic interaction. For total phenols, additive component [d] was found to be significant in PBC-631 x CW, PBC-631 x YW and IHR-546 x CW suggesting that simple selection will be useful for the improvement of this trait. Whereas, IHR-546 x YW had positive additive gene effect, but exhibited negative additive x additive as well as negative additive x dominance interaction thereby referring to delay

the selection in this cross. PBC-631 x CW recorded significant Chi-square value, whereas duplicate type of epistasis was observed in IHR-546 x PBC-631.

For ortho dihydroxy phenols, the cross combinations IHR-546 x CW, IHR-546 x YW and IHR-546 x PBC-631 exhibited significant dominance [h] estimates which pointed towards the effectiveness of heterosis breeding in these crosses. Positive additive [d] was noticed for PBC-631 x CW and PBC-631 x YW, though the latter cross exhibited negative additive x additive gene interaction. This implies that the selection in early generations can be fruitful in the former cross combination.

For total free amino acids, epistasis was observed in PBC-631 x YW, IHR-546 x YW and YW x CW. Additive component was significant and positive in PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and IHR-546 x YW along with dominance [h] component except in IHR-546 x CW. YW x CW exhibiting negative additive gene effect with positive additive x additive and additive x dominance gene interactions pointed towards the effectiveness of delaying selection. However, IHR-546 x YW exhibited significant Chi-square value indicating the presence of higher order interactions.

Estimates of simple scaling tests were significant in all the crosses except PBC-631 x YW for peroxidase activity, whereas for polyphenol oxidase activity these estimates were significant only in PBC-631 x YW and IHR-546 x YW indicating the presence of non-allelic interactions. For peroxidase activity, additive gene effects were found to be significant and positive in PBC-631 x CW and PBC-631 x YW indicating thereby the effectiveness of simple selection. Cross combinations IHR-546 x CW and IHR-546 x YW, though had positive additive gene effects, but preponderance of dominance x dominance gene interactions suggested to defer the selection to later

generations. Duplicate type of gene action was recorded in YW x CW, whereas IHR-546 x CW displayed significant Chi-square value.

For polyphenol oxidase activity, the importance of both additive and dominance genic effects were observed for PBC-631 x CW, PBC-631 x YW, IHR-546 x CW and IHR-546 x YW indicating the usefulness of simple selection as well as heterosis breeding. Recurrent selection would also be suitable breeding procedure to exploit both types of gene action as both dominance and additive effects are significant. On the other hand, YW x CW and IHR-546 x PBC-631 exhibited the significance of dominance and additive gene effects, respectively.

Present study suggests that the nature and magnitude of gene effects controlling the inheritance of various morphological and biochemical characters varied with the breeding material used in different crosses. So, specific breeding strategy has to be adopted for a particular cross to bring about desirable improvement in a particular trait. In some crosses, inbreds can be developed through hybridization following the pedigree method of selection. In other crosses, although high magnitude of dominance gene effects and dominance x dominance interactions were present, but it is difficult to exploit them due to the presence of duplicate epistasis, in such cases, some methods involving repeated crossing like diallel selective or biparental mating can be effectively utilized.

5.3 ASSOCIATION OF BACTERIAL WILT RESISTANCE WITH BIOCHEMICAL AND MORPHOLOGICAL TRAITS

Correlation studies

The correlation studies can prove to be highly useful for selecting characters, which are not easily observed or the genotypic values of which are over-shadowed by the environmental effects. Over the past twenty years, induced disease resistance was demonstrated in a number of plant pathogen systems by using biotic and abiotic inducing agents. The major hallmark of this form of resistance is the ability of the plants to defend themselves against a broad spectrum of pathogens by triggering plant species-specific defense responses (Metraux, 2001). The knowledge of relationship among such attributes particularly in relation to incidence of bacterial wilt and its contributing factors could be valuable in planning an effective and successful breeding programme. In the present study, genotypic correlations in general were found to be higher than the phenotypic correlations, which suggested that there is a strong inherent relationship between the various traits studied.

Ascorbic acid showed significant and positive correlation with plant survival (resistance). Ascorbic acid being a reducing agent is oxidized by ascorbic acid oxidase, thus creating environment for more activity of enzymes like peroxidase (PO) and polyphenol oxidase (PPO). Kumar *et al.* (2002) also reported higher levels of ascorbic acid content in resistant genotypes than susceptible genotypes while studying biochemical assay of bacterial wilt resistance of tomato. Total sugars along with reducing and non-reducing sugars showed significant and negative correlation with plant survival. It might be due to the fact that sugars being direct source of food for the pathogen may have enhancing effect in the growth and establishment of the later in the host. These results substantiated the findings of earlier workers, who have also reported higher levels of sugars in susceptible genotypes than the resistant ones (Chand, 1968; Chand and Walker, 1968; Azad, 1991 and Hegde and Anahosur, 2001)

Phenolic compounds and their precursors are toxic for the invading pathogens, therefore, their higher content in the plants is one of the important components for conferring resistance against the disease (Sindhan and Parashar, 1996). In the present study, total and ortho dihydroxy phenols (OD phenols) were positively associated with plant survival. These phenols as such or after conversion to toxic quinones or their other oxidation products might be responsible for the resistance mechanism in resistant cultivars either by inhibiting the pathogen activity or by reducing its rate of multiplication (Farkas and Kiraly, 1962). Sgarbi *et al.* (2003) have also reported a number of phenols as pre-infection inhibitors, providing the plants with a certain degree of basic resistance against pathogenic microorganisms. These results corroborate the findings of Bhullar *et al.* (1972), Thind *et al.* (1981), Azad (1991), Kumar *et al.* (2002) and Gopalakrishnan *et al.* (2002).

Total free amino acids also showed significant and positive association with plant survival. Amino acids have also been found to induce resistance against pathogens perhaps by distributing normal host protein/phenol metabolism (Papavizas and Davey, 1963). Chand (1968) and Chand and Walker (1968) have also reported changes in amino acids due to bacterial infection.

Certain key enzymes of secondary metabolism such as peroxidase (PO) and polyphenol oxidase (PPO) do not harm micro-organisms directly, but they contribute to the synthesis of secondary metabolites that are harmful for pathogens. In the present study, peroxidase and polyphenol oxidase revealed significant and positive association with plant survival. This association may be attributed to the phenol content of the genotypes, because phenols serve as substrate for peroxidase and polyphenol oxidase

enzymes (Kalia, 1998). The importance of enzymes in imparting disease resistance has also been emphasized by Manibhushanrao *et al*. (1988) and Sheela and Mathew (2002).

Among morphological characters *viz.,* fruit length, pedicel length, number of fruits per plant and number of pickings showed significant and positive correlation with plant survival. This may be on account of the fact that the resistant parents were having higher fruit length, pedicel length, number of fruits per plant and number of pickings. Contrary to this, susceptible genotypes were having blocky fruits with increased fruit diameter, pericarp thickness and average fruit weight, thus these characters revealed negative correlation with plant survival.

Path coefficient studies

The association between the characters, whose degree is being measured does not exist by itself but a complicated interaction pathway is involved in which various other attributes may also take part. Therefore, it would be interesting to study the direct and indirect contribution of each trait towards plant survival (resistance).

The present study revealed that the direct and indirect effects obtained at genotypic level were different from those at phenotypic level, which might be due to varying degree of influence of environment on various traits studied. Therefore, path analysis at phenotypic level may not provide true picture of direct and indirect causes and it would be advisable to understand the contribution of different traits towards plant survival at genotypic level. Plant survival (resistance) was taken as the resultant/dependent variable with rest of the biochemical and morphological characters studied in the present investigation. Among biochemical characters which revealed significant and positive correlation with plant survival, only ascorbic acid content, ortho dihydroxy phenols and polyphenol oxidase activity exhibited positive direct effects at

genotypic level. Whereas, the positive association of total phenols, total free amino acids and peroxidase activity with plant survival was contributed mainly via indirect contribution of ascorbic acid content thereby indicating the importance of ascorbic acid in plant survival. However, total sugars, reducing sugars and non-reducing sugars, which recorded significant and negative correlation with plant survival also revealed negative direct effects at genotypic level. Thus, ascorbic acid content, total sugars, reducing sugars, non-reducing sugars, ortho dihydroxy phenols and polyphenol oxidase activity play an important and crucial role in determining resistance to bacterial wilt. These results substantiated the findings of Azad (1991), Hegde and Anahosur (2001), Gopalakrishnan *et al.* (2002) and Kumar *et al.* (2002).

Among morphological traits which had shown significant and positive association with plant survival, only fruit length, pedicel length and number of fruits per plant showed positive direct effects also, whereas, number of pickings and plant height revealed negative direct effects. Further, it was noticed that their positive associations were mainly contributed by the indirect positive effects via number of fruits per plant.

Among the traits showing significant and negative association with plant survival, only pericarp thickness and average fruit weight showed negative direct effects. On the other hand, fruit diameter showed positive direct effect, however, negative association of this trait was mainly contributed via negative indirect effect of number of fruits per plant and average fruit weight.

5.4 HETEROSIS

The discovery of hybrid vigour by Shull (1908) has led to the development of heterosis breeding, an effective and efficient genetic tool in the hands of a breeder in

improving the yield and component traits of both self as well as cross pollinated crops. Heterosis studies provide information about per cent increase or decrease of F_1 over better parent or the standard check and thus help in pinpointing the best cross(s). Heterosis in desirable direction (hybrid vigour) is the ultimate aim of the breeder. Genetically diverse varieties are the main components of heterosis breeding to observe heterosis in F_1 hybrids. Capsicum has the advantage of producing a sufficient number of seeds in a single cross per fruit and lesser requirement of seeds per unit area. In the present study, no single cross could exhibit simultaneously significant desirable heterosis for all the characters. The results obtained after evaluating the six hybrids developed through hybridization of 4 parents (2 resistant and 2 susceptible to bacterial wilt) are discussed as follows:

Days to 50 per cent flowering and days to first picking are good indices of earliness. Only one cross combination PBC-631 x YW showed heterosis over better parent for days to 50 per cent flowering. Contrary to this, all the crosses except PBC-631 x YW displayed significant heterobeltiosis as well as standard heterosis for days to first picking. Differences in the results of days to 50 per cent flowering and days to first picking implies that there exist genotypic differences in the plant processes after flowering till fruit maturity. Variable magnitude of heterosis for flowering and days to first picking has been reported by Marfutina (1970), Chaim and Paran (2000), Gomide *et al.* (2003) and Sood and Kaul (2006b).

To develop a good looking hybrid/cultivar in bell pepper, it is important to strike a good balance between length and breadth of the fruit. For fruit length, all the crosses exhibited significant heterosis over better parent as well as over standard check. However, only IHR-546 x PBC-631 displayed significant heterobeltiosis, whereas none

of the hybrids recorded significant standard heterosis for fruit breadth. Only YW x CW exhibited bell shaped fruits. When the bell shaped cultivars (CW and YW) were crossed with PBC-631(long paprika fruits), their F_1s had long paprika type fruits and when IHR-546 was crossed either with CW or YW the F_1 fruits were triangular in shape like IHR-546. However, when PBC-631 was crossed with IHR-546 the fruit shape was similar to PBC-631. Heterosis for fruit length as well as fruit diameter has also been observed by Popova (1962), Marfutina (1970) and Mamedov and Pyshnaja (2001).

A long slender pedicel is desirable to allow expansion of the developing fruit, especially large-fruited bell peppers. A short pedicel on a determinate plant results in many deformed fruits. Only two crosses (IHR-546 x CW and IHR-546 x YW) showed significant positive heterosis over better parent, whereas all the crosses except YW x CW displayed significant standard heterosis. These findings are in line with those of Chaim and Paran (2000).

Bell pepper fruits are hollow and hence thicker pericarp not only withstands distant transportation, but also has invariably longer post harvest shelf life. None of the F_1s was able to display significant heterobeltiosis as well as standard heterosis in desirable direction for this trait. However, Mamedov and Pyshnaja (2001) have reported heterosis for pericarp thickness.

Number of fruits per plant and average fruit weight are the most important traits for obtaining higher yield in capsicum (Mishra *et al.,* 2002). All the crosses exhibited significant heterobeltiosis as well as standard heterosis for number of fruits per plant. However, only IHR-546 x PBC-631 and YW x CW showed desirable significant heterobeltiosis, while YW x CW displayed significant standard heterosis for average fruit

weight. These results are in close proximity to those of Marfutina (1970), Mamedov and Pyshnaja (2001), Gomide *et al.* (2003) and Sood and Kaul (2006b).

Higher yield is the prime objective of any breeding programme. All the crosses exhibited significant and positive heterosis over better parent. Similarly, all the crosses displayed standard heterosis in desirable direction except IHR-546 x PBC-631. Heterosis for higher yield has also been reported by Deshpande (1933), Thakur (1987), Kaul and Sharma (1988), Ahmed and Hurra (2000), Pandey *et al.* (2002), Gomide *et al.* (2003) and Sood and Kaul (2006b).

Higher the number of pickings more will be the yield, so heterosis in positive direction is desirable for this character. All the crosses exhibited significant positive standard heterosis for this trait, while only PBC-631 x YW was able to display significant positive heterosis over better parent. For branches per plant, only PBC-631 x YW exhibited significant and positive heterobeltiosis. Joshi (1986) has also reported heterosis for branches per plant.

Since sweet pepper is grown in the mid-hills of Himachal Pradesh during rainy season, taller plants are preferred to prevent fruit rot. Moreover, taller plants also ensure fruiting over a longer period of time. Four crosses over better parent and all the crosses exhibited significant positive economic heterosis for plant height. These results are in line with those of earlier workers (Popova, 1962; Joshi; 1986 and Chaim and Paran, 2000).

All the crosses except YW x CW displayed significant and positive standard heterosis for ascorbic acid content. Average heterosis for ascorbic acid content has also been reported by Pandey *et al.* (2002), while Betlach (1967) couldn’t get heterosis for this trait. None of the crosses displayed heterobeltiosis and economic heterosis for total

soluble solids (TSS) and total sugars. However, three crosses over better parent and two over standard check displayed significant desirable heterosis for reducing sugars. For non-reducing sugars, only PBC-631 x YW recorded significant and positive heterobeltiosis. Contrary to this, Marfutina (1970) has reported appreciable heterosis for sugars in sweet pepper and this may be on account of different genotypes studied in his study.

All the crosses recorded economic heterosis for total and ortho dihydroxy phenols except YW x CW for the former and IHR-546 x CW for the latter trait. Similarly, economic heterosis was displayed by three crosses for total free amino acids, whereas all the crosses exhibited the same for polyphenol oxidase activity. In addition, three crosses recorded significant positive heterobeltiosis for peroxidase activity.

Conclusions and future implications

- Studies on genetics of bacterial wilt resistance revealed that the resistance was dominant in nature and the degree varied from incomplete dominance to complete dominance depending upon not only the resistant parent used, but also the susceptible parent used.
- Single dominant gene was observed to govern bacterial wilt resistance in three crosses *viz.,* PBC-631 x CW, PBC-631 x YW and IHR-546 x CW.
- Since the fruits of most of F_1s were not bell shaped or blocky as preferred by the consumers, therefore, back-cross breeding programme with commercial cultivars accompanied by selection for bacterial wilt resistance is suggested.
- Sufficient genetic variability was generated through hybridization for all the horticultural and quality traits.

- The presence of dominance components for yield per plant in all the crosses along with complementary type of interaction in IHR-546 x YW suggested the exploitation of heterosis for obtaining higher yield.
- For number of fruits per plant, positive dominance components were recorded for most of the cross combinations, which also indicate the importance of exploiting hybrid vigour for this trait.
- For average fruit weight, most of the crosses exhibited negative additive component and positive additive x additive [i] component advocate to delay the selection for improving this trait.
- The nature and magnitude of gene effect varied with different crosses for most of the quantitative as well as qualitative traits. So, specific breeding strategy has to be adopted for a particular cross to get improvement in a particular trait.
- Plant survival exhibited significant and positive correlation with ascorbic acid content, total phenols, ortho dihydroxy phenols, peroxidase and polyphenol oxidase activity, whereas this association was significant and negative with total sugars, reducing sugars and non-reducing sugars.
- On the basis of path analysis, ascorbic acid content, total sugars, reducing sugars, non-reducing sugars, ortho dihydroxy phenols and polyphenol oxidase activity played an important and crucial role in determining the resistance to bacterial wilt.
- YW x CW was found to be the most promising and consistent heterotic combination for yield per plant, number of fruits per plant, average fruit yield per plant, number of pickings and plant height, however, this cross was highly susceptible to bacterial wilt.

CHAPTER - VI

SUMMARY

The present study entitled," **Genetics of bacterial wilt (*Ralstonia solanacearum*) resistance and some quantitative and qualitative traits in sweet pepper"** was aimed to obtain information on the genetics of bacterial wilt resistance, morphological and biochemical traits, to assess the association of these traits with bacterial wilt resistance and to study the extent of heterosis.

To study the genetics of bacterial wilt resistance, six generations (P_1, P_2, F_1, B_1, B_2 and F_2) of six crosses evolved by utilizing two resistant (PBC-631 and IHR-546) and two susceptible parents (California Wonder and Yolo Wonder) were evaluated in a Randomized Block Design in bacterial wilt sick plots with three replications at the experimental farm of Department of Vegetable Science and Floriculture, CSK HPKV, Palampur during summer-rainy, 2006. Sufficient plant population were maintained in different generations. Incidence of bacterial wilt was recorded at weekly intervals upto 90 DAT (days after transplanting).

Generation mean analysis was carried out to estimate the genetics of various morphological and biochemical traits. Six generations (P_1, P_2, F_1, B_1, B_2 and F_2) of six crosses were evaluated in a Randomized Block Design with three replications during summer-rainy, 2006 at the experimental farm HAREC, Bajaura, CSK HPKV. The generation means were used to determine the additive, dominance and epistatic components using the procedure given by Mather (1949) and Hayman and Mather (1955) and a perfect fit solution of Jinks and Jones (1958) and Mather and Jinks (1982). The phenotypic and genotypic coefficients of correlation were computed following Al-

Jibouri *et al.* (1958), whereas the path coefficient analysis of component traits with plant survival were carried out by following Dewey and Lu (1959).

Studies on genetics of bacterial wilt resistance revealed that the resistance was dominant in nature and the degree varied from incomplete dominance to complete dominance depending upon not only the resistant parent used, but also the susceptible parent. Single dominant gene was observed to govern bacterial wilt resistance in PBC-631 x CW, PBC-631 x YW and IHR-546 x CW and the segregation of their test cross (B_2) populations was in the ratio of 1(R) : 1(S).

Results revealed that sufficient genetic variability was generated through hybridization for all the horticultural and quality traits. The presence of dominance components for yield per plant in all the crosses along with complementary type of interaction in IHR-546 x YW suggested the exploitation of heterosis breeding for improving yield per plant. Similarly, positive dominance components were recorded in most of the cross combinations for number of fruits per plant, which further indicate the importance of exploiting hybrid vigour for this trait. However, most of the crosses had negative additive component and positive additive x additive [i] gene interactions suggesting to delay the selection for improving average fruit weight. In the present study, the nature and magnitude of gene effect varied with different crosses for most of the quantitative as well as qualitative traits. So, specific breeding strategy has to be adopted for a particular cross to get improvement. In some crosses, inbreds can be developed through hybridization following the pedigree method of selection. In other crosses, although high magnitude of dominance gene effects and dominance x dominance interactions were present, but it is difficult to exploit them due to the presence of

duplicate epistasis. In such cases, some form of recurrent selection like diallel selective or biparental mating can be effective.

Studies on correlation coefficient indicated that genotypic correlations were higher than the corresponding phenotypic correlations which suggested the existence of inherent association among these traits. Plant survival exhibited significant and positive correlation with ascorbic acid content, total phenols, ortho dihydroxy phenols, peroxidase and polyphenol oxidase activity, whereas this association was significant and negative with total sugars, reducing sugars and non-reducing sugars. However, in path analysis, some of the characters that showed positive or negative correlation were not able to display the corresponding direct effects in same direction. In such traits, majority of the association was contributed via the indirect effect of ascorbic acid content. Thus, on the basis of path analysis, ascorbic acid content, total sugars, reducing sugars, non-reducing sugars, ortho dihydroxy phenols and polyphenol oxidase activity played an important and crucial role in determining the resistance to bacterial wilt.

Studies on extent of heterosis and mean performance revealed that the hybrid YW x CW was the most consistent for yield per plant, number of fruits per plant, average fruit yield per plant, number of pickings and plant height. Although, other hybrids have also exhibited remarkable heterosis for yield per plant and number of fruits per plant, but these hybrids have low average fruit weight and are not bell shaped. Since the fruits of most of F_1s were not bell shaped or blocky as preferred by consumers, so the fruit shape of F_1s can be improved through repeated back crossing with commercial cultivars accompanied by selection for bacterial wilt resistance.