Electronic Journal of Plant Breeding, 9(3): 815-828 (Sep 2018) DOI: 10.5958/0975-928X.2018.00102.3
ISSN 0975-928X

Research Article

Heterosis, combining ability and gene action studies for insect-pest and disease resistance in cucumber

Ramesh Kumar[1], Sandeep Kumar ,[2*], Dharminder Kumar[1] and Sandeep Kansal[1]
[1] Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni-173 230, Solan, HP, India
[2] ICAR-Indian Agricultural Research Institute (IARI) Regional Station, Katrain-175 129 (Kullu Valley), HP, India
E-Mail: sandeepkdhatwalia@gmail.com

(Received: 09 Nov 2017; Revised: 14 Aug 2018; Accepted: 17Aug 2018)

Abstract

The paucity of research pertaining to the heterosis, combining ability, nature of gene action and proportional contribution of lines, testers and their interactions for insect-pest and disease resistance in cucumber motivated us to undertake this study. The experimental material comprised 48 F_1 hybrids, developed by crossing 16 lines (eight gynoecious) with three testers during the year 2011. Parents (16 lines and three testers) and their F_1 48 hybrids, along with two standard checks ("KH-1" and "Pusa Sanyog"), were planted in a Randomized Complete Block Design (RCBD) during the year 2012 for screening against different insect-pest and diseases under natural field conditions. In the present studies, genotypes LC-1-1, LC-2-2, LC-15-5, CGN-20969, CGN-20953, Poinsette and K-75 and crosses LC-1-1 × K-75, LC-15-5 × K-75, LC-3-3 × K-75, CGN-20969 × Japanese Long Green, and CGN-20953 × K-75 were found superior in response to insect-pest and disease incidence. Gene action studies indicated predominant role of non-additive gene action governing all the traits except fruit fly incidence, thereby, indicating usefulness of heterosis for disease resistance breeding in cucumber. Further, proportional contribution of lines was recorded highest for severity of powdery mildew and angular leaf spot, whereas testers were found superlative for fruit fly incidence and severity of downy mildew. Therefore, selection of parents should be done depending upon the trait of interest for resistant hybrid development in cucumber.

Key words
Angular leaf spot, Combining ability, Cucumber, Downy mildew, Fruit fly incidence, Heterosis, Powdery mildew

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops, infected by number of insect-pests and diseases. Extent of yield losses caused by the insect-pests in cucurbitaceous vegetables ranged from 30 to 100 per cent depending upon cucurbit species and the season in different parts of the world (Dhillon *et al.*, 2005). Like other cucurbits, cucumber is also being subjected to damage in India by wide array of insect-pests right from the initial stages of the crop to final harvesting (Ghule *et al.*, 2014). Fruit fly (*Bacrocera cucurbitae* Coq.) is one of the most destructive pests often rendering cultivation of cucumber unprofitable (Chaudhary and Patel, 2012). The fruits are damaged by the maggots of this fly as the female fly lays its eggs in the tissues of fruits. Due to fruit fly infestation, 73.83 per cent damage was reported from cucumber crop (Krishna *et al.*, 2006). Among the various diseases, powdery mildew caused by *Sphaerotheca fuliginea* is one of the most devastating diseases in cucurbits. Crop yield can decline as the disease severity increases. Severe infection by powdery mildew before the flowering stage can reduce the yield of cucumber fruit by 20-40 per cent (Lamsal *et al.*, 2011). Leaf infestation by this pathogen interferes with photosynthesis and respiration, leading to reduced fruit set, inadequate ripening and poor flavour development (McGrath, 1996). On the other hand, downy mildew of cucumber (*Pseudoperonospora cubensis* Rostow.) also causes serious losses under favourable environmental conditions. In many regions of the world having high humidity, it is main limiting factor for cucumber production (Wehner and Shetty, 1997). Downy mildew decreases flower set and fruit development by destroying the foliage (Hashmi, 1994). Besides this, angular leaf spot of cucurbits is caused by *Pseudomonas syringae* pv. *lachrymans* is the most widespread bacterial disease of cucurbits. It has been reported in a wide range of cucurbits throughout the world. Early infection results in significant reduction in the number of fruits and fruit weight. From these reports, it is evident that attack of these insect-pests and diseases is a key factor in reducing the yield and quality of cucumber. Today, management of these insect-pests and diseases is highly dependent on chemical fungicides

(Anand *et al.*, 2009), which is quite hazardous to human health and environment. Therefore, use of the cultivars that are resistant to these insect-pests and diseases can be effective in reducing damage and yield losses of cucumber. But, there are very few sources of cucumber germplasm available worldwide, which has resistance to insect-pests and diseases viz., EC-173934 (fruit fly), PI 200815, PI 200818, *C. hardwikkii* (powdery mildew), B-184, B159 (downy mildew) and H 603 and 859/1 (angular leaf spot). Hence, there is immense need of developing resistant varieties/hybrids of cucumber to minimize the severe yield losses caused by these biotic factors.

Heterosis breeding has come to play a pivot role in crop improvement for yield and quality attributes (Singh *et al*., 2014). But, before the exploitation of heterosis, nature and magnitude of gene action involved in the expression of trait of interest and choice of suitable parental lines is of utmost importance. The knowledge of nature and magnitude of gene action controlling the inheritance of various traits along with proportional contribution of parental lines in the expression of traits in F_1 hybrids would facilitates the choice of efficient breeding method and suitable parental lines for genetic improvement of any crop (Rattan and Chadha, 2009). The combining ability studies aiming to identify inbred lines with good general and specific combining ability effects rely on the availability of genetic diversity among the genotypes involved in a breeding program (Legesse *et al*., 2009). Moreover, combining ability also indicates the nature and magnitude of gene action involved in the expression of quantitative traits. But, till date very meager information is available in the literature pertaining to the heterosis, combining ability, nature of gene action and proportional contribution of lines, testers and their interactions for insect-pest and disease resistance in cucumber. Hence, major objective of this study was to develop insect-pest and disease resistant cucumber hybrids through the knowledge of different estimates of combining ability, gene action and heterosis.

Materials and Methods

The present investigations were carried out at Experimental Research Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP) during *Kharif* (June-September) 2012. The experimental material for the present investigations was comprised of already tested high yielding 16 inbred lines (eight gynoecious) and three testers with broad genetic base (Table 1). The crosses were attempted during the year 2011 as per Line × Tester design suggested by Kempthorne (1957). The F_1 population of 48 hybrids along with parents was planted at a spacing of 100 cm × 75 cm in a plot having size of 4.0 x 3.0 m^2, accommodating 16 plants per plot in Randomized Complete Block Design (RCBD) with three replications during the year 2012. The standard cultural practices for raising a healthy crop of cucumber as recommended in the "Package of Practices" for Vegetable Crops, published by the Directorate of Extension Education, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan (Anonymous, 2009) have been followed during entire period of study.

The observations for fruit fly incidence (%) were recorded on five randomly selected plants in each entry (genotype/hybrid) over the replications. The total number of fruits per plant and fruits infested with fruit fly were counted from the randomly selected plants to work out the incidence of fruit fly as per the following formula:

Fruit fly incidence (%)

$$= \frac{\text{Number of fruit fly infested fruits}}{\text{Total number of fruits}} \times 100$$

The occurrence and severity of powdery mildew (%), downy mildew (%) and angular leaf spot (%) was recorded periodically under natural conditions. For each disease 15 different leaves were randomly selected from different levels of height (from top to bottom) from five plants of each genotype/hybrid. Angular leaf spot is characterized by appearance of water-soaked areas on the plants foliage. They later on become dry, chalky and cracked. While, in downy mildew initial symptoms include large, blocky, yellow areas visible on the upper surface. As lesions mature, they expand rapidly and turn brown. We have confirmed it microscopically as mycelial growth was observed in case of downy mildew, while bacterial ooze was seen in the leaves infected with angular leaf spot. Disease severity for powdery mildew was recorded by adopting the 0-5 scale given by Ransom *et al.* (1991), while disease severity for downy mildew was recorded by adopting the 0-4 scale given by Reuveni (1983). On the other hand, disease severity for angular leaf spot was recorded by adopting the 0-5 scale given by Bhat *et al.* (2007). Per cent disease severity (PDI) in all the diseases was calculated by using the formula as given below (McKinney, 1923):

$$\text{PDI (\%)} = \frac{\sum (n \times v)}{Z \times N} \times 100$$

Where, n=number of leaves in each category; v=numerical value of each category; Z=numerical value of highest category; N= total number of leaves in a sample

The data recorded on the 48 hybrids, along with 19 parents (16 lines and three testers) and two standard check cultivars were subjected to analysis of variance manually in MS Excel-2007 worksheet as per the formulae given by Panse and Sukhatme (1967). For line × tester analysis, replication-wise mean values of parents and their 48 F_1 hybrids for each trait were subjected to statistical analysis as per the model suggested by Kempthorne (1957) by using OPSTAT software. The additive and dominance components of variance were computed by following Singh and Chaudhary (1997) and Dabholkar (1992). The per cent contribution of lines, testers and their interactions were estimated as per the formulae given by Singh and Chaudhary (1997) by using SPAR-1 software. The estimates of heterosis were calculated manually in MS Excel-2007 worksheet as the deviation of F_1 mean from the mid-parent (MP), better parent (BP) and standard check-I (KH-1) and standard check-II (Pusa Sanyog), respectively, by using the following formulae (Singh, 1973):

$$\text{H } (F_{1,} \text{MP}) \ \% = [(\overline{F}_1 - \overline{MP})/\overline{MP} \times 100],$$

$$\text{H } (F_1, \text{BP}) \ \% = [(\overline{F}_1 - \overline{BP})/\overline{BP} \times 100],$$

$$\text{H } (F_{1,} SC_1) \ \% = [(\overline{F}_1 - \overline{SC}_1)/\overline{SC}_1 \times 100],$$

$$\text{H } (F_{1,} SC_2) \ \% = [(\overline{F}_1 - \overline{SC}_2)/\overline{SC}_2 \times 100]$$

Where,

F_1: First filial generation; MP: Mid-parent;
BP: Better parent; SC_1: Standard check-I
SC_2: Standard check-II

Further, statistical significance of all the estimates of heterosis was assessed via t-test (Wynne *et al.*, 1970).

Results and Discussion

All the 19 parents and their 48 F_1 hybrids studied, responded differently to the attack of different insect-pest and diseases *viz.*, fruit fly incidence, severity of powdery mildew, downy mildew and angular leaf spot (Table 2). Substantial variation was observed among the parents and hybrids for fruit fly incidence (parents=16.86-29.65 and hybrids =10.87-33.71 %), severity of powdery mildew (parents=10.20-23.60 and hybrids=8.90-28.20 %), downy mildew (parents=12.77-38.30 and hybrids=10.17-41.73 %) and angular leaf spot (parents=9.07-31.23 and hybrids =8.23-36.03 %). The lowest fruit fly incidence was recorded in the genotype LC-2-2 and the cross-combination LC-1-1 × K-75. Minimum severity of powdery mildew was recorded in the parental line LC-15-5, while cross combination LC-15-5 × K-75 recorded least severity of powdery mildew. The parental line, CGN-20969 and the cross combination, LC-3-3 × K-75 recorded minimum severity of downy mildew. Minimum severity of angular leaf spot was observed in the parental line LC-1-1 and cross combination, LC-1-1 × K-75 recorded least severity of angular leaf spot. Variation in response to fruit fly incidence was also reported earlier by Thakur *et al.* (1992) in bitter gourd and Kumar (2006) and Sharma (2010) in cucumber. Wide variations with respect to severity of different diseases in cucumber were also recorded by Morishita *et al.* (2003), Block and Reitsma (2005), Sakata *et al.* (2008) and Kumar *et al.* (2012) for severity of powdery mildew; Charoenwattana (2009), Brar *et al.* (2011) and Call *et al.* (2013) for severity of downy mildew and Bhat *et al.* (2007), Woltman *et al.* (2008) and Kumar *et al.* (2012) for severity of angular leaf spot in cucumber. On the basis of mean performance, parents LC-1-1, LC-2-2, LC-15-5 and CGN-20969 among lines, and Poinsette among the testers, were superior for different traits under study. Among the hybrids, LC-1-1 × K-75, LC-15-5 × K-75, LC-3-3 × K-75 and CGN-20969 × Japanese Long Green were found to be most promising. Among above mentioned parents and hybrids, parental line LC-1-1 and the cross-combination LC-1-1 × K-75 were also found promising for yield and yield contributing traits (Kumar *et al.*, 2017). The common approach of selecting parents on the basis of *per se* performance does not necessarily lead to fruitful results (Allard, 1960). Therefore, before drawing any conclusions, we determined combining ability for the different traits under study.

The analysis of variance for combining ability revealed significant differences among the parents and hybrids for all the traits under study (Table 3). The genotypes, LC-1-1 and CGN-20953 (for fruit fly incidence, severity of powdery mildew and angular leaf spot), LC-2-2 (for fruit fly incidence, severity of downy mildew and angular leaf spot), LC-3-3 and LC-15-5 (for fruit fly incidence, severity of powdery mildew and downy mildew), Poinsette (for fruit fly incidence, severity of powdery mildew and downy mildew), K-75 (for fruit fly incidence and severity of downy mildew) and Japanese Long Green (for severity of angular leaf spot) were found good general combiners as reflected from their consistent performance for desirable negative GCA effects (Table 4). Significant negative general combining ability (GCA) effects of different parental material for biotic stresses were also reported by earlier workers *viz.*, Kumar (2006) and Sharma (2010) for fruit fly incidence, Sharma (2010) for severity of powdery mildew and Brar *et al.* (2011) for severity of downy mildew in cucumber. But, no report is available in the literature pertaining to the GCA effects for severity of angular leaf spot in cucumber. On the basis of present investigations for GCA effects, it may be concluded that the five parental lines, *viz.*, LC-1-1, LC-2-2, LC-3-3, LC-15-5 and CGN-20953 along with the tester, K-75 were found to be good general combiners for different traits under study. These genotypes may be utilized in hybridization programs for obtaining superior resistant hybrids or transgressive segregants. For marketable yield per plant, the genotype LC-1-1, CGN-20953 and K-75 had exhibited highest positive GCA effects (Kumar *et al.*, 2017).

Specific combining ability (SCA) effect helps in identifying the best cross combinations for various traits. These effects arise due to non-additive gene interactions. Among all the hybrids, five best crosses *viz.*, LC-1-1 × K-75 (good × good), CGN-20953 × K-75 (good × good), LC-15-5 × Poinsette (good × good), LC-3-3 × Poinsette (good × good) and LC-2-2 × K-75 (good × good) for fruit fly incidence; LC-15-5 × K-75 (good × poor), CGN-20953 × K-75 (good × poor), Gyne-5 × Poinsette (average × good), LC-1-1 × K-75 (good × poor) and LC-3-3 × K-75 (good × poor) for severity of powdery mildew; CGN-20969 × Japanese Long Green (good × poor), CGN-19533 × K-75 (poor × good), CGN-22930 × Poinsette (poor × good), LC-25-7 × Japanese Long Green (good × poor) and LC-15-5 × Japanese Long Green (good × poor) for severity of downy mildew; CGN-20953 × K-75 (good × poor), LC-1-1 × K-75 (good × poor), LC-25-7 × K-75 (good × poor), CGN-20969 × Japanese Long Green (good × good) and LC-2-2 × Poinsette (good × average) for severity of angular leaf spot revealed significant negative SCA effects (Table 5). Most of the above crosses have the parents with good × poor GCA effects, which indicated the involvement of both additive and non-additive genetic variances. Such types of cross combinations are most desirable for genetic improvement of any crop through heterosis breeding. The other crosses had the involvement of either good × good or average × good combiners, which indicated the presence of additive × additive or additive × dominance type of gene interactions. Significant negative estimates of heterosis with the involvement of parents with different GCA effect have been reported earlier by Brar *et al.* (2011) for severity of downy mildew and Kumar (2006) for fruit fly incidence in cucumber. On the basis of overall performance, the cross combinations LC-1-1 × K-75, LC-15-5 × K-75, CGN-20969 × Japanese Long Green, and CGN-20953 × K-75 were found to be the best hybrids for different traits under study. Among the above-mentioned hybrids, SCA effect for marketable yield per plant was also found significantly high for the cross-combination LC-1-1 × K-75 (Kumar *et al*., 2017).

The estimates of genetic components of variance facilitate to adopt suitable breeding strategy for the purposeful management of generated variability for the traits under genetic improvement (Cockerham, 1961 and Sprague, 1966). The mean sum of squares due to GCA and SCA were highly significant for all the traits under study, indicating the importance of both additive and non-additive genetic components of variance (Table 3). Further, the mean sum of squares due to GCA and SCA were used to estimate the variances for GCA and SCA, respectively, based on which nature of gene action has been worked out.

The estimates of σ^2sca were higher in magnitude as compared to σ^2gca (average) for all the traits except fruit fly incidence (Table 6), thereby indicating predominant role of non-additive gene action governing these traits. Among the traits under study, where SCA variances were higher than GCA values, dominant components of variance (σ^2s) were also higher than the additive components (σ^2g), indicating the role of non-additive gene action. Further, variance ratio was found less than one for all the traits except fruit fly incidence. Again, it confirmed the role of non-additive gene action controlling most of the traits under study. After having an insight into the GCA and SCA variances as well as additive (σ^2A) and dominant (σ^2D) components of variance, it may be worthwhile to effect improvement in cucumber by developing superior open-pollinated varieties through selection in segregating population for fruit fly incidence (Kumar, 2006). Alternatively, exploitation of hybrid vigor or reciprocal recurrent selection, which capitalizes on both additive and non-additive variances, might be more effective for severity of powdery mildew, downy mildew and angular leaf spot, which had either high or equal dominant (σ^2D) components of variance to that of additive (σ^2A) components (Ghaderi and Lower, 1979; Lower *et al.*, 1982; Musmade and Kale, 1986).

The proportional contribution of lines, testers and their interactions to the total variance showed that both the lines and testers played equal role towards the total variance for the traits under study (Table 6). The contribution of lines was found highest for severity of powdery mildew and angular leaf spot as compared to individual contribution of testers and lines × testers interactions. It revealed higher estimates of GCA variance *i.e.,* additive gene action among the lines for the above-mentioned traits (Nadali and Nadali, 2010). The proportional contribution of testers was found higher than the individual contribution of lines and lines × testers interactions for fruit fly incidence and severity of downy mildew, which is also due to the additive gene action among the testers for these traits. The contribution of lines × testers interactions was found lower than the individual contribution of lines and testers for all the traits under study. The lower contribution of lines × testers interactions than lines or testers for all the traits indicates lower estimates of specific combining ability variance. There are no reports available in literature about the proportional contribution of lines, tester and their interactions for insect-pests and disease incidence in cucumber.

The estimation of heterosis for different traits revealed significant differences among different cross combinations (Table 7). In the present study, number of the hybrids revealed the significant negative heterosis for fruit fly incidence. But, the cross combinations LC-1-1 × K-75, CGN-20953 × Poinsette, LC-3-3 × Poinsette, LC-15-5 × K-75 and Gyne-5 × K-75 were rated as best heterotic crosses due to their significant negative values for all the estimates of heterosis under study. Kumar (2006) and Sharma (2010) had also reported negative heterosis for fruit fly incidence in cucumber. Besides this, ample number of the hybrids recorded the significant negative heterosis for severity of different diseases under study. But, CGN-20515 × Poinsette, CGN-20953 × K-75, LC-3-3 × Poinsette, LC-15-5 × K-75 and Gyne-5 × Poinsette for severity of powdery mildew, LC-3-3 × K-75 for severity of downy mildew and CGN-20969 × Japanese Long Green and LC-1-1 × K-75 for severity of angular leaf spot, revealed significant negative values for all the estimates of heterosis. Significant negative heterosis for severity of powdery mildew and downy mildew was also reported by Sharma (2010) and Brar *et al.* (2011), respectively. In our study, we have computed the different estimates of heterosis for insect-pest and disease resistance by using gynoecious parental lines, whereas earlier workers studied only one or two types of heterosis for monoecious cultivars of cucumber. On the basis of overall performance, heterosis studies revealed that hybrids LC-1-1 × K-75, LC-15-5 × K-75, LC-3-3 × K-75 and CGN-20969 × Japanese Long Green had significantly high negative heterotic values for different traits under study. Among these cross combinations, LC-1-1 × K-75 had significant positive values for different estimates of heterosis for number of marketable fruits per plant, harvest duration and marketable yield per plant (Kumar *et al.*, 2017), hence it is designated as best heterotic cross combination among all the hybrids under study. Hence, hybrid vigor may be exploited commercially for the improvement of these traits in cucumber.

On the basis of mean performance and general combining ability studies, we concluded that among the parents, lines LC-1-1, LC-2-2, LC-15-5, CGN-20969 and CGN-20953, and testers Poinsette and K-75 were found superior in response to insect-pests and disease incidence. The cross combinations LC-1-1 × K-75, LC-15-5 × K-75, LC-3-3 × K-75, CGN-20969 × Japanese Long Green, and CGN-20953 × K-75 were found best on the basis of mean performance, specific combining ability and heterosis for different traits under study. However, among above mentioned parents and hybrids only parental line LC-1-1 and cross combination LC-1-1 × K-75 were found superior for yield and its attributing traits, hence it is designated as best parental line and hybrid, respectively. Further, gene action studies concluded that all the traits except fruit fly incidence were inherited by dominance components of variance. Hence, heterosis breeding could be exploited commercially in cucumber for the development of insect-pests and disease resistance parthenocarpic gynoecious hybrids/transgressive segregants. Further, proportional contribution of lines was recorded highest for severity of powdery mildew and angular leaf spot. Besides this, testers were found superlative for fruit fly incidence and severity of downy mildew. Therefore, depending upon the trait of interest due attention should be given on the lines and testers for the development of insect-pests and disease resistance parthenocarpic gynoecious hybrids/transgressive segregants in cucumber.

Acknowledgements

The authors are highly thankful to Centre for Crop Genetic Resources, the Netherlands and ICAR-Indian Agricultural Research Institute (IARI) Regional Station, Katrain, Kullu, HP, India for providing cucumber germplasm for conducting the present investigation.

References

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and sons, New York, 485p.

Anand, T., Chandrasekaran, A., Kuttalam, S., Raguchander, T. and Samiyappan R. 2009. Management of Cucumber (*Cucumis sativus* L.) Mildews through Azoxystrobin-Tolerant Pseudomonas fluorescens. *J. Agric. Sci. Technol.,* **11**: 211-226.

Anonymous. 2009. Package of practices for vegetable crops. Directorate of Extension Education, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, 202p.

Bhat, N.A., Masoodi, S.D., Ahmad, M. and Zargar, M.Y. 2007. Occurrence and Severity of Angular Leaf Spot of Cucumber in Kashmir. *Annl. Pl. Protect. Sci.,* **15** (2): 410-413.

Block, C.C. and Reitsma, K.R. 2005. Powdery Mildew Resistance in US National Plant Germplasm System Cucumber Collection. *HortSci.,* **40** (2): 416-420.

Brar, P.S., Singh, G., Singh, M. and Batth, G.S. 2011. Genetic Analysis for Quality Traits and Reaction to Downy Mildew in Cucumber (*Cucumis sativus* L.). *J. Res. PAU.,* **48** (1&2): 28-33.

Call, A.D., Wehner, T.C., Holmes, G.J. and Ojiambo, P.S. 2013. Effects of Host Plant Resistance and Fungicides on Severity of Cucumber Downy Mildew. *HortSci.,* **48** (1): 53-59.

Charoenwattana, P. 2009. Four Downy Mildew Patho-Types are Present on Cucumbers in the Northern Region of Thailand. *Asian J. Food Agro-Indust.,* (Special Issue): 387-391.

Chaudhary, F.K. and Patel, G.M. 2012. Effect of Abiotic Factors on Population Fluctuation of Melon Fly, *Bactrocera cucurbitae* Coquillett. *Life Sci. Leaflets,* 365-369.

Cockerham, C.C. 1961. Implication of Genetic Variances in Hybrid Breeding Programme. *Crop Sci.,* **1**: 47-52.

Dabholkar, A.R. 1992. Elements of Biometrical Genetics. Concept Publishing Company, New Delhi, pp. 187-214.

Dhillon, M.K., Singh, R., Naresh, J. and Sharma, H.C. 2005. The Melon Fly, *Bactrocera cucurbitae*: A Review of its Biology and Management. *J. Insect Sci.,* **5**: 40.

Ghaderi, A. and Lower, R.L. 1979. Analysis of Generation Means for Yield in Six Crosses of Cucumber. *J. Amer. Soci. Horti. Sci.,* **104** (4): 567-572.

Ghule, T.M., Uikey, B.L., Barma, P. and Jha, S. 2014. Incidence Studies on Some Important Insect-Pests of Cucumber (*Cucumis Sativus* L.). *The Ecoscan,* **8** (1&2): 177-180.

Hashmi, A.A. 1994. Horticulture Insect Pest Management of Vegetables compiled by Elina Bashir, National Book Foundation of Pakistan, pp. 633.

Kempthorne, O. 1957. An Introduction to Genetic Statistics. John Wiley and Sons, New York, London, pp. 458-471.

Krishna K.N.K., Verghese A., Shivakumara B., Krishnamoorthy P.N. and Ranganath H.R. 2006. Fruit Flies of Economic Importance: From Basic to Applied Knowledge. In: Proceedings of the 7th International Symposium on fruit flies of economic importance, Salvador, Brazil, pp. 249-253.

Kumar, A. 2006. Studies on Heterosis and Inheritance of Resistance to Fruit Fly in Cucumber (*Cucumis sativus* L.). Ph.D. Thesis, Dr. Y S Parmar University of Horticulture and Forestry, Nauni, Solan (H P). 109p.

Kumar, S., Kumar, R. and Kansal, S. 2012. Response of Cucumber Accessions to Economically Important Diseases Under Open Field Conditions in Mid-Hill Conditions of Himachal Pradesh. *Crop Improv.,* **39** (2): 200-201.

Kumar, S., Kumar, R., Kumar, D., Gautam, N., Singh, N., Parkash, C., Dhiman, M.R. and Shukla, Y.R. 2017. Heterotic potential, potence ratio, combining ability and genetic control of yield and its contributing traits in cucumber (*Cucumis sativus* L.). *New Zealand J. Crop Horticult. Sci.* **45**(3): 175-190.

Lamsal K., Kim S.W., Jung J.H., Kim Y.S., Kim K.S. and Lee, Y.S. 2011. Inhibition Effects of Silver Nanoparticles against Powdery Mildews on Cucumber and Pumpkin. *Mycobio.,* **39** (1): 26-32.

Legesse, B.W., Pixley, K.V. and Botha, A.M., 2009. Combining Ability and Heterotic Grouping of Highland Transition Maize Inbred Lines. *Maydica,* **54**: 1-9.

Lower, R.L., Nienhuis, J. and Miller, C.H. 1982. Gene Action and Heterosis for Yield and Vegetative Characteristics in a Cross between a Gynoecious Picking Cucumber Inbred and a *Cucumis sativus* var. *hardwickii* Line. *J. Amer. Soci. Horti. Sci.,* **107** (1): 75-78.

McGrath, M.T. 1996. Successful Management of Powdery Mildew in Pumpkin with Disease Threshold-Based Fungicide Programs. *Plant Dis.,* **80**: 910-916.

McKinney, H.H. 1923. Influence of Soil Temperature and Moisture on Infection of Wheat Seedlings by *Helminthosporium sativum*. *J. Agri. Res.,* **26**: 195-217.

Morishita, M., Sugiyama, K., Saito, T. and Sakata, Y. 2003. Powdery Mildew Resistance in Cucumber. *JARQ,* **37** (1): 7 -14.

Musmade, A.M. and Kale, P.N. 1986. Heterosis and Combining Ability in Cucumber (*Cucumis sativus* L.). *Veg. Sci.,* **13** (1): 60-68.

Nadali, B. and Nadali, B.J. 2010. Heterosis and Combining Ability Analysis for Yield and Related-Yield Traits in Hybrid Rice. *Intl. J. Bio.,* **2** (2): 222-231.

Panse, V.G. and Sukhatme, P.V. 1967. Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research, New Delhi, 381p.

Ransom, L.M., Briens, R.G.O. and Glass, R.J. 1991. Chemical Control of Powdery Mildew in Green Peas. *Aus. Pl. Patho.,* **20** (1): 16-20.

Rattan, P. and Chadha, S. 2009. Gene Action Studies for Yield and its Contributing Characters. *Bio. Forum-An Intl J.,* **1**(2):8-10.

Reuveni, R. 1983. Resistance of *Cucumis melo* to *Pseudoperonospora cubensis*. *Annl. Appl. Bio.,* **102**: 533-537.

Sakata, Y., Morishita, M., Kitadanib, E., Sugiyama, M., Oharac, T., Sugiyamad, K. and Kojima A. 2008. Development of a Powdery Mildew Resistant Cucumber (*Cucumis sativus* L.). *Kyuri Chukanbohon Nou 5 Go,* **7** (2)**:** 173-179.

Sharma, M. 2010. Gene Action and Heterosis Studies Involving Gynoecious Lines in Cucumber (*Cucumis sativus* L.). Ph.D. Thesis, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H P), 192p.

Singh, D. 1973. Diallel Analysis Over Environments-I. *Ind. J. Genet.Pl. Breed.,* **33**: 127-136.

Singh, R.K. and Chaudhary, B.D. 1997. Line × Tester Analysis. In: Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana, pp. 191-200.

Singh, S.K., Singh, S.V. and Srivastava, J.P. 2014. Heterosis and Inbreeding Depression for Yield and its Component Traits in Cucumber. *Agriways,* **2** (1): 47-51.

Sprague, G.F. 1966. Quantitative Genetics in Plant Improvement. In: Plant Breeding: a symposium held at Iowa State University. The Iowa State University Press, Ames, Iowa. pp. 315-354.

Thakur, J.C., Khattra, A.S. and Brar, K.S. 1992. Comparative Resistance to Fruit Fly in Bitter Gourd. *Haryana J. Horti. Sci.,* **21** (3&4): 285-288.

Wehner, T.C. and Shetty, N.V. 1997. Downy Mildew Resistance of the Cucumber Germplasm Collection in North Carolina Field Tests. *Crop Sci.,* **37**: 1331-1340.

Woltman, H.O., Schollenberger, M, Mądry, W and Szczytt, KN. 2008. Evaluation of Cucumber (*Cucumis sativus* L.) Cultivars Grown in Eastern Europe and Progress in Breeding for Resistance to Angular Leaf Spot (*Pseudomonas syringae* pv. *lachrymans*). *Euro. J. Pl. Patho.,* **122:** 385-393.

Wynne, J.C., Emery, D.A. and Rice, P.M. 1970. Combining Ability Estimates in *Arachis hypogeae* L. II. Field Performance of F_1 Hybrids. *Crop Sci.,* **10**: 713-715.

Table 1. List of the cucumber genotypes used in the hybridization along with standard check cultivars

Sr. No.	Genotypes	Source	Pollination Mechanism
(a)	Lines		
1.	CGN-19533	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
2.	CGN-20256	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
3.	CGN-20515	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
4.	CGN-20953	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
5.	CGN-20969	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
6.	CGN-21585	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
7.	CGN-22930	Centre for Crop Genetic Resources, the Netherlands	Gynoecious
8.	LC-1-1	Dhangota, Hamirpur, Himachal Pradesh, India	Monoecious
9.	LC-2-2	Bhota, Hamirpur, Himachal Pradesh, India	Monoecious
10.	LC-3-3	Awahdevi, Hamirpur, Himachal Pradesh, India	Monoecious
11.	LC-12-4	Gagal, Kangra, Himachal Pradesh,India	Monoecious
12.	LC-15-5	Sarkaghat, Mandi, Himachal Pradesh, India	Monoecious
13.	LC-21-6	Dangar, Bilaspur, Himachal Pradesh, India	Monoecious
14.	LC-25-7	Saru, Chamba, Himachal Pradesh, India	Monoecious
15.	LC-28-8	Sambha, Jammu, Jammu and Kashmir, India	Monoecious
16.	Gyne-5	ICAR-IARI Regional Station, Katrain, Kullu, HP, India	Gynoecious
(b)	Testers		
1.	K-75	UHF, Nauni, Solan, Himachal Pradesh,India	Monoecious
2.	Japanese Long Green	ICAR-IARI Regional Station, Katrain, Kullu, HP, India	Monoecious
3.	Poinsette	National Seeds Corporation, New Delhi, India	Monoecious
(c)	Standard check cultivars		
1.	KH-1	UHF, Nauni, Himachal Pradesh,Solan	Monoecious
2.	Pusa Sanyog	ICAR-IARI Regional Station, Katrain, Kullu, HP, India	Gynoecious

Table 2. Top five parents and hybrids identified on the basis of insect-pest and disease response in cucumber

Traits	Range		Mean ± S.E. (d)	Top five parents	Top five cross combinations along with mean performance of check cultivars
	Parents	Hybrids			
Fruit fly incidence (%)	16.86-29.65	10.87-33.71	22.15±0.96	LC-2-2 (16.86), LC-1-1 (17.37), LC-15-5 (19.18), LC-3-3 (19.48), CGN-20953 (20.86)	LC-1-1 × K-75 (10.87), LC-3-3 × Poinsette (11.20), LC-15-5 × Poinsette (11.40), LC-2-2 × K-75 (12.80), CGN-20953 × K-75 (13.24)
					KH-1 (Check-I)-(18.52) Pusa Sanyog (Check-II)-(19.66)
Severity of powdery mildew (%)	10.20-23.60	8.90-28.20	15.62±1.26	LC-15-5 (10.20), Poinsette (10.30), LC-21-6 (11.33), CGN-20953 (11.68), †JLG (12.23)	LC-15-5 × K-75 (8.90), CGN-20515 × Poinsette (9.47), LC-3-3 × Poinsette (9.57), Gyne-5 × Poinsette (9.90), CGN-20953 × K-75 (10.20)
					KH-1 (Check-I)-(12.83) Pusa Sanyog (Check-II)-(15.70)
Severity of downy mildew (%)	12.77-38.30	10.17-41.73	19.76±1.52	CGN-20969 (12.77), Poinsette (12.90), K-75 (13.20), LC-3-3 (14.70), LC-25-7 (16.17)	LC-3-3 × K-75 (10.17), CGN-20969 × JLG (10.43), LC-2-2 × Poinsette (11.30), LC-15-5 × K-75 (11.50), Gyne-5 × K-75 (12.87)
					KH-1 (Check-I)-(16.30) Pusa Sanyog (Check-II)-(14.17)
Severity of angular leaf spot (%)	9.07-31.23	8.23-36.03	17.29±1.45	LC-1-1 (9.07), CGN-20969 (9.37), LC-12-4 (11.27), CGN-20953 (11.33), JLG (12.27)	LC-1-1 × K-75 (8.23), CGN-20969 × JLG (8.80), LC-2-2 × Poinsette (10.30), CGN-20953 × K-75 (10.37), LC-1-1 × Poinsette (11.40)
					KH-1 (Check-I)-(15.50) Pusa Sanyog (Check-II)-(12.80)

†Japanese Long Green

Table 3. Analysis of variance for Line × Tester analysis including parents in cucumber

Source →	**Mean Sum of Squares**								
Traits ↓	**Replications**	**Treatments**	**Parents**	**P *vs* C**	**Crosses**	**Lines**	**Testers**	**Lines × Testers**	**Error**
d.f. →	2.00	66.00	18.00	1.00	47.00	15.00	2.00	30.00	132
Fruit fly incidence (%)	2.32	105.70*	31.13*	27.02*	135.93*	43.80*	2530.74*	22.34*	1.40
Severity of powdery mildew (%)	4.47	55.64*	41.52*	5.72*	62.11*	85.62*	377.52*	29.33*	2.42
Severity of downy mildew (%)	2.09	141.36*	177.46*	151.33*	127.32*	133.31*	1074.19*	61.20*	3.51
Severity of angular leaf spot (%)	12.78	93.62*	119.97*	29.94*	84.88*	163.67*	291.57*	31.71*	3.14

*Significant at 5% level of significance

Table 4. Estimates of general combining ability (GCA) effects of parents for economically important insect-pests and diseases in cucumber

Parents/Traits → ↓	Fruit fly incidence (%)	Severity of powdery mildew (%)	Severity of downy mildew (%)	Severity of angular leaf spot (%)
Lines				
CGN-19533	0.32	2.87*	5.17*	2.83*
CGN-20256	2.87*	2.92*	2.20*	4.12*
CGN-20515	0.36	-2.65*	2.24*	2.02*
CGN-20953	-1.49*	-3.84*	-0.41	-3.74*
CGN-20969	3.09*	3.26*	-4.99*	-2.37*
CGN-21585	2.78*	5.03*	2.15*	12.16*
CGN-22930	-0.58	4.86*	9.59*	-0.61
LC-1-1	-3.26*	-2.01*	0.81	-6.62*
LC-2-2	-2.41*	-0.96	-2.06*	-3.85*
LC-3-3	-3.38*	-3.40*	-3.23*	-0.59
LC-12-4	2.20*	-0.07	-0.36	-1.37*
LC-15-5	-3.05*	-4.91*	-4.47*	1.14
LC-21-6	0.67	0.54	0.79	-0.21
LC-25-7	-0.09	-0.90	-4.91*	-3.41*
LC-28-8	1.01*	-1.44*	-0.93	-0.61
Gyne-5	0.96*	0.71	-1.59*	1.12
Testers				
K-75	-3.95*	2.61*	-2.65*	2.36*
Japanese Long Green	8.38*	0.34	5.46*	-2.55*
Poinsette	-4.42*	-2.95*	-2.80*	0.18
S.E. (g_i) Lines	0.39	0.51	0.62	0.59
S.E. (g_j) Testers	0.17	0.22	0.27	0.25
S.E. (g_i- g_j) Lines	0.55	0.73	0.88	0.83
S.E. (g_i- g_j) Testers	0.24	0.31	0.38	0.36
C.D.$_{(0.05)}$ (g_i) Lines	0.77	1.01	1.22	1.15
C.D.$_{(0.05)}$ (g_i) Testers	0.33	0.43	0.52	0.50
C.D.$_{(0.05)}$ (g_i- g_j) Lines	1.09	1.43	1.73	1.63
C.D.$_{(0.05)}$ (g_i- g_j) Testers	0.47	0.62	0.74	0.71

*Significant at 5% level of significance

Table 5. Estimates of specific combining ability (SCA) effects of hybrids for economically important insect-pests and diseases in cucumber

Hybrids/Traits → ↓	Fruit fly incidence (%)	Severity of powdery mildew (%)	Severity of downy mildew (%)	Severity of angular leaf spot (%)
CGN-19533 × K-75	-1.15	4.75*	-5.49*	3.52*
CGN-19533 × Japanese Long Green	-0.04	-2.43*	8.71*	-1.15
CGN-19533 × Poinsette	1.19	-2.31*	-3.21*	-2.36*
CGN-20256 × K-75	4.20*	3.75*	5.70*	4.66*
CGN-20256 × Japanese Long Green	-2.46*	-2.32*	-4.21*	-1.91
CGN-20256 × Poinsette	-1.73*	-1.43	-1.48	-2.75*
CGN-20515 × K-75	-0.34	-1.99*	-1.39	1.13
CGN-20515 × Japanese Long Green	-1.54*	2.68*	3.88*	0.58
CGN-20515 × Poinsette	1.89*	-0.68	-2.48*	-1.71
CGN-20953 × K-75	-3.31*	-4.34*	0.95	-5.40*
CGN-20953 × Japanese Long Green	3.89*	1.90*	-0.22	2.58*
CGN-20953 × Poinsette	-0.58	2.43*	-0.72	2.81*
CGN-20969 × K-75	1.90*	2.97*	4.26*	1.26
CGN-20969 × Japanese Long Green	-1.74*	-2.30*	-9.38*	-3.41*
CGN-20969 × Poinsette	-0.16	-0.66	5.11*	2.14*
CGN-21585 × K-75	2.20*	1.71	3.65*	4.35*
CGN-21585 × Japanese Long Green	0.53	-0.44	-2.19*	-2.22*
CGN-21585 × Poinsette	-2.74*	-1.27	-1.46	-2.13*
CGN-22930 × K-75	0.80	4.94*	-2.42*	-2.43*
CGN-22930 × Japanese Long Green	-2.73*	-2.80*	7.32*	0.51
CGN-22930 × Poinsette	1.93*	-2.14*	-4.90*	1.91
LC-1-1 × K-75	-3.91*	-3.44*	-2.44*	-4.65*
LC-1-1 × Japanese Long Green	2.79*	2.23*	0.97	3.96*
LC-1-1 × Poinsette	1.12	1.20	1.47	0.69
LC-2-2 × K-75	-2.84*	-1.90*	2.56*	0.21
LC-2-2 × Japanese Long Green	2.72*	1.48	0.61	2.96*
LC-2-2 × Poinsette	0.12	0.42*	-3.18*	-3.17*
LC-3-3 × K-75	4.05*	-3.25*	-3.28*	-2.91*
LC-3-3 × Japanese Long Green	-1.05	3.09*	1.06	-0.25
LC-3-3 × Poinsette	-2.99*	0.15	2.22*	3.17*
LC-12-4 × K-75	-1.57*	1.42	-0.03	0.40
LC-12-4 × Japanese Long Green	-1.29	-2.93*	1.91	-1.41
LC-12-4 × Poinsette	2.86*	1.51	-1.88	1.01
LC-15-5 × K-75	0.73	-4.56*	-0.72	1.17
LC-15-5 × Japanese Long Green	2.39*	0.87	-4.30*	0.69
LC-15-5 × Poinsette	-3.12*	3.69*	5.02*	-1.87
LC-21-6 × K-75	-0.15	1.73	-3.65*	3.26*
LC-21-6 × Japanese Long Green	-0.77	-3.15*	3.06*	-2.68*
LC-21-6 × Poinsette	0.92	1.41	0.59	-0.58
LC-25-7 × K-75	3.50*	-2.25*	2.89*	-4.60*
LC-25-7 × Japanese Long Green	-1.72*	2.16*	-4.66*	2.11*
LC-25-7 × Poinsette	-1.77*	0.09	1.77	2.48*
LC-28-8 × K-75	-1.51*	-1.64	1.64	2.83*
LC-28-8 × Japanese Long Green	-0.18	0.43	-0.57	-0.88
LC-28-8 × Poinsette	1.69*	1.20	-1.07	-1.95
Gyne-5 × K-75	-2.59*	2.10*	-2.23*	-2.83*
Gyne-5 × Japanese Long Green	1.23	1.51	-1.98	0.51
Gyne-5 × Poinsette	1.36*	-3.61*	4.21*	2.31*
S.E. (S_{ij})	0.68	0.89	1.08	1.02
S.E. (S_{ij}-S_{kj})	0.96	1.27	1.53	1.44
C.D.$_{(0.05)}$(S_{ij})	1.34	1.76	2.12	2.01
C.D.$_{(0.05)}$(S_{ij}-S_{kj})	1.89	2.48	2.99	2.84

*Significant at 5% level of significance

Table 6. Estimates of genetic components of variance for different traits and proportional contribution of lines, testers and their interactions to sum of squares of the hybrids in cucumber

Traits	**σ^2 GCA† (Lines)**	**σ^2 GCA (Testers)**	**σ^2 GCA (Average)**	**σ^2 SCA††**	**σ^2g**	**σ^2s**	**σ^2g/σ^2s (Variance Ratio)**	**Per cent contribution of**		
								Lines	**Testers**	**Lines × Testers**
Fruit fly incidence (%)	2.38	52.26	44.38	6.95	177.52	27.80	6.39	10.28	79.23	10.49
Severity of powdery mildew (%)	6.25	7.25	7.09	8.99	28.36	35.96	0.79	43.99	25.86	30.15
Severity of downy mildew (%)	8.01	21.10	19.04	19.71	76.16	78.84	0.97	33.42	35.90	30.68
Severity of angular leaf spot (%)	14.66	5.41	6.87	9.81	27.48	39.24	0.70	61.54	14.62	23.84

†GCA = general combining ability
‡ SCA= specific combining ability

Table 7. Estimates of heterosis for economically important insect-pests and diseases in cucumber (Top 10 hybrid combinations)

	Fruit fly incidence (%)					Severity of powdery mildew (%)			
	Per cent increase/decrease over					Per cent increase/decrease over			
Cross combination(s)	**Mid parent**	**Better parent**	**Standard Check-I**	**Standard Check-II**	**Cross combination(s)**	**Mid parent**	**Better parent**	**Standard Check-I**	**Standard Check-II**
CGN-19533 × K-75	-22.15*	-19.08*	-7.02	-12.41*	CGN-20515 × Poinsette	-16.67	-8.06	-26.19*	-39.68*
CGN-20953 × K-75	-37.16*	-36.53*	-28.51*	-32.66*	CGN-20953 × K-75	-25.22*	-12.67	-20.50*	-35.03*
CGN-20953 × Poinsette	-28.34*	-25.65*	-16.25*	-21.11*	CGN-20953 × Poinsette	3.73	10.68	-11.15	-27.39*
LC-1-1 × K-75	-43.75*	-37.42*	-41.31*	-44.71*	LC-1-1 × K-75	-21.33*	-17.12*	0.78	-17.64*
LC-2-2 × K-75	-32.88*	-24.08*	-30.89*	-34.89*	LC-1-1 × Poinsette	-12.95	16.5	-6.47	-23.57*
LC-3-3 × Poinsette	-46.55*	-42.51*	-39.52*	-43.03*	LC-3-3 × K-75	-19.46*	-13.3	-8.57	-25.29*
LC-15-5 × K-75	-22.24*	-17.99*	-15.06*	-19.99*	LC-3-3 × Poinsette	-19.68	-7.09	-25.41*	-39.04*
LC-15-5 × Poinsette	-45.21*	-40.56*	-38.44*	-42.01*	LC-12-4 × JLG	-5.18	7.11	2.1	-16.56*
LC-25-7 × Poinsette	-31.46*	-29.96*	-15.17*	-20.09*	LC-15-5 × K-75	-31.01*	-12.75	-30.63*	-43.31*
Gyne-5 × K-75	-29.74*	-22.84*	-11.34*	-16.48*	Gyne-5 × Poinsette	-35.57*	-3.88	-22.84*	-36.94*
	Severity of downy mildew (%)					**Severity of angular leaf spot (%)**			
	Per cent increase/decrease over					**Per cent increase/decrease over**			
Cross combination(s)	**Mid parent**	**Better parent**	**Standard Check-I**	**Standard Check-II**	**Cross combination(s)**	**Mid parent**	**Better parent**	**Standard Check-I**	**Standard Check-II**
CGN-20969 × JLG	-35.02*	-18.32	-36.01*	-26.39*	CGN-20953 × K-75	-31.78*	-8.47	-33.10*	-18.98
LC-1-1 × K-75	-20.26*	14.17	-7.55	6.35	CGN-20953 × JLG	13.81	18.53	-13.35	4.92
LC-2-2 × Poinsette	-23.98*	-12.4	-30.67*	-20.25	CGN-20969 × JLG	-18.67*	-6.08	-43.23*	-31.25*
LC-3-3 × K-75	-27.10*	-22.95*	-37.61*	-28.23*	LC-1-1 × K-75	-41.51*	-9.26	-46.90*	-35.70*
LC-12-4 × Poinsette	-16.93*	10.85	-12.27	0.92	LC-1-1 × JLG	11.81	31.53*	-23.03*	-6.8
LC-15-5 × K-75	-22.48*	-12.88	-29.45*	-18.84	LC-1-1 × Poinsette	-17.39*	25.69*	-26.45*	-10.94
LC-21-6 × K-75	-24.22*	4.77	-15.15	-2.4	LC-2-2 × Poinsette	-35.42*	-22.96*	-33.55*	-19.53
LC-25-7 × JLG	-14.2	-5.81	-6.56	7.48	LC-12-4 × JLG	0.25	4.7	-23.87*	-7.81
LC-28-8 × Poinsette	-11.21	12.64	-10.86	2.54	LC-21-6 × JLG	-17.61*	-4.65	-24.52*	-8.59
Gyne-5 × K-75	-15.52	-2.5	-21.04*	-9.17	LC-25-7 × K-75	-29.96*	-16.49	-25.81*	-10.16

*Significant at 5% level of significance