

STUDIES ON GENETIC AND MOLECULAR DIVERSITY IN CUCUMBER (*Cucumis sativus* L.)

Thesis

Submitted to the



**G. B. Pant University of Agriculture and Technology
Pantnagar–263 145 (U.S. Nagar), Uttarakhand, India**

By

Sandeep Yadav

Id. No. 52603

**IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE DEGREE OF**

Doctor of Philosophy

Horticulture (Vegetable Science)

FEBRUARY, 2021

ACKNOWLEDGEMENT

I actually feel that happiness lies not only in pursuit but also in reaching the goal and at this juncture, I stand with the kernel of my endeavour in my hand, with the shower of blessing bestowed on me by esteemed "GOD" while pursuing this course of study many known and unknown hands pushed me forward on the right path and enlightened me with their knowledge and experience.

Indeed, the words in my lexicon are not sufficient either in form or in thought to elucidate my profound sense of reverence and indebtedness to Dr. D. K. Singh, Professor Department of Vegetable Science, and the chairman of my advisory committee, who graciously provide me an opportunity to derive advantage of his meticulous guidance, supervision, prolific discussion, healthy criticism from time to time, outstanding cooperation, diligence and soothing parental affection during the entire course of investigation and construction of this manuscript.

I am immensely beholden to the members of my Advisory Committee, Dr. Dharendra Singh, Professor and Head, Department of Vegetable Science, Dr. N. K. Singh, Professor, Department of Genetics and Plant Breeding and Dr. K. P. Singh, Professor, Department of Plant Pathology for their full-fledged cooperation, able guidance and valuable suggestions during the whole course of this investigation and preparation of this manuscript.

I am grateful to Dean, College of Agriculture; Dean, College of Post Graduate Studies; Director, Experiment Stations and Joint Director, V.R.C., Pantnagar for providing necessary facilities for conducting this research.

With a deep sense of gratitude and great pleasure, I acknowledge my sincere thanks to Dr. Dharendra Kumar Singh, Dr. Manoj Raghav, Dr. J.P. Singh, Dr. S. K. Maurya, Dr. Alka Verma, Dr. Lalit Bhatt, Devendra Ji, Dinsh Ji, Sunil Ji, Rawat Ji and other Staff members of Department of Vegetable Science for their constant help and encouragement.

Although, it is likely a drop in the ocean, yet I would like to express my heartiest sense of reverence and immense love to my most venerable parents Shri Ram Prit and Smt. Tara Devi, whose endless love, blessings, sacrifice, confidence in me, untiring support and persistent encouragement has brought me to where I stand today.

Indeed, it is with the personal touch of emotion that I seize this opportunity to express my heartfelt affectionate gratitude to my brother and sister and all family members for their appreciable patience, endless inspiration and constant encouragement which made this dream in a reality.

I cannot forget the love and co-operation received from my respected seniors Yogendra Sir, Neeraj Sir, Hirdesh sir, Ankit Sir, Praveen Sir, Asheesh Sir, Lavlesh Sir, Sajal Sir.

It is indeed a pleasure to acknowledge the love, inspiration, encouragement, selfless help and cheerful company of my batchmates Garima, Vivek, Ankit, Nima and Rashmi.

I would like to express my sincere thanks to my loving juniors especially, Yashpal, Rajkumar, Rajendra Bhatt, Shubham, Pushpendra, Abhilash, Rajat, Paras, Anand, Shivran and Rajendra Thakur.

I express heartfelt and deepest sense of gratitude to all my teachers since my school time for their blessings, encouragement and suggestions.

I am also thankful to Bhanu bhaiya for their support during preparation of this manuscript.

The financial assistance provided by the Department of Science and Technology, New Delhi as "INSPIRE Fellowship" during the tenure of this degree programme is gratefully acknowledged.

At last, I would like to convey my grateful thanks to all those unmentioned persons who helped me to see my dreams come true.

*Pantnagar
February, 2021*

*Sandeep Yadav
(Sandeep Yadav)
Author*

CERTIFICATE - I

This is to certify that the thesis entitled “**STUDIES ON GENETIC AND MOLECULAR DIVERSITY IN CUCUMBER (*Cucumis sativus* L.)**” submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy** with major in **Horticulture (Vegetable Science)** and minor in **Genetics and Plant Breeding** of the College of Post-Graduate Studies, G.B. Pant University of Agriculture and Technology, Pantnagar, is a record of *bona fide* research carried out by **Mr. Sandeep Yadav, Id. No. 52603** under my supervision and no part of the thesis has been submitted for any other degree or diploma.

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

Pantnagar
February, 2021



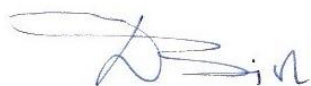
(Dinesh Kumar Singh)
Chairman
Advisory Committee

CERTIFICATE-II

We, the undersigned, members of the Advisory Committee of **Mr. Sandeep Yadav, Id. No. 52603**, a candidate for the degree of **Doctor of Philosophy** with major in **Horticulture (Vegetable Science)** and minor in **Genetic and Plant Breeding** agree that the thesis entitled “**STUDIES ON GENETIC AND MOLECULAR DIVERSITY IN CUCUMBER (*Cucumis sativus* L.)**” may be submitted in partial fulfillment of the requirements for the degree.



(Dinesh Kumar Singh)
Chairman
Advisory Committee



(Dhirendra Singh)
Member



(N.K. Singh)
Member



(K.P. Singh)
Member



(Ex-officio member)
Head of the Department

CONTENTS

S. No.	Chapters	Pages
1.	Introduction	1-7
2.	Review of Literature	8-36
	2.1 Genetic variability for different yield related traits.	8
	2.2 Heterosis studies.	14
	2.3 Combining ability	21
	2.4 Screening of parents and F ₁ against downy mildew (<i>Pseudoperonospora cubensis</i>).	31
	2.5 Molecular markers for studying genetic diversity of cucumber genotypes.	32
3.	Materials and Methods	37-63
	3.1 Cite of experiment and climate	37
	3.2 Experiment materials	37
	3.3 Experiment method	40
	3.4 Experiment design	40
	3.5 Observation recorded	44
	3.6 Downy mildew of cucumber	45
	3.7 Statistical analysis	46
	3.8 Assessment of genetic diversity using SSR marker	56
4.	Results and Discussion	64-141
	4.1 Analysis of variance (ANOVA)	64
	4.2 Genetic variability for different yield related traits	66
	4.3 To estimate the extent of heterosis over its parents	74
	4.4 Estimation of combining ability.	105

4.5	To screen the parents and F ₁ hybrids of cucumber against downy mildew (<i>Pseudoperonospora cubensis</i>)	118
4.6	To assess the molecular diversity of cucumber genotypes.	131
5.	Summary and Conclusion	142-146
	Literature Cited	
	Appendices	
	Vita	
	Abstract	

LIST OF TABLES

Table No.	Title	Page No.
3.1	List of parents with resistant check for downy mildew studies	38
3.2	List of F ₁ hybrids developed through half diallel mating design	38
3.3	List of cucumber lines used for molecular diversity analysis	39
3.4	Analysis of variance	46
3.5	Analysis of variance for method 2, model 1 with expectations of mean squares	53
3.6	List of SSR primers used for DNA amplification	59
3.7	Reagents with their concentration and quantity used for single PCR reaction	61
3.8	PCR amplification protocol for SSR primers	61
4.1	Analysis of variances for fourteen yield related traits in cucumber	65
4.2	Mean performance of cucumber genotypes for different yield and its contributing traits	72
4.3	Estimation of coefficient of variance and other genetic parameters for different yield and its contributing traits in cucumber	77
4.4	Heterosis for days to first male flower	80
4.5	Heterosis for node number to first male flower	82
4.6	Heterosis for days to first female flower	84
4.7	Heterosis for node number to first female flower	85
4.8	Heterosis for days to first	87
4.9	Heterosis for days to last harvest	88
4.10	Heterosis for internodal length (cm)	90
4.11	Heterosis for plant height (m)	92
4.12	Heterosis for fruit length (cm)	93
4.13	Heterosis for average fruit diameter (cm)	95

4.14	Heterosis for number of fruits per plant	97
4.15	Heterosis for average fruit weight (g)	98
4.16	Heterosis for fruit yield per plant (kg)	100
4.17	Heterosis for fruit yield (q/ha)	102
4.18	Summary table showing top three promising heterotic crosses with respect to each yield and its contributing traits in desired direction	104
4.19	Analysis of variance for combining ability in cucumber genotypes for yield and its contributing traits	106
4.20	General combining ability effect of parents for different yield and its contributing traits in cucumber	110
4.21	Estimation of specific combining ability effects for different yield and its contributing traits in F ₁ 's of diallel cross of cucumber	111
4.22	Best general combiner for different traits in cucumber	116
4.23	Downy mildew incidence at weekly interval	121
4.24	Downy mildew disease severity at weekly interval	128
4.25	Grading of F ₁ hybrids and their parental population with check against Downy mildew (<i>Pseudoperonospora cubensis</i>)	129
4.26	Level of polymorphism revealed by ten SSR primers in thirty six genotypes of cucumber	137
4.27	Pair wise similarity matrix based upon Jaccard's coefficient for 36 genotypes of cucumber	140

LIST OF PLATES AND FIGURES

Table No.	Title	Page
1	Experimental field view	41
2	Crossing block maintained open field conditions	42
3	Fruit harvesting, seed extraction and drying	43
4	PCR amplification of 36 cucumber genotypes by SSR 13262	134
5	PCR amplification of 36 cucumber genotypes by SSR 69	134
6	PCR amplification of 36 cucumber genotypes by SSR 60	135
7	PCR amplification of 36 cucumber genotypes by SSR 54	135
8	PCR amplification of 36 cucumber genotypes by SSR 61	136
9	PCR amplification of 36 cucumber genotypes by SSR 52	136
Fig. 1	Dendrogram of Cucumber lines based on the SSR marker data set using UPGMA based on Jaccard's similarity coefficient	141

LIST OF ABBREVIATIONS

%	Per cent
@	At the rate
°C	Degree Celsius
µg	Microgram
C.D.	Critical Difference
C.V.	Coefficient of Variation
cm	Centimeter
cm ³	Cubic Centimeters
cv.	Cultivar
<i>viz.,</i>	Videlicet (Namely)
<i>et.al</i>	Etalia, (Co-worker)
Fig.	Figure
FW	Fresh Weight
g	Gram
ha	Hectare
<i>i.e.</i>	That is



Introduction



Cucumber (*Cucumis sativus* L.) is one of the important Asiatic species and member of the Cucurbitaceae family having chromosome number $2n=2X=14$ which has 120 genera and more than 800 species (Jeffrey, 1980). Out of these, 34 genera and 108 species occur in India, including 38 endemic species and another 38 non-endemic species. Cucumber is originated in India (Sebastian, 2010) from its wild progenitor *Cucumis sativus* var. *hardwickii* R., which is still found in southern foothills of the Himalayas. Its spread eastwards to China and westwards to Asia Minor, North Africa and Southern Europe (Seshadri and Parthasarathy, 2002). Cucumber has been cultivated in India for more than 3000 years and records indicate that it was used for food by ancient Egyptians, Greeks and Romans. It was grown in France in 9th century and in England during 14th century. Columbus is supposed to have brought Cucumber in America. China is considered as a secondary centre of diversity (De Candolle, 1882), where it occupies second largest area among vegetables after Chinese cabbage. China is the highest producer country which accounts for nearly half of the total world production. The other main producers are Iran, Turkey and USA.

Cucumber is grown throughout the world and is the fourth most important vegetable crop after tomato, cabbage and onion and the second most widely cultivated cucurbit after watermelon (Tatlioglu, 1993). It is well known for its economic importance as food plant, primarily cultivated for tender fruits, which are used as salad, pickles and also used with curd for preparation of “Rayata”. Mature fruits are also used as vegetable in India. The fruits and seed have cooling effect. Fruits are good for people suffering from constipation, jaundice and indigestion. Fruits are demulcent and diuretic. Fruits contain proteolytic enzyme, ascorbic acid oxidase, succinic and malic dehydrogenase. Fruits are also used as an astringent and antipyretic and the seed oil of cucumber is highly valuable for development of brain, therefore it is also used in Ayurvedic medicines (Robinson and Decker-Walters, 1999). The fruit has about 95 per cent water content which makes it diuretic, possessing a deep cleansing action due to the presence of some natural chemical constituents such as glycolic, lactic and salicylic acids (Uzodike and Onuoha, 2009).

One hundred gram of edible cucumber fruits contain 96g water, 0.6g protein, 0.1g fat, 2.2g carbohydrate, 45IU Vitamin A, 0.03mg Vitamin B1, 0.02mg Vitamin B2, 0.3mg Niacin, 12mg Vitamin C, 12mg Calcium, 0.3mg Iron, 15mg Magnesium and 24mg phosphorus (Alcazar and Gulick, 1983).

Cucumber is highly cross pollinated crop and usually monoecious in nature preferring warm weather and bright light for its better growth and development. It is an all year round out door vegetable in the tropics opined that cucumber is a typical vegetable of warm, temperate and cool tropical areas that can be cultivated at any time of the year (Chikezie *et al.*, 2016). It is a thermophillic, day-neutral, frost susceptible and annual plant having climbing or trailing habit through axillary un-branched tendrils. The fruit is a special type of berry, commonly known as ‘pepo’.

Cucumber is commercially grown in the tropical and subtropical regions of the world. In India, cucumber is cultivated from higher altitude to plains under open field condition as well as under protected conditions including river beds. In north Indian plains, generally two crops are grown in a year i.e. spring-summer and kharif season, while in hills it is cultivated as an autumn summer crop. The global area under cucumber cultivation is 19.845 mha with a production of 75.219 MT and productivity 37.90 tonnes ha⁻¹ (FAO, 2018). China holds rank 1st in both area and production of cucumber with an area of 1.044 mha and production 5.620 mt (FAO, 2018). In India, the harvested area and production of cucumber is 0.082 mha and 1.259 mt respectively with average productivity of 15.35 tonnes per hectare (NHB, 2018). Haryana is leading in both area and production of cucumber with area of 0.017 mha and 0.2744 mt production (NHB, 2018). In Cucumber, sex expression is generally influenced by environment. Under long day and high light intensities staminate flowers predominate, whereas under short day and low light intensities female flower predominate. For crossing purpose, pistillate flowers are closed with a rubber band or covered by paper bag to protect against unwanted pollen 1 day prior to opening in the afternoon. Unopened male flowers are also covered similarly at the same time. Anthesis takes place around 5.30-7.00 hr. Dehiscence occurs around 4.30-5.00 hr. Pollen fertility is up to 14 hr. Next day morning, pollination is carried out from pollen of protected staminate flower. A thread is tied on selfed flowers and a label is tied on the crossed flowers.

In any crop improvement programme, it is necessary to assess the nature and magnitude of genetic variability, heritability and genetic advance in the initial parental material. The efficiency of selection largely depends upon the magnitude of variability present in the breeding population. Hence, knowledge of variability present in the gene pool of a crop species is essential to start a judicious breeding programme. Selection is also effective when there is genetic variability among the individuals in population. Earlier variability used to be assessed by visual observation. Now biometrical methods are available for systematic assessment of genetic variability. A quantitative measure which provides information about the correspondence between genotypic variance and phenotypic variance is heritability. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1981). It is the ratio of variance due to hereditary differences to the total phenotypic variance. This ratio is expressed in percentage. If the percentage is large, characters regarded as highly heritable. On the other hand, if it is smaller, environmental agency is considered as mostly responsible for phenotypic manifestation of the character.

An unambiguous, reliable, fast and cost effective assessment of genetic diversity is important for the conservation, evaluation and utilization of genetic resources, for studying the diversity of pre-breeding and breeding germplasm and for determining the uniqueness and distinctness of the phenotypic and genetic constitution of genotypes to protect breeder's intellectual property rights (Franco *et al.*, 2001).

Today public sector varieties are not much used by farmers for commercial cultivation. So, in order to isolate desirable genotypes with higher yield and better quality, there is an urgent need to assess the existing variability under specific environment (Saikia *et al.*, 1995).

Heterosis term was coined by Shull in 1914. Heterosis refers to the superiority of F_1 hybrid in one or more characters over its parents. In other words, heterosis refers to increase of F_1 in fitness and vigour over the parental values. In current usage heterosis and hybrid vigour are used as synonyms and interchangeable. Heterosis can be estimated over mid-parent value (relative heterosis), better parent value (heterobeltiosis) and check parent (standard heterosis). Generally, positive heterosis is considered as desirable, but in some cases negative heterosis is also desirable (such as

earliness, days to first flowering, days from flowering to first fruit setting, days from fruit setting to maturity). The very basic problem in cucumbers is concerning with the low marketable yield. Heterosis breeding provides an opportunity for achieving unique improvement in yield and other desirable attributes in one generation that would be more time consuming and difficult with other conventional breeding methods. It has direct relevance for developing hybrids and an effective tool for improvement in yield, earliness, quality and resistance to diseases. In cucumber too, success of F₁ hybrids has encouraged the breeders to develop hybrids which are early, high yielding, tolerant to biotic and abiotic stresses. For achieving this, availability and characterization of germplasm, estimation of heterosis and working out combining ability of parents and crosses is a useful step for development of new varieties.

Hays and Jones (1916) two British scientists, were the first to report heterosis in cucumber. They found that F₁'s from crosses between unrelated parents showed increase in yield over the better parent by as much as 24-39 per cent. Heterosis has contributed significantly towards increased crop production and it has become the basis of multi-billion dollar agro business in the world (Phillips, 1999). The exploitation of heterosis is much easier in cross pollinated crops and being cucumber monoecious, provides ample scope for the utilization of hybrid vigour on commercial scale.

Combining ability analysis is useful for the study and comparison of homozygous inbred lines in hybrid combination (Sprague and Tatum, 1942). It is one of powerful tools available which gives the estimates of combining ability effects and aids in selecting desirable parents for heterosis breeding. General combining ability (GCA) is a measure of additive genetic action, and specific combining ability (SCA) is deviation from additivity (Kempthorne, 1969; Mayo, 1980). General combining ability is a main effect and SCA is an interaction (Olfati *et al.*, 2012). The aim is to determine the breeding value of the cross (Griffing, 1956).

The concept of general and specific combining ability is of practical importance to the breeders. It is therefore, in the interest of breeders to know how the two combining abilities are related to various components of heritable variations. It helps in the selection of suitable parents for hybridization and in identification of superior cross combinations. General combining ability (GCA) can be defined an

average performance of a genotype in series of hybrid combination, whereas average performance of a parent in specific cross combination is the specific combining ability (SCA).

Downy mildew is common disease in cucumber caused by the pathogen [*Pseudoperonospora cubensis* (Berk. & Curt.) Rostov.]. It is a major foliar disease of cucumber (Palti and Cohen, 1980). Studies on the host range of *Pseudoperonospora cubensis* indicate approximately 20 genera, including 50 species in the Cucurbitaceae, are hosts. A total of 19 host species are in the genus *Cucumis* (Palti and Cohen, 1980; Lebeda, 1992; Lebeda and Widrechner, 2003). The cucurbit downy mildew pathogen is an obligate parasite and, with the rare exception of oospore production, can only survive and reproduce on living host tissue (Bains and Jhooty, 1976). Environmental conditions affect overwintering capacity as well as disease development and intensity (Cohen, 1977). In production regions where conditions are too harsh for *Pseudoperonospora cubensis* to survive all year, the pathogen is introduced through the spread of sporangia in wind and storms originating in warm regions where the pathogen can overwinter on wild and cultivated hosts (Bains and Jhooty, 1976).

Symptoms of cucumber downy mildew generally occur only on the foliage. Infection first appears as small water soaked lesions on the underside of leaves. The disease is characterized by formation of yellow, more or less angular spots on the upper surface of the leaves. White purplish spores appear on the under surface of the leaves. Chlorotic lesions eventually turn necrotic. Eventually the entire leaf will become necrotic and die. Symptoms vary depending on relative susceptibility of the cultigens. The most resistant cultigens exhibit a hypersensitive response (HR) with small necrotic or chlorotic flecks and sparse sporulation, while the most susceptible cultigens are highly chlorotic and necrotic. The HR type resistance was first described by Barnes and Epps (1954) in cucumber PI 197087, from a single resistance gene *dm-1*. Resistance from PI 197087 was used intensively in breeding new cultivars, and most current cultivars are thought to have some resistance derived from PI 197087. This resistance proved effective for many years but has since been overcome. *Pseudoperonospora cubensis* has high evolutionary potential and qualitative resistance is generally easily defeated.

Environmental conditions play a fundamental role in disease intensity (Cohen, 1977). Leaf wetness is critical for infection to occur, with sporangia requiring free moisture to germinate, but temperature determines the rate of disease. Sufficient leaf moisture can be supplied by rainfall, dew formation, or irrigation. The ideal temperature for sporulation and subsequent infection is 15°C, but a range between 5 and 30°C will suffice. The pathogen generally thrives in warm humid regions. Variability in the pathogen population may also play a role in cucumber response to downy mildew.

Genetic diversity between individuals or populations can be determined using morphological or molecular markers. Phenotypic traits have certain limitations as they are influenced by environmental factors and the developmental stage of the plant. Molecular markers based on DNA sequence polymorphism are more informative and independent of environmental conditions. Genetic markers (morphological, biochemical and molecular) have been employed for the characterization of genetic diversity present in cucumber (Knerr *et al.*, 1989; Meglie *et al.*, 1996; Staub *et al.*, 1997).

DNA markers are becoming more popular and effective to study the genetic diversity and choosing right parents. DNA markers have numerous application in plant breeding such as assessing the level of genetic diversity within germplasm and cultivar identity (Solanki and Seth, 1980; Huang *et al.*, 2009). Advent of polymer chain reaction (PCR) has revolutionarized the DNA based diagnostic. Simple-sequence repeats (SSRs), also known as microsatellites, are short tandem repeated motifs that may vary in the number of repeats at a given locus (Tautz, 1989). SSR markers have many advantages over other molecular markers, such as genetic co-dominance. It is widely used as a versatile tool in plant breeding programs, as well as in evolutionary studies, because of their high ability for showing diversity among cultivars (Adato *et al.*, 1995; Mhameed *et al.*, 1996; Levi and Rowland, 1997).

Diallel cross refers to all possible crosses among 'n' lines and the analysis based on the estimation of such a set of crosses is known as diallel analysis. It is extensively used for the evaluation of varieties or strains in terms of their genetic makeup. Diallel analysis provides a sensitive approach for large scale studies of quantitative characters.

It yields reliable information on the components of variance and on GCA and SCA variances and effects. Thus it helps in the selection of suitable parents for hybridization as well as in the choice of appropriate breeding procedures.

Diallel analysis developed by Jinks and Hayman (1953) and Hayman (1954) offer means of obtaining useful information on differential parental combinations through an assessment of the overall genetic architecture of parental lines in relation to the characters studied. On the basis of diallel analysis, Griffing (1956) described a method for the precise measurement of general and specific combining ability which is very useful technique in classifying parental lines in terms of their hybrid performance and as such an aid in selecting parents which when crossed may give to more desirable segregants. Such information forms the backbone of any breeding programme and is of great significance to the breeders.

Keeping all above facts in consideration, the present investigation entitled **“Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.)”** will be taken with following objectives.

1. To estimate the extent of genetic variability for different yield related traits.
2. To estimate the extent of heterosis over its parents.
3. To study the general combining ability (gca) and specific combining ability (sca) of parents and hybrids.
4. To screen of parents and F₁ against downy mildew (*Pseudoperonospora cubensis* L.).
5. To assess the molecular diversity of cucumber lines.



*Review
of
Literature*



An attempt has been made to review the relevant literature of present study which has been described under following heads and sub-heads:

- 2.1 Genetic variability for different yield related traits.
- 2.2 Heterosis studies.
- 2.3 Combining ability.
- 2.4 Screening of parents and F₁ against downy mildew (*Pseudoperonospora cubensis*).
- 2.5 Molecular markers for studying genetic diversity of cucumber genotypes.

2.1. Genetic variability for different yield related traits

In 1889, Galton reported that continuous variation is due to heredity. Genetic variability is an obvious phenomenon of considerable importance in crop improvement. Vavilov (1951) for the first time perceived the importance of genetic variability and advocated that the wide range of variability provides better scope and future of selecting desired genotypes.

The degree to which the variability of quantitative character is transferred to the next generation is referred as heritability. Genetic advance is the result of heritability and infers the potentiality of selection intensity. Genetic advance, when considered along with heritability gives reasonable assessment of the resultant effects of selection in breeding populations (Johnson *et al.*, 1955).

In another study, Das *et al.* (2005) demonstrated considerable variability among 18 diverse cucumber genotypes for stability during summer and rainy seasons. Observations recorded were vine length, fruit number, fruit length, fruit diameter, fruit weight and yield per vine. The variance for genotypes and environment was found highly significant for all the characters, thus revealed the presence of genetic variability in the material for all the various characters.

In one more experiment, Kumar (2006) evaluated genetic variability in 35 diverse genotypes of cucumber. Analysis of variance showed significant differences

among all the genotypes for the characters like node number at which first female flower appears, days to first female flower appearance, days to marketable maturity, fruit weight, fruit length, flesh to seed cavity ratio, number of fruits per plant, yield per plant, rind firmness, total soluble solids and cucurbitacin content.

Uddin *et al.* (2006) examined the considerable genetic variability in 25 diverse genotypes of cucumber. The results from the experiment revealed significant differences among all the studied genotypes with significant variation for all the characters. Bhat *et al.* (2007) conducted an extensive survey to study the presence of angular leaf spot in all cucumber growing areas of Kashmir valley with incidence and intensity ranging from 23.3 to 74.4 per cent and 10.5 to 26.0 per cent, respectively. The pooled data demonstrated that angular leaf spot of cucumber was prevalent in all the locations surveyed with varying degrees of incidence and intensity, which was minimum in first but maximum in last (third) stage of survey. Highest disease incidence and intensity at all the three stages was observed at Narain Bagh, Srinagar, followed by Waskura, Shadipora, Dal area, and Mangnipora, respectively. Minimum disease incidence and intensity was recorded at Krimsher (Badgam).

Munshi *et al.* (2007) collected 31 accessions of wild and feral form of cucumber (*Cucumis sativus* var. *hardwickii*) from different regions of India and examined for days to first fruit set and first picking, fruit weight, fruits per plant, fruit length: diameter (L:D ratio) and yield per plant. Highly significant variation was obtained among the genotypes for all the characters studied; hence individual plant selection could be an effective way for isolation of superior genotypes for these traits.

Hanchinamani *et al.* (2008) conducted a trial on 45 diverse genotypes of cucumber to evaluate the mean variability for 20 characters. All the genotypes exhibited significant differences for all the characters under study. The genotype, BGD-L recorded the maximum mean value for number of primary branches per vine, fruit length, average fruit weight, number of fruits per vine and fruit yield per vine, however; DWD-2 gave maximum mean value for fruit diameter, flesh thickness and days to first male flower appearance, while BNGL-1 recorded maximum mean value for vine length. The genotype LL-02 registered maximum mean value for days to first female flower appearance and inter-nodal length, while the two genotypes CL-1 and

CHC-2 had the maximum mean value for node number at which first male and female flower appears, respectively.

In an experiment, variability in 25 diverse cucumber genotypes for fruit yield and yield contributing trait was evaluated. A wide range of variability along with estimates of phenotypic coefficients of variation and genotypic coefficients of variation was recorded for days to first female flower anthesis, number of primary branches per plant, number of fruits per plant, node number bearing first female flowers, fruit length, fruit weight, cavity of fruit at edible stage and fruit yield per plant. Therefore, these traits are more reliable for effective selection (Kumar *et al.*, 2008). Yadav *et al.* (2009) used 20 cucumber genotypes and observed considerable amount of genetic variability for all the traits except cavity of fruit at edible stage. Number of days to first female flower anthesis showed the maximum phenotypic and genotypic coefficient (PCV and GCV).

A field study was conducted by Hossain *et al.* (2010) to evaluate the field performance, variability, characters association and genetic divergence of 58 long type cucumber accessions. The results revealed that the highest GVC was obtained in yield per plant (42.75%) where number of fruits per plant (33.41%), fruit length (27.57%), number of lateral shoots (24.19%), average fruit weight (22.14%), petiole length (16.10%), node order at which male and female flower opened (13.28% and 12.62%) were recorded. Among the long type cucumber accessions, CSL51 gave the highest yield per plant (2.69kg). The correlation co-efficient studies revealed that yield per plant had highly positive and significant association with fruit length and diameter, average fruit weight and number of fruits per plant.

Gaikwad *et al.* (2011) found substantial role of environment in the expression of the traits as exhibited by lower estimates of GCV than PCV for those traits. The coefficient of variation were high for traits percent diseases index (PDI), length of fruit, number of fruits per vine, and weight of fruit as was the broad sense heritability estimates. Final vine length and weight of fruit recorded high estimates of heritability

Call *et al.* (2012) screened the 86 cucumber cultigens (cultivars and breeding lines) for higher yield and resistance to the new strain of downy mildew. None of the cultigens tested in this study indicated a high level of resistance, although differences in resistance were detected. Lines WI 2757 and M 21 and cultivar Picklet were consistent

among the top resistant lines in North Carolina and Michigan. The cultivars Coolgreen, Wis. SMR 18 and Straight 8 were identified as moderately to highly susceptible. An unreleased hybrid, Nun 5053 F₁ and the cultivar Cates were the top yielding lines overall. The best cultivars in this study were found moderately resistant and would likely require application of fungicide to attain high yield and quality in the presence of downy mildew. Until high resistance becomes available, growers would benefit by using fungicides in combination with tolerant and moderately resistant cultivars.

In another study, Chikezie *et al.* (2016) evaluated sixteen exotic and indigenous cucumber genotypes (*Cucumis sativus* L.) under early and late seasons planting and results showed a highly significant difference among the genotypes in all the traits studied in both seasons. Beit Alpha genotype gave the highest fruit yield/ha in early season planting, while in the late season, the highest yield producer was Ashely. In both seasons, vine length, number of branches and leaves, leaf area, number of pistillate and staminate flowers/plant, number of fruit and fruit weight/plant showed positive and significant correlation with total fruit yield/ha. In both seasons, the highest positive direct effect on yield was recorded in fruit weight/plant. Significantly highest total fruit yield/ha was recorded in the early rainy season planting in this agro ecological zone. Based on high fruit yield, Beit Alpha genotype for early season planting and Ashley genotype for late season are recommended for cultivation in the Southeast Nigeria agro ecological zone.

Kumar *et al.* (2013) found high genotypic coefficient of variation in thirty cucumber genotypes for seed vigour index- I and yield per plot, whereas, it was moderate for node number bearing first female flower, severity of powdery mildew, angular leaf spot and anthracnose, average fruit weight, harvest duration, fruit length, seed vigour index-II, total soluble solids, number of marketable fruits per plant and fruit breadth. It was low for traits namely, seed germination and days to marketable maturity.

Basavarajeshwari *et al.* (2014) assessed fifty two cucumber genotypes and recorded highly significant variation for vine length, number of primary branches per plant, number of leaves per plant, leaf area index, days taken to first male and female flower, node number bearing first female flower and days to first harvest. Moderate to high coefficient of variation were recorded for vine length, number of primary branches

and node number bearing first female flower at both genotypic and phenotypic levels.

An experiment was conducted by Ranjan *et al.* (2015), where they recorded wide genetic variation for all the characters studied namely, vine length, number of primary branches per plant, number of fruits per plant, shelf life of fruits, seed length, hundred seed weight, number of seeds per fruit, fruit colour, flesh colour, total soluble solid content and susceptibility towards downy mildew and three viral diseases. Both phenotypic and genotypic coefficients of variation were high for node number bearing first female flower, number of primary branches per plant, fruit weight, number of fruits per plant, shelf life of fruits, hundred seed weight and number of seeds per fruit whereas, vine length and seed cavity diameter showed low genotypic coefficient of variation. Ullah *et al.* (2012) observed high GCV and PCV values for yield per plant, fruits per plant, fruit weight and fruit length in cucumber, whereas the broad sense heritability ranged from 42.26 to 89.55% for various traits.

In a field study, variability, heritability and genetic advance for yield and contributing traits in 38 advanced lines of cucumber (*Cucumis sativus* L.) were assessed. GCV and PCV were highest for node at first female flower appearance followed by node at first male flower appearance, yield per plant, seed cavity breadth, average fruit weight and number of fruits per plant. High estimated genetic advance over mean and heritability values were observed for nodes per vine, node at first female flower appearance, days to first female flower opening etc (Veena *et al.*, 2012). Similarly, Golabadi *et al.* (2012) observed a high variation for all the studied traits like total fruit yield per pickling between genotypes.

Afangideh and Uyoh (2007) evaluated eleven exotic and six indigenous cultivars of cucumber (*Cucumis sativus*) for yield and quality characteristics. Total fruit yield was significantly higher ($P < 0.01$) and fewer days to flowering ($P < 0.001$ and 0.01 , respectively). Genetic analyses indicated that Phenotypic Coefficients of Variation (PCV) were higher than genotypic coefficients of variation in all of the attributes studied; while length of vine at 6 weeks had the highest genetic gain. High heritability (broad sense) estimates of 94% and 85% were obtained for days to flower initiation and days to 50 percent flowering, respectively. Length of vine at 6 weeks, days to flower initiation and days to 50% flowering had high to moderate genotypic

variance, high to moderate heritability. Selection can, therefore, be based on these characters, and their phenotypic expression would be a good indicator of their genotypic potentiality.

An experiment was carried out by Kandasamy (2017) where he examined twenty diverse genotypes of cucumber collected from Tamil Nadu and Kerala regions to study the morphological characters like days to first female flowering, node number of first female flower, vine length, number of secondary branches, days to fruit harvest, fruit length, fruit girth, fruit diameter, average fruit weight, number of fruits per plant, 1000 seed weight and yield per plant to estimate the variability, heritability, genetic advance. In variability studies, the yield per vine was recorded with highest mean value CS 6 genotype. The maximum phenotypic and genotypic co-efficient of variation (PCV and GCV) was for yield per plant followed by average fruit weight, fruit diameter and number of fruits per plant. High heritability was observed for all the characters except node number of first female flower. Genetic gain was maximum for yield per plant followed by average fruit weight, fruit diameter, number of fruits per plant, number of secondary branches, fruit length, fruit girth and 1000 seed weight.

Karthick *et al.* (2019) assessed the PCV, GCV, heritability and genetic gain for various horticultural traits and states that phenotypic coefficient of variation (PCV) were higher than the corresponding values of genotypic coefficient of variation (GCV). While the difference between PCV and GCV was very less for length of vine, number of primary branches, number of nodes per vine, node number bearing first male flower, node number bearing first female flower, days for first male flower, days for first female flower, days for first harvest, number of male flower, number of female flower, number of fruits per plant, fruit length, fruit diameter, fruit weight and yield per plant and these traits are less influenced by environment. High phenotypic and genotypic coefficient of variation were observed number of primary branches, node number bearing first male flower, number of male flower, number of female flower, number of fruits per plant, fruit length, fruit weight and yield per plant. In this experiment, all the studied traits had high heritability coupled with high to moderate genetic advance except days for first male and female flower appearance.

2.2 Heterosis

The two British scientists, Hays and Jones (1916) were the first to report heterosis in cucumber. They observed that F_1 from crosses between unrelated parents resulted increase in yield over the better parent by as much as 24-39 per cent. Heterosis breeding is the well-organized and effective way to exploit the gene diversity present in crop plants. Heterosis is generally manifested in positive direction like superiority in adaptation, increase in yield and quality, disease resistance, maturity and general vigour over its parents but in some cases it is in negative direction like for earliness, plant height, maturity duration and toxic substances, which is also a desirable character in crop breeding. Heterosis is well known in cross-pollinated species (Hayes and Footer, 1976). Among cucurbits, cucumber has distinct and unique sex mechanism which can be manipulated easily for F_1 hybrid production. Further, cucumber has distinct advantage in commercial exploitation of heterosis because of favourable genetic mechanism, low inbreeding depression, high heterosis percentage for yield and related traits, large number of seeds per pollination and requirement of low seed rate per unit area.

In an experiment, Prasad *et al.* (2002) carried out multivariate analysis of 32 cucumber lines for eight characters and identified six genetically diverse parents. These parents were then used to make all possible combinations and high residual heterosis was observed for yield per plant (10.41-111.49%), fruit number per plant (12-188.37%), flesh thickness (4.71-53.9%), fruit length (4.6-37.57%), vine length (19.4-67.9%). The crosses with higher percentage of heterosis and residual heterosis were advanced for successive generations to select transgressive segregant lines.

Bairagi *et al.* (2002) identified PCUC-98-25 \times DC-1 as the best heterotic combination for the characters like days to first flowering (-8.75%), nodal position of first female flower (-3.81%), number of primary branches per plant (40.6%) and vine length (32.9%). The F_1 hybrid, DC-1 \times PCUC-28 showed 121.96% and 91.921% heterosis for number of fruits per plant and yield per plant, respectively. In another study, Bairagi *et al.* (2005) evaluated 28 non-reciprocal F_1 's derived from 8 diverse cucumber genotypes during to study heterosis over better parents and the check cultivar, Pant Cucumber Hybrid-1 (PCUCH-1). The hybrids PCUC-83 \times PCUC-15, PCUC-83 \times PCUC-25 and PCUC-25 \times PCUC-15 were found most promising ones.

Kumbhar *et al.* (2005) evaluated 28 F₁ hybrids of cucumber for yield and its components. The highest heterosis of 80.69% was recorded for yield per plant followed by number of fruits per vine (67.12%) and days to first fruit harvest (61.7%). Similarly, Pandey *et al.* (2005) revealed that F₁ hybrids DC-1 × B-159 and VRC-11-2 × Bihar 10 were observed to be the best hybrids for total fruit yield as they recorded high significant positive heterosis over better parent (100.8 and 60.19%) and mid parent (140.66 and 71.29%).

In a field study, Sudhakar *et al.* (2005) used fifteen lines of cucumber to develop 77 F₁ hybrids in different combinations. The results revealed that there was a wide variation in magnitude and direction of heterosis for all the traits. Branches per plant, fruits per plant, fruit weight, fruit length, fruit diameter and total fruit yield were the high heterotic characters. Appreciable heterosis in desirable direction was obtained over better and mid parents for all the characters. The hybrids DC-1 × B-159 and VRC-11-2 × Bihar-10 were the best hybrid combinations for total fruit yield as they observed significant positive heterosis over better and mid parent. The high yield recorded in these attributed to high number of fruits per plant.

Munshi *et al.* (2005) studied heterosis in 15 F₁ hybrids of cucumber. The F₁ hybrids DC-1 × PCUC-8, CHC-1 × PCUC-8 and DC-1 × Poinsette were observed to be best performing F₁ hybrids for yield per plant. The hybrid DC-1 × PCUC-8 showed 29.2% and 45.0% increase in yield, over top parent and standard parent, respectively. Moreover, Nehe *et al.* (2007) observed that heterosis and heterobeltiosis were superior for many traits including fruit number per vine, followed by yield per plant, and fruit diameter. The F₁ crosses Talegaon Local × Poona Khira, Sheetal × Junnar Local and Himangi × Shubhangi, recorded the maximum level of heterosis and heterobeltiosis for yield per plant and its component traits in cucumber.

Yadav *et al.* (2008) conducted a field trial in 18 cucumber lines at Uttar Pradesh. Among these lines, 15 lines were selected as female parents (lines) and 3 as male parents (testers). The line × tester analysis was used to assess the performance of 12 characters *viz.*, days to flowering of first male flower, days to flowering of first female flower, length of vine, number of primary branches per plant, number of nodes of first male flower, number of nodes of first female flower, number of nodes per vine,

length of fruit, diameter of fruit, number of fruits per plant, fruit weight and fruit yield per plant. The average heterosis for yield per plant ranged between 19.03 to 60.00 per cent. The heterotic response of these crosses was also exhibited in most of the yield attributing traits and can be used in commercial hybrid seed production.

Godoy *et al.* (2008) studied heterosis for yield traits and found that F₁ hybrids, H-35 and H-43 had the maximum yields. Hybrids recorded positive heterosis over the parental lines and also general heterosis in relation to the superior parents. Hachinamani and Patil (2009) demonstrated that parental lines BGD L, DWD-2, GBGL and Pointsette were superior for number of fruits per plant. The maximum heterosis in positive direction over mid (94.03) and better (31.73) parents were obtained in hybrid combinations of L₄ × T₁ and L₄ × T₂, respectively. The maximum yield is because of increase in average fruit weight and number of fruits per plant.

An experiment was carried out by Choudhary and Singh (2010) to study heterosis in *Cucumis sativus* var. *hardwickii* and reported that only PCUC 15 × P7 was superior over better parent PCUC 15 for days to female flower anthesis. Three crosses which showed significant heterobeltiosis for number of fruits per plant were PCUC 8 × P7 (44.22%), PCUC 28 × P5 (18.61%) and PCUC 15 × P7 (18.44%). Four F₁ crosses were superior over better parent for fruit yield per plant. The highest heterobeltiosis was reported in cross PCUC 15 × P3 (61.61%), followed by PCUC 15 × P7 (50.90%), PCUC 8 × P7 (43.01%) and PCUC 15 × P5 (28.43%).

In another study, Kumar *et al.* (2010) reported that Pusa Uday, DC-1 and CH-20 were the superior performing parental lines for yield per plant. Appreciable amount of heterosis was recorded over better, top and standard parents for all the characters. CRC-8 × Pusa Uday, CHC-2 × Pusa Uday and G-338 × Pusa Uday were three best performing F₁ crosses for yield. Singh *et al.* (2010) used half diallel method to study heterosis involving ten cucumber parents with six characters. VRC-18-2 × Patna-3 showed the maximum heterosis for yield. They also suggested that traits like polar and equatorial diameter of fruit and yield should be used to improve through selection, whereas vine length, number of branches and individual fruit weight might be improved through hybridization.

Dogra and Kanwar (2011) attempted the crosses among eight parents (including two gynoecious lines) in half diallel fashion. Twenty eight F₁'s, eight parents and one check were grown in a randomized complete block design with three replications at two different locations viz., Nauni (L-1) and Chambaghat (L-2). Heterobeltiosis and standard heterosis for earliness was maximum in EC-173934 × LC-40 and G-2 × Gyn-1, respectively. The crosses G-2 × Gyn-1 and EC-173934 × LC-40 exhibited maximum negative heterobeltiosis and standard heterosis for earliness, while the cross K-90 × G-2 revealed maximum positive heterobeltiosis and standard heterosis for number of fruits per plant and yield. In the same year, Kushwaha *et al.* (2011) studied heterosis in 21 F₁ crosses of cucumber. The hybrids BC-11 × BC-12, BC-16 × Poinsette, BC-14 × BC-16, BC-15 × BC-16 and BC-11 × BC-16 showed maximum significant heterobeltiosis for node number to first female flower, fruit length, diameter, weight, and number of fruits per plant and total yield per vine, respectively.

Brar *et al.* (2011) crossed eight genetically divergent parental lines in a diallel pattern to investigate extent of heterosis for quality traits and reaction to downy mildew. Cross combination Long Green × Bhari Mansa had the maximum heterosis over better parent for vitamin C and over standard check cultivar Punjab Naveen for shelf life of fruits. Hybrid Long Green × Bhari Mansa registered best overall performance for studied quality traits.

A field trial was conducted to study heterosis for yield and its components in cucumber through 10 × 10 diallel analysis. The three best performing F₁ hybrids for total yield per plant were DC-2 × PCUC-28, PCUC-28 × VRC-11-1 and DC-2 × VRC-11-1, which showed 50.43, 43.61 and 35.32 per cent significant heterosis over top parent DC-2, respectively (Sarkar and Sirohi, 2011). Rabou and Hamed (2011) while studying ten F₁ hybrids for estimation of heterosis for some economic characters observed that seven out of ten evaluated hybrids showed significant positive heterosis over the better parent ranging from 18.24% to 138.39% for total yield per plant. The cross combination Cus 2-11-519 × Cus 2-23-576 showed maximum heterosis (138.39%) followed by Cus 2-11-519 × Cus 1-12-26 (60.26%) and Cus 3-2-14 × Cus 1-12-26 (49.80%).

Singh *et al.* (2012) studied heterosis in 36 F₁ hybrids for different fruit characters. The crosses BSC-1 × BSC-2, BSC-1 × CHC-1, VRC-11-2 × CC-5 and CC-7 × CHC-1 recorded positive and significant heterosis over standard parent and better parent, and concluded that these hybrids can be commercialized for high yield in cucumber cultivation. In the same year, Mule *et al.* (2012) studied heterosis for fruit yield and its components in a set of 27 F₁ hybrids of cucumber obtained from a Line x Tester method involving twelve diverse parents. Hybrids Pilibhit Local × K-90 followed by Sheetal × SPP-44 and Sheetal × CC-9 have exhibited high heterobeltiosis for fruit yield and its component characters. These crosses involved Poor × Poor and Poor × Good combiner parents. Further improvement in fruit yield could be possible through the hybridization and selection in transgressive segregants.

In another study, Airina *et al.* (2013) observed significant heterosis for most of the characters studied except for average weight of the fruit. The F₁ crosses EC 709119 × IC 538155, EC 709119 × IC 527427, EC 709119 × IC 538186 and EC 709119 × IC 410617, recorded high heterobeltiosis for fruit yield and number of fruits per plant in cucumber. In the following year, Singh *et al.* (2014) conducted an experiment to estimate heterosis for yield and its component traits in a 8×8 parent diallel cross excluding reciprocals. They observed that the maximum heterosis for yield per vine was expressed by the cross combinations PCUC-15 × PCUC-15-1 (211.70) followed by CHC-2 × C 99-12 (177.66), PCUC-15 × CHC 2 (97.35), PCUC 15-1 × BIHAR (69.84) and EC 43342 × C 99-12 (62.10). The cross CHC 2 × C 99-12 also showed significant heterosis for fruit weight, number of fruits per vine and vine length and was found to be one of the best crosses for yield per vine.

Pati *et al.* (2015) reported heterosis in cucumber for yield components in 28 F₁ crosses and reported that GBS-1 × Pusa Uday showed heterosis for earliness characters, fruits number per plant and yield per plant, whereas, GBS-4 × Pusa Uday recorded appreciable amount of heterosis for fruit length, average fruit weight and fruit diameter. In the same year, Jat *et al.* (2015) developed twenty one F₁ hybrids by using seven parental lines including two gynocious lines in a half diallel mating design to determine heterosis for earliness, yield and yield related traits. PPC-2 × Pusa Uday, GPC-1 × Pusa Uday and PPC-2 × Punjab Naveen were the three best heterotic hybrids for yield per plant, showing 64.51, 55.61 and 54.57% heterosis, respectively, over standard check Pusa Uday.

Singh *et al.* (2015) studied heterosis for yield and its related characters in an 8x8 parent diallel cross excluding reciprocals and observed wide range of economic heterosis for most of the characters studied. Heterosis over better parent for yield per vine ranged from -66.16 to 162.43%. Maximum heterosis for yield per vine was shown by the cross combinations PCUC 15 × PCUC 15-1, PCUC 15-1 × BIHAR 1, EC 43342 × C 98-6, EC 43342 × C 99-10 and PCUC 15-1 × C 98-6. In the following year, Singh *et al.* (2016) while evaluating eight parental lines and their 28 hybrids along with a standard check reported that the extent of heterosis varied from -14.31 to 18.27 over better parent and -21.26 to 2.24 over standard check. Hybrid ACC-2 × ACC-6 and ACC-5 × ACC-7 were found to exhibit maximum heterosis over better parent and standard check, respectively. For number of fruits per vine, the extent of heterosis ranged from -28.15 to 32.15 over better parent and -17.80 to 35.17 over standard check. Maximum heterosis over better parent and standard check was exhibited by ACC-3 × ACC-4 and ACC-2 × ACC-8, respectively.

Kaur *et al.* (2016) crossed eight diverse cucumber genotypes in a half diallel mating design to obtain 21 F₁ hybrids for estimation of heterosis for quality attributing traits. JLG × NCH-1 was found to exhibit the maximum heterosis for flesh to seed cavity ratio over better parent (16.67%) and standard check NS-404 (11.11%), while that for total soluble solids was shown by JLG × Summer Kheera over better parent (31.06%) and standard check (34.39%).

Sandeep *et al.* (2017) evaluated F₁ population of 48 crosses, developed by crossing 16 lines (8 gynocious) and 3 testers and revealed that parental lines LC-1-1, CGN-20953, CGN-19533, Gyne-5, LC-15-5 and testers Japanese Long Green and K-75 were found superior on the basis of mean performance and general combining ability effects. The cross combinations LC-1-1 × K-75 (monoecious), CGN-19533 × K-75 (gynocious), CGN-20953 × Poinsette (gynocious), Gyne-5 × K-75 (gynocious) and LC-3-3 × Poinsette (monoecious) excelled based on per se performance, specific combining ability and heterosis studies. In the same year, Shailaza *et al.* (2017) used gynocious *Pgyn-1*, *Pgyn-4*, *Pgyn-5* and ten monoecious cucumber genotypes *viz.*, PCUC-28, PCUC-8, PCUC-83 US-832, PCUC-15, PCUC-25, PCUC-35, PCUC-208, PCUC-126 and Punjab Naveen were selected and crossed in line × tester mating design to produce 30 cross combinations during 2013. The F₁ and parents were evaluated

during spring-summer 2014. The cross Pgyn-1 × PCUC-35 showed positive heterosis over better parent and Pgyn-5 × US-832 over standard parent for days to first female flower and days to first harvest. Eighteen crosses showed heterobeltiosis for node numbers to first female flower. Highest heterobeltiosis was observed in Pgyn-5 × PCUC-28 (31.79%) for average fruit weight. For fruit yield highest value of heterobeltiosis was recorded in cross Pgyn-5 × PCUC-28. Highest heterobeltiosis was observed in Pgyn-4 × US-832 for number of fruit/vine.

A field trial was carried out by Simi *et al.* (2017) to investigate the heterosis for quantitative characters in 39 cucumber genotypes (19 parents and 20 F₁) were investigated. The analysis of variance indicated the highly significant differences among the parents and hybrids for 19 characters studied. Considerable coefficient of variation was observed for branches per plant, flesh thickness, placental thickness, fruit length, fruit width, male and female flowers per plant, leaf length, leaf breadth, vine length, fruits per plant, fruit yield per plant indicating the scope of selection for those characters. The characters like branches per plant, male and female flowers per plant, fruit length, fruit weight, fruits per plant, fruit yield per plant contributed the maximum variability towards divergence among cucumber genotypes. Heterosis study depicted that the crosses Sobujsathi × Baromashi, Sobujsathi × Khira, Himaloy × Khira, exhibited significant positive heterosis for 50% female flowering; Himaloy × Baromashi, Baromashi × Greenking for fruit length; Baromashi × Hero, Yuvraj × Khira for single fruit weight. Where Sobujsathi × Baromashi, Shila × Khira, Modhumoti × Hero and Modhumoti × Khira exhibited significant positive heterosis and heterobeltiosis for yield per plant. The highest positive heterotic effect for no. of fruits per plant was observed in Modhumoti × Baromashi (20%). The highest heterobeltiosis effect was found in hybrid Himaloy × Yuvraj (24.5%) followed by Sobujsathi × Khira (11.2 %), Modhumoti × Baromashi (10.0 %). Four crosses exhibited significant positive better parent heterotic effect for this trait and the combination Sobujsathi × Baromashi had the maximum heterosis on yield (47.6%). The maximum heterobeltiosis effect was found in Shila × Khira (27.73 %) followed by Modhumoti × Hero (15.14%) and Modhumoti × Khira (10%) for fruit yield.

In an experiment, Bhutia *et al.* (2018) studied the heterosis for yield and its component traits in eight parental lines and 28 F₁ hybrids obtained from 8 × 8 half

diallel cross excluding reciprocals in randomized block design (RBD) with three replication. P₄ (Pusa Uday), P₆ (DC-1) and P₅ (Punjab Naveen) were observed to be three best performing parents for total yield per plant. Appreciable heterosis was recorded over standard check (Pusa Uday) for all the traits studied except for fruit width. Three best performing hybrids were Pusa Uday × DC-1 followed by Pusa Uday × Kalyanpur Green and Pusa Uday × Punjab Naveen which showed significant heterosis of 86, 62.9 and 56.11%, respectively over standard parent for yield and other desirable traits and these hybrid combinations may be exploited for commercial cultivation.

Ene *et al.* (2019) estimated heterosis and revealed that cross ‘Zna Capso’ had the highest Better Parent (BP) heterosis in total fruit yield/ha while ‘BA Capso’ had the highest Mid Parent (MP) heterosis in the same trait. Significant general (GCA) and specific (SCA) combining ability variances were obtained in all the traits implying that both the additive and non-additive gene effects operated in the genetic expression of the traits. Relative magnitude of GCA and SCA variances indicated preponderance of additive gene action for all the traits. ‘Beit Alpha’ and ‘Straight 8’ are best general combiners while ‘BA Capso’ and ‘Capso Strght 8’ were the best specific combiners for total fruit yield.

2.3 Combining ability

The combining ability analysis gives useful information regarding the selection of parents in terms of the performance of their hybrids. The term general combining ability (GCA) indicates the performance of a line in several hybrid combinations and specific combining ability (SCA) to designate those effects in certain combinations which significantly departed what would be expected on the basis of average performance of the lines involved. The analysis of combining ability is the most important and efficient tool in selecting desirable parents for hybridization. General combining ability (GCA) is due to additive genetic variance and additive × additive epistasis, whereas specific combining ability (SCA) is due to dominance genetic variance and all types of epistasis *i.e.* additive × additive, additive × dominance and dominance × dominance. The estimation of GCA manifests selection of suitable parents for hybridization whereas; SCA helps in the identification of superior cross

combinations. Griffing (1956a) revealed combining ability analysis, to estimate the type of gene action involved in the study of inheritance of important quantitative traits, and Griffing (1956b) suggested that it can be estimated by combining ability analysis. Balliu *et al.* (2000) crossed five long fruited cucumber lines in diallel design. They reported that most yield components appeared to be under additive gene control. Sex expression appeared to be under both additive and non-additive control.

Verma *et al.* (2000) reported parent K-27080, CC-3, C-12, Gy-2 were found good general combiner for yield and its component traits. High SCA effect for yield and other trait were exhibited by cross combination JLG \times C-12, K-27080 \times C-12, K-27080 \times CC-3. Similarly, Bairagi *et al.* (2001) observed that parental lines PCUC-98-25, DC-1 and C-31 were superior and good general combiners for the characters studied. Among F₁ crosses, PCUC-98-25 \times C-31 recorded significant SCA effects for each and every character under study. The GCA variance was superior to the SCA variance, which suggests the predominance of additive gene action for the characters.

Sharma *et al.* (2001) studied the combining ability in cucumber using line \times tester mating design. The lines GYNL and Poona Khira were good general combiner for earliness, whereas Sel. 72-5, Swarapurna followed by GYNL and Sheetal were good general combiner for marketable fruit yield and its attribute. The hybrids Sel. 72-5 \times Poinsette and Swarapurna \times Poinsette observed significant SCA effects for 4 and 6 characters out of 7 characters studied, respectively.

In a field study, Lopez and Staub (2002) studied combining ability in three *Cucumis sativus* varieties (Gy-14, H-19 and Gy-7) and one *C. sativus* var. *hardwickii* (WI-5551). GCA was significant for fruit number, length/diameter ratio, number of female flowering nodes and days to anthesis whereas, SCA was significant for fruit number and days to anthesis. Fang *et al.* (2004) found that GCA variance for earliness of yield comprised 91.92% of the genotypic variation. The SCA variation for the total yield comprised of 82.92% of the total genotypic variance. Parental line 04 reported the highest GCA for earliness and total yield per plant, whereas parental line 03 and 06 reported the maximum SCA for earliness and total yield, respectively.

Kumbhar *et al.* (2005) studied combining ability for yield and its components *viz.*, days to first female and male flowers, number of female and male flowers, days to

first fruit picking, fruit length and diameter, number of fruits per vine and average fruit weight during summer 2001 in Pune, Maharashtra, India, with 28 F₁ hybrids of cucumber obtained by 8 × 8 diallel among 8 parents. The characters studied were governed by additive and non-additive gene action. There was close agreement between per cent performance of parents and general combining ability effects for all the characters. The best specific combinations were those involving parents with low and/or high combining ability. Shubhangi and Sheetal were identified as the best combiners for yield. The specific combinations Improved Long Green × Himangi and Poona Khira × Junnar Local were identified as the best hybrids.

Li *et al.* (2005) analyzed general (GCA) and specific combining ability (SCA) for five main quality characters *viz.*, protein content, total sugar content, fruit length, flesh thickness and fruit dry weight of pickling cucumber. GCA effects were high for protein content, total sugar content, flesh thickness and fruit dry weight of line ZR22, indicating its potential for use as parent in hybridization. SCA effects were high for all quality characters in LN11 × ZR22, indicating that this hybrid can be used in breeding for high-quality pickling cucumber. Munshi *et al.* (2006a) reported that mean square due to GCA and SCA were highly significant for mostly all the characters under study, showed the role of both additive and non-additive genetic components of variation. SCA was higher than the GCA component of variance in every character which indicated the role of non-additive gene action. The parents P₁, P₂ and P₄ were found to be the good combiners for yield/plant. The hybrids P₄ × P₆, P₂ × P₆ and P₃ × P₄ were most capable combinations for many traits including yield/plant. In the same year, Shushir *et al.* (2005) observed Shubhangi, Sheetal and Talegaon local as the best general combiner for yield. The SCA effect was highest for the cross Long Green × Himangi and Poona Khira × Junagarh Local.

Yudhvir and Sharma (2006) reported that SCA variances were higher than GCA for each and every character except length of the fruit and fruit diameter, showing the importance of non-additive gene action. The parental lines AAUC-2 and Sel-75-1-10 were good general combiners for yield and other related traits. The crosses Sel-75-1-10 × K- Paprola and CHC-2 × Sel-75-2-10 found significant SCA for yield and fruits number per plant. In the same year, Munshi *et al.* (2006) conducted field studies to analyse the combining ability of a 6 × 6 diallel cross of cucumber excluding

reciprocals. The mean square due to general (GCA) and specific combining abilities (SCA) were highly significant for almost all the characters indicating the importance of both additive and non-additive genetic components of variation. The SCA component of variance was higher than the GCA component of variance in all characters which indicated the importance of non-additive gene action for the control. Predictability ratio and average degree of dominance observed to be less than 0.5 and more than 1, respectively, for all the characters studied further confirmed the role of non-additive component of variance. The parents P₁, P₂ and P₄ were found to be good combiners for number of characters including yield per plant. The crosses P₄ x P₅, P₂ x P₅ and P₃ x P₄ were the most promising combinations for different characters including yield per plant. The results indicated the importance of heterosis breeding for effective utilization of non-additive gene action.

A field experiment was conducted by Singh and Sharma (2006) to evaluate the combining ability in 15 cross combinations (5 x 3) with 8 parents for 12 characters. Significant differences in the parents indicated that the majority of the parents had diversity for almost all the characters studied. Variance due to SCA was higher than that of GCA for all the characters except fruit length, fruit diameter and TSS, indicated the importance of non-additive gene action. The presence of non-additive gene action was predominant for most of the characters studied suggested the importance of hybrid vigour for these characters. In the subsequent year, Yadav *et al.* (2007) found that the parental lines 2020, 2017, 2231 and 2336 recorded a significant GCA effect. On the basis of SCA, seven superior heterotic crosses, namely 2237 x 2226, 2237 x 2238, 2015 x 2014, 2228x2238, 2028 x 2238, 2336 x 2014 and 2229 x 2226 were found superior for yield and yield related traits.

Hanchinamani and Patil (2009) studied thirty five F₁ hybrids of cucumber involving 12 parents to work out the combining ability for yield and its contributing traits. Significant differences in the parents revealed that majority of the parents had diversity for total yield per vine, total number of fruits per vine, fruit length, vine length, fruit diameter, average fruit weight, number of branches per vine, days to first female flower appears, node number at which first female flower appears. Considering combining ability values, parents BGDL, DWD-2, GBGL and Poinsette were found to be superior for total fruit number per vine, parents BGDL, DWD-2 and Vejundra Dosa

for total fruits yield per vine, parent BGD, White Long, Vejudra Dosa and BGBL for average fruit weight and parents BGD, PAU-1 and ARABL for high vigorous plants. The cross BGD \times Hot Season showed significant positive SCA for total fruit yield per vine and total number of fruits per vine.

In an experiment, Tiwari *et al.* (2009) studied combining ability analysis in a half-diallel cross of cucumber resulted the mean square due to general combining ability (gca) and specific combining ability (sca) were highly significant for almost all the characters. Specific combining ability components of variance were higher than general combining ability components of variance in all the characters which indicated the importance of non-additive gene action. Predictability ratio and average degree of dominance confirmed the role of additive and non-additive gene action. The parents CRC-8, CHC-2, G-338, Pusa Uday, DC-1 and CH-20 were observed to be good combiner for number of characters including yield per plant. The crosses CRC-8 \times Pusa Uday, CHC-2 \times Pusa Uday and CHC-2 \times DC-1 were most promising combination different characters including yield per plant.

Kumar *et al.* (2009) studied combining ability using cross combinations of salinity-tolerant and salinity sensitive inbreds and indicated that the mean square due to GCA and SCA were significant in desirable direction for all the characters. The potential cucumber hybrid CRC-8 \times Pusa Uday and CHC-2 \times Pusa Uday were found superior for earliness; yield and its attributing traits based on high SCA effects and could be exploited in saline areas of our country. In the same year, Uddin *et al.* (2009) reported significant differences among the parents and hybrids/crosses for GCA and SCA respectively. The lines F₁, M₁, F₈ and F₇ were found as the good general combiners for fruit yield per plant. F₈ \times M₂ was the best specific combiner for fruit yield per plant.

Yoshioka *et al.* (2010) reported that GCA effects were more significance than the SCA effect in determining the performance of the hybrid. Estimates of the GCA effects were highly significant for most parental genotypes and were highly correlated with the actual performance of parental genotypes. Sarkar and Sirohi (2010) revealed that the mean square due to general combining ability and specific combining ability were highly significant for every characters studied, further revealed that both additive and non-

additive gene actions played an important role for inheritance of these traits. The parental line DC-1 recorded highest GCA for weight of the fruit, length of fruit and yield per plant and parental line DC-2 recorded maximum favourable GCA effects for node number of first female flower and fruits per plant. The hybrid DC-1 × PCUC-28 and CH-20 × Himangi, were superior hybrids over its top parent for total yield per plant.

Chirani *et al.* (2011) demonstrated combining ability and heterosis in a 6x6 partial diallel cross to see the nature of gene action in cucumber (*Cucumis sativus* L.) and analysis of variance revealed high significant differences among all the F₁ hybrid means and among their respective six parental values for all the traits examined. The mean squares attributed to general combining ability (GCA) and specific combining ability (SCA) was also highly significant. SCA genetic variances were greater than those of GCA and more important for the traits of marketable yield as well as simple weight index, showing the dominance of non-additive gene action. Early yield and non-marketable yield were controlled by additive and non-additive type of gene action due to high GCA variances. Line 504 with its bearing of high general and specific combining ability is finally found desirable regarding cucumber hybrid seed production and therefore is recommended.

In the field experiment, Dogra and Kanwar (2011) reported that the high estimates of GCA were exhibited by parental line G2 and *Gyn1* for most of the characters under study. The cross combinations K-90 × G2 and K-90 × *Gyn1* recorded high SCA estimates and per cent performance for yield and number of fruits/plant. Similarly, Kushwaha *et al.* (2011) observed that both GCA and SCA variances were significant for all the characters studied. In general, the mean squares for GCA were larger than SCA for all the characters except yield per plant. BC-11 × BC-16, BC-15 × Poinsette and BC-13 × BC-14 were the most promising hybrids and showed highest SCA effects for yield per plant.

Olfati *et al.* (2012) made a comparison among two forms of half-diallel analysis in cucumber. The different half-diallel techniques used were Griffing's model I, method 2 and 4. These methods of diallel analysis were found to be interrelated. However, as Griffing's model I, method 4 partitioned heterosis into different components as well as gave information about combining ability and this method had

certainly some advantages over the other. The results further indicated using parental generations in the second Griffing method may cause biased estimate of the GCA and SCA variances. Thus, using the fourth Griffing method is more suitable than the other methods in providing time, cost, and facilities, and it is recommended as an applicable method.

In another trial, Singh *et al.* (2012) evaluated the F₁ and F₂ progenies of a 8 × 8 parent diallel cross (excluding reciprocals) of cucumber (*Cucumis sativus* L.) to analyze the combining ability and found that analysis of variance for combining ability revealed highly significant GCA and SCA variances for all the characters studied in F₁ and F₂ generations. However, the estimated values of GCA variance were lower than the SCA variance for all the traits in both F₁ and F₂ generations indicating the predominance of non-additive genetic variance. The parent C 99-12 was best general combiner for yield per vine, days to first male flower, fruit length, fruit weight and vine length in both the generations. The cross combinations EC 43342 × C 99-10, EC 43342 × C 98-6 and PCUC 15-1 × C 98-6 were observed as good general combiners for yield/vine in both F₁ and F₂ progenies.

An attempt was made to cross 6 diverse cucumber lines (*Cucumis sativus* L.) in diallel fashion excluding reciprocals. The 15 F₁ hybrids along with six parental lines were grown in randomized block design with three replications. The mean square due to GCA and SCA were highly significant for almost all the traits under experiment. The parents P₁, P₂, P₅ and P₆ were observed to be the good combiners for a number of characters, including yield per plant. The crosses, P₁ × P₅, P₂ × P₅ and P₂ × P₆ were most promising combinations for earliness and other desirable characters including yield per plant (Kumar *et al.*, 2013).

Olfati *et al.* (2013) studied general and specific combining ability and heterosis estimation of some cucumber lines for qualitative traits in partial diallel design in a 6 × 6 partial diallel cross to see the nature of gene action for fruit quality indices in cucumber (*Cucumis sativus* L.) and they observed highly significant differences among all the F₁ hybrid means and their respective six parental values for all the traits examined. The mean squares of general combining ability (GCA) and specific combining ability (SCA) were highly significant. In the same year, Bairagi *et al.* (2013)

reported that genotypes PCUC-25, PCUC-15, and PCUC-83 were good general combiners for maximum of the economic traits including number of fruits and fruit yield per plant where as the crosses PCUC-83 × PCUC-25, PCUC-83 × PCUC-15, PCUC-25 × PCUC-15 and PCUC-8 × PCUC-15 were good specific combiners for most of the economic traits studied including number of fruits and fruit yield per plant.

In an experiment, Kumar *et al.* (2013) demonstrated that the mean square due to GCA and SCA were highly significant for most the characters studied indicating the importance of both additive and non-additive type of genetic components. The parental lines CRC8 CHC-2, Pusa Uday, DC-1 were good combiners for many of the characters, including yield per plant. The hybrids, CRC-8 × Pusa Uday, CHC-2 × Pusa Uday and CHC-2 × DC-1 were superior performing for earliness traits and other characters which includes yield per plant. In the subsequent year, Vidhya and Kumar (2014) evaluated five genotypes namely CS-36, CS-10, CS-17, CS-37 and CS-39 for studying combining ability effects. CS-37 and CS-39 exhibited high gca for almost all the traits. High sca effects were recorded by hybrids CS-39 × CS-19, CS-37 × CS-17, CS-37 × CS-39 and CS-17 × CS-39.

Reddy *et al.* (2014) evaluated thirty six F₁ hybrids along with their parents for their combining ability for ten important quantitative characters and the results revealed that specific combining ability component of variance (σ^2_s) was higher than general combining ability component of variance (σ^2_g) for all the characters, which indicated the importance of non-additive gene action for improvement. The predictability ratio was observed to be < 0.5 for all the traits except node number of first female flower, which further confirmed the predominant role of non-additive component of variance for improvement of these traits.

In a field study, combining ability of fruit yield and morphological traits in greenhouse cucumber (*Cucumis sativus* L.) using a 9 × 9 full diallel population was analyzed. Data were collected on internode length, leaf length, leaf width, fruit length, and fruit diameter, number of fruits per plant, yield per fruit and yield per plant. Variance components showed that both the additive and the dominant gene effects played significant roles in the genetic control of the traits studied. Genetic control of internode length, leaf width and number of fruits per plant was accomplished by

additive effects. The significant mean squares of reciprocal crosses for all the studied traits suggested that maternal inheritance also played an important role in the inheritance of these traits. Significant general combining ability for fruit yield revealed that both selection and hybridization methods would lead to desirable genetic improvements in cucumber through accumulation of desirable alleles from parents in the target genotype, but that hybridization would be preferred (Golabadi *et al.*, 2015)

Pati *et al.* (2015) studied combining ability for yield and its related traits. The magnitudes of variance due to GCA as well as SCA were highly significant which indicated the significance of both additive and non-additive gene action. In order of superiority the gynoeocious based hybrids GBS-1 × Pusa Uday and GBS-1 × Punjab Naveen followed by monoecious hybrid GS-4 × Pusa Uday, exhibited highest SCA effects for many characters including yield per plant. In case of yield and other yield contributing characters where SCA component of variance (s^2_s) is higher than GCA component of variance (s^2_g), indicated preponderance of non- 15 additive gene action. Hence, the improvement programme based on heterosis breeding would be appropriate for improving these traits.

Kaur *et al.* (2016) while studying eight diverse cucumber genotypes and their 28 F₁ hybrids for combining ability analysis for quality traits found that the parent Gy-14 (flesh to seed cavity ratio and β -carotene) and Swarna Sheetal (ascorbic acid and dry matter content) were the best general combiner. The cross combination EC-27075 × Summer Kheera showed highest sca effect for total soluble solids whereas Pant Kheera-1 × Japanese Long Green had highest sca for ascorbic acid content. In the same year, Kumar *et al.* (2016) worked on the development of parthenocarpic gynoeocious hybrid in cucumber. They evaluated 48 F₁ crosses developed by crossing sixteen lines and three testers along with two standard checks, namely, KH-1 and Pusa Sanyog. Lines LC-1-1, CGN- 9 21585, LC-28-8, CGN-20953 and testers Japanese Long Green and K-75 were found to be superior on the basis of mean performance and general combining ability. Best cross combinations exhibiting high sca effects were observed to be LC-1-1 × K-75 (monoecious), CGN-21585 × Japanese Long Green (gynoeocious), CGN-19533 × K-75 (gynoeocious), CGN20953 × Poinsette (gynoeocious) and LC-28-8 × K-75 (monoecious).

Airina *et al.* (2017) studied twelve F₁ hybrids of cucumber derived from a top cross involving twelve monoecious parents and a stable gynoeious inbred (EC 709119) as female parent were evaluated in randomized block design (RBD) with three replications to assess general combining ability (GCA). Significant GCA effects were observed for all the characters except days to first male flower anthesis. The estimates of GCA effects revealed that none of the parents exhibited good GCA for all the characters together. Among 12 parents, CS123 was observed good general combiner for fruit yield per vine, length of main vine, branches per plant, number of harvests, duration of the crop, fruits per plant and number of seeds per fruit. The parents, CS128 and IC 538186 were good general combiners for earliness. The parent CS127 was found to be superior for fruit length, weight and girth.

In a field study, four selected advanced inbred lines were crossed as females with three testers as males in a Line \times Tester scheme to produce 12 F₁ crosses. Seven parents and their 12 crosses along with Hesham F₁ as a check hybrid, were evaluated for agronomic traits under greenhouse at a private farm in El-Nubaria city, during the winter season of 2016-2017, to estimate the extent of heterosis and combining ability. The experiment was conducted in a randomized complete blocks design with three replications. The results indicated significant differences among parents, crosses, lines, testers, and their interaction for all studied traits. Non-additive gene action was more important than the additive one for most traits. The lines 62 and 62A as well as the tester 54A, were good combiners for most traits. The cross 63 \times 54A has the greatest specific combining ability effects for early yield and total yield traits. Moreover, it had the greatest heterotic and superiority values for early yield and total yield traits, except for the superiority over the check hybrid for total yield, since, the crosses 62 \times 54A and 62 \times 54C, for total weight and total number of fruits in addition to the crosses, 62 \times 54D, 62A \times 54A, and 62A \times 54C for total weight of fruits, had the greatest values of superiority over the check hybrid (Al-Araby *et al.*, 2019).

Rajguru *et al.* (2020) crossed seven cucumber genotypes (3 lines and 4 testers) in a line \times tester mating design. The resultant 12 hybrids and their parents were studied using Randomized Block Design with two replications. They observed sufficient genetic variability for all the characters under study. The parents L₂ (Koradacherry local), T₂ (Orathanadu local) and T₃ (Aipatti local) exhibited high positive GCA

(General Combining Ability) effects for yield related traits and high negative GCA effects for earliness characters. The parent T₂ identified in this study may be used in multiple crossing programme to isolate high yielding varieties. Among the hybrid combinations, L₂×T₃, L₁×T₂ and L₃×T₄ expressed the maximum positive significant SCA (Specific Combining Ability) effects for yield and yield associated characters.

2.4 Screening of parents and F₁ against downy mildew (*Pseudoperonospora cubensis*)

Call *et al.* (2012) evaluated 1300 cultigens in Clinton, NC, and Skierniewice, Poland under natural field epidemics. The most resistant and susceptible cultigens were further studied in replicated experiments in North Carolina and India. Fungicide experiments were conducted in 2008 and 2009 to identify tolerance, involving weekly applications to one of two sets of material at a location. Results from this study confirmed the results of the initial screening. The most resistant cultigens over all environments were PI 605996, PI 330628, and PI 197088. Cultigens have been found that significantly outperform checks in all resistance traits. High yielding and tolerant cultigens have also been identified that could be used in developing improved cultivars.

Later in 2015, Metwally *et al.* (2015) examined 133 such accessions for downy mildew resistance under natural field epidemics during the summer 2013 at El-Beheira Governorate, Egypt. Mean ratings for downy mildew leaf damage ranged from 1 to 9 on a 0 to 9 scale. They classified 18 PI accessions (13.5%) as highly resistant (rating of 1.0-2.0), 46 (34.5%) as moderately resistant (rating 2.1-4.0), 40 (30%) as intermediate (rating 4.1-6.0), 12 (9%) as moderately susceptible (rating 6.1-7), and 17 (13%) as highly susceptible (rating > 7.1). They found most resistant PI accessions were PI 432870, PI 432873, PI 432878, PI 432884, and PI 432886 with a rating of 1, which originated from China. The most susceptible PI accessions were Ames7736, PI 211979, PI 288991, PI 288992 and PI 289698 with a rating of 9. The five most resistant and five most susceptible accessions were further evaluated in replicated experiments during the summer 2014. Results from the repeated test confirmed the results from the first screening. No PI accession was found immune to downy mildew. However, high levels of resistance were observed in several PI accessions.

In an experiment, Kumar *et al.* (2018) planted 48 F₁ hybrids, developed by crossing 16 lines (eight gynocious) with three testers. Parents (16 lines and three

testers) and their F₁ 48 hybrids, along with two standard checks (“KH-1” and “Pusa Sanyog”), were planted in a Randomized Complete Block Design (RCBD) for screening against downy mildew diseases under natural field conditions. In the study, 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. Whereas testers were found good for severity of downy mildew.

In the following year, Manisha *et al.* (2019) conducted experiment comprised 15 F₁ crosses, developed by crossing 6 genotypes during the year 2015. Parents and the 15 hybrids, along with standard check (KH-1), were planted in a randomized complete block design during the year 2016 for screening against different insect-pest and diseases under natural field conditions. In the present studies, genotypes PI-618860, UHF-CUC-1, UHFCUC-2 and Khira-75 and crosses Khira-75 × PI-618860, Khira-75 × UHF-CUC-1 and Khira-75 × UHF-CUC-2 were found superior in response to downy mildew disease incidences.

2.5 Molecular markers for studying genetic diversity of cucumber lines

Molecular marker technology provides information that can help to define the distinctiveness of germplasm and helps to rank them according to the number of close relatives and their phylogenetic position. It is a complementary approach for genetic characterization. Genetic markers have been employed for the characterization of genetic diversity present in cucumber (Meglie and Staub, 1996).

2.5.1 SSR Markers

Molecular- markers are special segments of DNA which flag the presence of genes that control particular trait. DNA markers reveal neutral sites of variation at the DNA sequence level, *i.e.* variation are not evident in morphology and each might be nothing more than a single nucleotide difference on a gene or a piece of repetitive DNA. Since the advent of polymerase chain reaction, many techniques have been developed to detect DNA polymorphism. Such polymorphism has utility in plant genetics and breeding. DNA fragment and sequence analysis have been used for genetic mapping experiments, diversity analysis and more recently marker assisted selection in many crop species.

Fazio *et al.* (2002) studied development and characterization of PCR markers in cucumber. Experiments were designed to develop simple sequence repeats (SSR), sequence characterized amplified region (SCAR), and single nucleotide polymorphisms (SNP) markers and optimize reaction conditions for PCR. A set of 110 SSR were constructed using a unique methodology. Four SCARs and two PCR markers based on SNPs that are tightly linked to multiple lateral branching (*i.e.* a yield component) were also developed. SNP markers were developed from otherwise monomorphic SCAR markers, producing genetically variable amplicons. This array of markers substantially increased the pool of genetic markers available for genetic investigation in cucumber.

In an experiment, Lang *et al.* (2007) studied random amplification of polymorphic DNA (RAPD) markers to evaluate the relationships among 14 cucumber cultivars. A total of six RAPD primed sites were used to calculate Jaccard's distance coefficients for cluster analysis using an un-weighted pair-group method using an arithmetic averaging (UPGMA) algorithm. The genetic relationships identified using RAPD markers were highly concordant, such that the correlation between SSR and RAPD genetic distance (GD) estimates was $r=0.73$ through RAPD analysis of 14 accessions allowed for their grouping into two distinct groups designated as CS and CM. In the same year,

Yeboah *et al.* (2007) constructed a genetic map based on sequence related amplified polymorphism (SRAP) and ISSR markers for cucumber based on the segregation of SRAP and ISSR markers in 112 plants of F_2 population derived from a cross between two cucumber inbred lines PW0832 and PW0801. In the investigation of polymorphism with 50 ISSR and 132 SRAP primer combinations, 13 (26%) ISSR primers and 26 (20%) SRAP primer pairs were polymorphic. The average polymorphic bands were four for ISSR and two for SRAP.

Parvathaneni *et al.* (2011) generated 109 polymorphic alleles with 15 ISSR primers. The ISSR primer UBC 825 was highly informative with a PIC value of 0.8934. III contained the highest number of genotypes, namely Kanivellari, Sankagiri Local, Perundurai Local, Long Melon, and Sempatti Local, while clusters I, II, IV, and V (Karur local, Andaman Local, Edapaddi Local, and N 78, respectively) contained the minimum number of genotypes.

Manohar *et al.* (2013) evaluated the genetic diversity among 39 cucumber collections from Karnataka using 23 RAPD and 18 ISSR primers. Out of 309 bands scored 147 (47.57 %) were polymorphic. UBC855 primers revealed the highest PIC (polymorphism information content) value of 0.49, whereas Jaccard's similarity coefficients ranged from 0.36 to 0.84. The UPGMA phenogram and the PCA (Principle component analysis) indicated that the populations formed five major clusters. CSC 83 (774 g per fruit) and CSC 71 (yellow skin) are considered to be the most important collections to be stressed for further breeding purpose. In the same year, Pandey *et al.* (2013) used morphological and SSR markers to study the genetic variation among 44 cucumber accessions. They found high genetic variability in days to 50% female flowering, number of fruits per plant, individual fruit weight and root length. The accessions represented genetically diverse populations (Jaccard's similarity coefficient = 0.25 to 0.85) and allelic diversity of polymorphic markers ranged from 0.001 to 0.9396 (average= 0.31). They further reported that clustering pattern of SSR markers was not in consonance with the groupings based on quantitative traits.

Pandey *et al.* (2013) examined genetic variation in 44 cucumber accessions using SSR markers and found the pair-wise Jaccard's similarity coefficient ranged from 0.25 and 0.85 indicating that the accessions represent genetically diverse populations. The allelic diversity of polymorphic markers ranged between 0.001 to 0.9396 with an average of 0.31 based on polymorphic information content.

In the year 2014, Innark *et al.* (2014) demonstrated a total of 17 ISSR primers (85%) could amplify in all 40 cucumber accessions with the percent of polymorphic bands of each primer ranged from 0.12 to 0.45 with the mean of 0.25, while the resolving power (RP) averaged at 1.82 and ranged in between 0.50 to 3.20. Similarly, Singh *et al.* (2016) investigated the genetic diversity and similarity among 11 cucumber genotypes using 8 ISSR markers. The 6 ISSR primers generated a total of 49 polymorphic alleles. On the basis of ISSR data, dendrogram clustered the genotypes into two major clusters and five sub-clusters. Among all the genotypes a total of 40-100% polymorphism was observed. The similarity value ranged from 35% to 96%. Three monocious genotypes *viz.*, PCUC-8, PCUC-15 and PCUC-28 (Pant Khira-1) were grouped in one cluster with 96% similarity, whereas parthenocarpic genotypes in another cluster.

Normohamadi *et al.* (2017) evaluated 10 morphological traits of 20 genotypes of local cucumbers using 9 SSR primers. They revealed high genetic variability for the number of flowers per plant. Jaccard's similarity coefficient ranged between 0.51 and 0.92, indicating a high diversity among all the genotypes. A cluster analysis using the UPGMA method was performed to evaluate the genetic similarity among genotypes. The clustering pattern of the SSR markers did not coincide with the groupings based on quantitative traits. A dendrogram of the cluster analysis of molecular data showed a high diversity among the studied genotypes.

In an experiment, Dar *et al.* (2017) investigated genetic variation, marker attributes and population structure in 104 genotypes of cucumber using 23 SSR primer pairs. They further revealed that total number of alleles produced was 67 with an average of 2.91 per locus. Allele frequency ranged from 0.215 to 0.561 with mean value of 0.403, polymorphic information content ranged from 0.158 to 0.495 with the mean of 0.333, marker index ranged from 0.316 to 1.54 with an average value of 0.954 and resolving power ranged from 0.346 to 2.692 with mean of 1.392. The maximum allele frequency was reported with primer SSR 65, whereas the maximum value of polymorphic information content and resolving power was found with SSR 61 and the maximum value of marker index was reported with SSR60. Jaccard's similarity coefficient ranged between 0.07 to 0.897 with maximum similarity between genotype G₄₀ and G₄₁ and minimum ranged between G₁₆ and G₂₀, and G₁₆ and G₁₀₀.

Valcarcel *et al.* (2018) studied molecular genetic diversity of 131 Spanish accessions using 23 simple sequence repeat (SSRs) markers and found eighteen of these SSRs were polymorphic; the mean number of alleles, mean observed heterozygosity and mean polymorphic information content were 3.2, 0.065 and 0.229, respectively. Seven SSRs showed a polymorphic information content (PIC) ranging from 0.31 to 0.44, therefore they were reasonably informative. Around 60% of the alleles showed a frequency higher than 0.05, and only one allele in the SSR31399 showed a frequency lower than 0.01.

In a field trial, Pati *et al.* (2019) assessed the genetic diversity of 36 of cucumber genotypes based on 17 polymorphic simple sequence repeat (SSR) markers. They revealed that genetic distance based on 17 SSR markers among 36 genotypes was quantified ranging from 0.03 to 0.70 indicated a wide diversity present among the

genotypes evaluated in the study. These primers produced 2-4 number of alleles with an average 2.76. Polymorphism information content varied from 0.005 to 0.550 with an average of 0.348. The observed heterozygosity mean was 0.098, while gene diversity or expected heterozygosity was 0.625 to 0.057.

Kumar *et al.* (2020) evaluated the genetic diversity among 78 cucumber (*Cucumis sativus* L.) accessions using 60 SSR markers. A total of 171 alleles were amplified with a mean of 2.85 alleles per locus. The polymorphism information content (PIC) ranged between 0.05 (UW084478) to 0.59 (UW084186) with a mean value of 0.36. The major allele frequency, gene diversity, and heterozygosity of these SSR markers were 0.36-0.97, 0.05-0.67 and 0.00-0.68, respectively. The dendrogram based on SSR marker analysis classified the 78 genotypes into two major groups those were subdivided into ten subgroups.



*Materials
and
Methods*



The present investigation entitled “**Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.)**” was carried out at Vegetable Research Centre (V.R.C.) of the Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand in the year 2017-18 and 2018-19 respectively. The details of the materials used and the techniques adopted in the study are described in this chapter.

3.1 Cite of experiment and climate

Geographically Pantnagar is situated at the latitude of 29.5° North and longitude 79.2° East and at an elevation of 243.83 meters above the mean sea level. The weather conditions were quite favourable for the normal growth of the crop. The climate of Pantnagar is humid sub-tropical with maximum temperature ranging from 35.10°C to 45.40°C in summer and minimum temperature ranging from 4.80°C to 13.60°C in winter. Generally, monsoon starts from the third week of June and ends in September. The average annual rainfall is 1300 mm. The mean relative humidity remains almost 80-90 per cent from mid-June to the end of February and then it steadily decreases to 50 per cent by the first week of May and remains so till mid-June. The weekly average of various weather parameters that prevailed during the investigation was recorded at Meteorological Observatory of Norman E. Borlaug Crop Research Centre of the University and are presented in Appendix I. Considering the eco-geographical conditions, Pantnagar is located at the foothills of *Shivalik* range in the Himalayas and falls under the humid sub-tropical climate in a narrow belt called *Tarai*. The soil of the *Tarai* region has been developed from calcareous, medium to coarse-textured materials under the predominant influence of tall vegetation and moderate to well drain condition. The molecular experiment was carried out at the National Agricultural Innovation Project (NAIP) laboratory, Department of Vegetable Science.

3.2 Experimental materials

The experimental material comprised of 8 genotypes which were selected based on their diversity for different characters. From these 8 genotypes, 28 F₁ hybrids crosses were developed in a half diallel mating design. The parents and their F₁'s are presented in Table 3.1 and 3.2 respectively.

Table 3.1: List of parents with resistant check for downy mildew studies

S.No.	Parent line	Source
1	PCPGR - 50	Baruasagar, Jhansi, U.P.
2	PCPGR - 51	Givathikapurawa, Faizabad, U.P.
3	PCPGR - 59	Chetia, Siddarth Nagar, U.P.
4	PCPGR - 83	Mukhautia, Rai bareilly, U.P.
5	PCPGR - 112	Sultanpur, U.P.
6	PCPGR - 126	Ghosi, Mau, U.P.
7	PCPGR - 138	Hannumanganj, Prayagraj, U.P.
8	PCPGR - 149	Sultanpur, U.P.
9	Pant Khira-1(Check)	V.R.C. Pantnagar, Uttarakhand
10	Poinsette (resistant check for downy mildew screening)	NSC, New Delhi

Table 3.2: List of F₁ hybrids developed through half diallel mating design

S.No.	F ₁ hybrids	S.No.	F ₁ hybrids
1	PCPGR- 50 × PCPGR - 51	15	PCPGR -59 × PCPGR -112
2	PCPGR-50 × PCPGR-59	16	PCPGR - 59 × PCPGR -126
3	PCPGR-50 × PCPGR-83	17	PCPGR - 59 × PCPGR -138
4	PCPGR-50 × PCPGR-112	18	PCPGR - 59 × PCPGR -149
5	PCPGR-50 × PCPGR -126	19	PCPGR - 83 × PCPGR -112
6	PCPGR - 50 × PCPGR -138	20	PCPGR - 83 × PCPGR -126
7	PCPGR - 50 × PCPGR -149	21	PCPGR - 83 × PCPGR -138
8	PCPGR - 51 × PCPGR -59	22	PCPGR - 83 × PCPGR -149
9	PCPGR - 51 × PCPGR -83	23	PCPGR - 112 × PCPGR -126
10	PCPGR - 51 × PCPGR -112	24	PCPGR - 112 × PCPGR -138
11	PCPGR - 51 × PCPGR -126	25	PCPGR - 112 × PCPGR -149
12	PCPGR - 51 × PCPGR -138	26	PCPGR - 126 × PCPGR -138
13	PCPGR - 51 × PCPGR-149	27	PCPGR - 126 × PCPGR -149
14	PCPGR - 59 × PCPGR -83	28	PCPGR - 138 × PCPGR -149

Table 3.3: List of cucumber genotypes used for molecular diversity analysis

S.No.	Genotype	Source
1	PCPGR-50	Baruasagar, Jhansi, U.P.
2	PCPGR-51	Givathikapurawa, Faizabad, U.P.
3	PCPGR-59	Chetia, Siddarth Nagar, U.P.
4	PCPGR-66	Kalyanmadarasa, Faizabad, U.P.
5	PCPGR-112	Sultanpur, U.P.
6	PCPGR-126	Ghosi, Mau, U.P.
7	PCPGR-138	Hannumanganj, Prayagraj, U.P.
8	PCPGR-149	Sultanpur, U.P.
9	PCPGR-4	Palampur, H.P.
10	PCPGR-123	Faridpur, Bareilly, U.P.
11	PCPGR-25	Aashapur, Varanasi, U.P.
12	PCPGR-83	Mukhautia, Rai bareilly, U.P.
13	PCPGR-106	Ghosi, Mau, U.P.
14	PCPGR-199	Chumal, Champawat, U.K.
15	PCPGR-73	Saung, Tehari, U.K.
16	PCPGR-7657	Akhandnagar, Sultanpur, U.P.
17	PCPGR-8	Jammu
18	PCPGR-478	Barparwa, Gorakhpur, U.P.

S.No.	Genotype	Source
19	PCPGR-4273	Barogh, Lucknow, U.P.
20	PCPGR-196	Chumal, Champawat, U.K.
21	PCPGR-210	Sitapur, U.P.
22	PCPGR-87	Kanatal, Tehri, U.P.
23	PCPGR-211	Sitapur, U.P.
24	PCPGR-3888	Sultanpur, U.P.
25	PCPGR-44	Palampur, H.P.
26	PCPGR-264	Almora, U.K.
27	PCPGR-20	Chetia, Siddarth Nagar, U.P.
28	EUC-1-07	Majhra, Nainital, U.K.
29	PCPGR-36	Sikandrabad, Bulandshahar, U.P.
30	PCPGR-37	Sikandrabad, Bulandshahar, U.P.
31	PCPGR-202	Sultanpur, U.P.
32	PCPGR-55	Sekha, Aligarh, U.P.
33	PCPGR-62	Jaipurpadly, Nainital, U.K.
34	PCPGR-135	Hannumanganj, Prayagraj, U.P.
35	PCPGR-160	Vikrampur, Basti, U.P.
36	PCPGR-7566	Dilipnagar, U.S. nagar, U.K.

3.3 Experimental Method

The investigation consisted of a number of inter related field experiments conducted during different seasons from February, 2018 to June, 2019. The research programme was carried out with following experiments.

- I. To determine genetic variability, heritability and genetic advance on yield and yield contributing traits
- II. To estimate the extent of heterosis
- III. To determine the combining ability of parental lines and crosses
- IV. To screen of parents and F₁ hybrids against downy mildew.
- V. Molecular diversity analysis of cucumber lines.

3.3.1 Experiment 1: Development of F₁ population

Eight genotypes of cucumber were crossed in Half Diallel mating design during February to June, 2018 in open field condition to obtained 28 F₁, hybrid combinations. Seeds from mature fruits were collected for evaluation of 28 F₁ hybrid combinations in next season (Plate 1).

3.3.2 Experiment 2:

The collected seeds are shown in the field for following study.

- (A) Evaluation of cucumber genotypes for quantitative characters.
- (B) Study of heterosis and combining ability of Parents and their F₁ hybrid.
- (C) Screening of parents and F₁ hybrids against downy mildew.

F₁ hybrid along with their parents were evaluated during February, 2019 to June, 2019 in open field condition. All cultural operations were carried out and data for all fourteen quantitative characters were recorded. Downy mildew disease screening also done in above mentioned year (Plate 1).

3.4 Experimental Design

The experiment was laid out in a RBD with three replications. Each genotype within a replication consisted of nine plants. The spacing between rows was kept 1.0 m



Plate 1: Experimental field view



Seedling stage



Healthy crop stand in field



Crossed flower



Well developed crossed Fruit

Plate 2: Crossing block maintained open field conditions



Mature fruit harvested for seed extraction



Seed extraction



Seed drying

Plate 3: Fruit harvesting, seed extraction and drying

and within plants 0.75 m. Initially 5 seeds were sown in a pit and later 1 plant per pit was maintained after thinning.

3.5 Observations recorded

Fourteen quantitative characters were scored on each genotype in this experiment. Five plants were randomly selected from each genotype in each replication for recording of observations for all the plant traits. The observations were recorded for following yield and yield contributing traits.

3.5.1 Days to first male flower

Number of days taken from the date of sowing to the appearance of first male flower in 50 per cent of plants.

3.5.2 Node number to first male flower

The number of node to which first male flower appeared was counted from base of the plant.

3.5.3 Days to first female flower

Number of days taken from the date of sowing to the appearance of first female flower in 50 per cent of plants.

3.5.4 Node number to first female flower

The number of node to which first female flower appeared was counted from base of the plant.

3.5.5 Days to first harvest

Number of days taken from the day of sowing to first harvest was recorded.

3.5.6 Days to last harvest

Number of days taken from the day of sowing to last harvest was recorded.

3.5.7 Internodal length (cm)

The distance between 5th node and 10th node was recorded and the mean value was calculated for average distance between two nodes.

3.5.8 Plant height (m)

The length of main shoot was measured from base of the plant to the tip of main shoot at the time last fruit harvesting stage.

3.5.9 Fruit length (cm)

The length of five randomly selected fruits was measured with the help of scale and the average length was calculated in cm.

3.5.10 Average fruit diameter (cm)

The diameter of five randomly selected fruits was measured with the help of scale and the average diameter was calculated in cm.

3.5.11 Number of fruits per plant

Total number of fruits was calculated by adding number of fruits from all harvest in each genotype and the mean value was calculated for the number of fruits per plant.

3.5.12 Average fruit weight (g)

Five fruits were randomly taken from each genotype and then mean fruit weight was calculated in gram.

3.5.13 Fruit yield per plant (kg)

Total fruit weight of five plants from all harvest was recorded and the mean yield per plant was calculated in kg

3.5.14 Fruit yield (q/ha)

Total fruit weight of five plants from all harvest was recorded and the mean fruit yield per plant was calculated in kg and then converted into quintals per hectare.

3.6 Downy mildew of cucumber

Parents and F₁ hybrids were evaluated in three replication with resistant check Poinsette. In each replication, disease incidence for downy mildew was recorded for all twelve plants. And five plants were randomly selected for disease severity. Following observations were recorded for downy mildew disease:

3.6.1 Disease incidence:

Data of different parents and F₁ hybrids against downy mildew incidence in present experiment taken at weekly interval day after initiation (DAI) of disease. Disease incidence was calculated for downy mildew disease under:

$$\text{Disease Incidence} = \frac{\text{Number of plants infected}}{\text{Total Number of plants}} \times 100$$

3.6.2 Disease severity:

Disease severity was evaluated weekly in all planting dates after the onset of observable symptoms in the first planting date for six consecutive weeks. Ratings were based on the percentage of symptomatic leaf area [disease rating scale 0 to 9, where 0 = no damage, 1 = 1% to 10%, 2 = 11% to 20%, 3 = 21% to 30%, 4 = 31% to 40%, 5 = 41% to 50%, 6 = 51% to 60%, 7 = 61% to 70%, 8 = 71% to 80% and 9 = 81% to 100% (or dead)]; as described by Jenkins and Wehner (1983).

PDI was calculated using the given formula and the genotypes were categorized into four groups namely resistant (0-20%), moderately resistant (21-40%), susceptible (41-60%) and highly susceptible (>60%) (Reddy, 2002).

$$\text{PDI} = \frac{\text{Sum of numerical value}}{\text{No. of leaves graded} \times \text{Maximum disease grade}} \times 100$$

3.7 Statistical Analysis

3.7.1 Analysis of variance

The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications according to procedure given by Panse and Sukhatme (1967) and the software used for analysis was STPR-3 in the following manner.

Table 3.4: Analysis of variance

Source of variation	Degree of freedom	Sum of squares	Mean sum of square	'F' Value
Replications	r-1	RSS	RSS/r-1= Mr	Mr/me
Treatments	t-1	TSS	TSS/t-1= Mt	Mt/Me
Error	(r-1)(t-1)	ESS	ESS/(r-1)(t-1)= Me	
Total	Rt-1			

Where,

r = number of replications

t = number of treatments (genotypes, including parents)

Mr = mean sum of square due to replications

Mt = mean sum of square due to treatments

Me = mean sum of square due to error

σ_g^2 = genotypic variance

σ_e^2 = error variance

Coefficient of variance (C.V.)

Standard deviation expressed as percentage of mean is known as coefficient of variation (CV). It was calculated as:

$$CV (\%) = \frac{SD}{\bar{x}} \times 100$$

Where,

\bar{x} = mean of character

SD = standard deviation

This statistic is generally used to judge the precision of the experiment.

3.7.2 Estimation of genotypic, phenotypic and environmental variances

The variance due to genotype, phenotype and environment were computed as follows.

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MS due to genotypes (adj)} - \text{MS due to error (intra block)}}{r \text{ (replication)}}$$

$$\text{Environmental variance } (\sigma_e^2) = \text{Error mean sum of squares Phenotypic variance}$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2 \text{ (MS due to error)}$$

Where, 'r' is number of replications.

Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Environment co-efficient of variation (ECV)

$$\text{ECV (\%)} = \frac{\text{Environmental standard deviation}}{\text{Mean}} \times 100$$

Where,

\bar{X} = General mean

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

GCV and PCV were classified as suggested by Burton and Devane (1953)

<10% : Low

10-20% : Moderate

>20% : High

σ_p = Phenotypic standard deviation

GCV and PCV were classified as suggested by Burton and Devane (1953)

<10% : Low

10-20% : Moderate

>20% : High

3.7.3 Estimation of heritability

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

$$\text{Heritability } (h^2) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$$h^2 (\%) = \text{Heritability (Broad sense)}$$

$$\sigma^2_g = \text{Genotypic variance}$$

$$\sigma^2_p = \text{Phenotypic variance}$$

Heritability (h^2) in broad sense was categorized as suggested by Hanson *et al.*, 1956 and the same is given below.

<50% - Low

50-75% - Moderate

>75% - High

3.7.4 Genetic advance (GA)

Expected genetic advance was estimated by the method proposed by Johnson *et al.* (1955).

$$GA = h^2 \cdot K \cdot \sigma_p$$

Where,

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation of given character

K = Selection differential at 5 % selection intensity (2.06).

3.7.5 Genetic advance as percent of mean (GA %)

$$\text{G.A. } (\%) = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

Genetic advance as percent of mean was categorized as low, moderate and high as given by Johnson *et al.* (1955). It is as follows:

- <10% - Low
- 10-20% - Moderate
- >20% - High

3.7.6 Estimation of heterosis

The magnitude of heterosis was estimated in relation to mid-parent, better parent and standard parent. They were thus, calculated as percentage increase or decrease of F_1 s over the mid-parent (MP), better parent (BP) and standard parent (SP) using the methods of Turner (1953) and Hayes *et al.* (1956). The formula used for estimation of heterosis given by Fonseca and Patterson (1968) was used.

Heterosis for each trait was computed and the significance of F_1 heterosis values were tested by comparing them with critical difference (CD) values obtained separately for MP and BP employing the formulae given below.

3.7.6.1 For mid-parent heterosis

$$\text{Percent heterosis over mid-parent (MP)} = \frac{F_1 - MP}{MP} \times 100$$

Where,

$$\text{Mid-parent} = \frac{P_1 + P_2}{2}$$

Where, P_1 and P_2 are parents of a hybrid combination.

The deviations for heterosis were tested for their significance by the following standard errors.

$$SE = \sqrt{\frac{3 \text{ MSE}}{2 r}}$$

Where,

MSE = Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

C.D. = S.E. (d) x 't' value at error df (P = 0.05 and P 0.01 levels of significance)

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{MP}}{\text{S.E. of heterosis over MP}}$$

Calculated value was compared with table value at error degrees of freedom for significance.

3.7.6.2 For better parents heterosis

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

Percent heterosis over better parent is also called as heterobeltiosis (BH).

CD for better parents heterosis = SE x 't' value.

$$SE = \sqrt{\frac{2MSE}{r}}$$

Where,

MSE= Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

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

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{MP}}{\text{S.E. of heterosis over SP}}$$

Calculated 't' value was compared with table value at error degrees of freedom for significance.

3.7.6.3 For standard parents heterosis

$$\text{Percent heterosis over standard parent (SP)} = \frac{F_1 - SP}{SP} \times 100$$

Percent heterosis over standard parent is also called as standard heterosis.

CD for standard parents heterosis = SE x 't' value.

$$SE = \sqrt{\frac{2MSE}{r}}$$

Where,

MSE = Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

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

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{SP}}{\text{S.E. of heterosis over SP}}$$

Calculated 't' value was compared with table value at error degrees of freedom for significance.

3.7.7 Combining ability analysis

The combining ability analysis for different characters was carried out following the method 2 model 1 of Griffing (1956), where parents and F_1 's were included but not the reciprocals. Thus the experimental material for this method comprises of $n(n+1)/2$ genotypes.

The mathematical model for the combining ability analysis is assumed to be:

$$Y_{ij} = \mu + g_i + g_j + S_{ij} + 1/bc \sum \sum e_{ijkl}$$

Where,

ij = 1, 2, -----, p (p = number of parents involved in diallel)

k = 1, 2, -----, r (r = number of replications)

l = 1, 2, -----, c (c = number of observations taken in each plot)

μ = the population mean

g_i, g_j = GCA effect of i^{th} and j^{th} parents, respectively

S_{ij} = the interaction, *i.e.* the specific combining ability (SCA) for the cross between i^{th} and j^{th} parents such that $S_{ij} = S_{ji}$.

e_{ijkl} = environmental effect associated with $ijkl^{\text{th}}$ observation

The restriction imposed on this mathematical model is:

$$(i) \sum_i (g_i) = 0$$

$$(ii) \sum_j (S_{ij}) = 0$$

The orthogonal partitioning of the variety sum of squares in the ANOVA is as follows:

Table 3.5: Analysis of variance for method 2, model 1 with expectations of mean squares

Sources	d.f.	Sum of square	Mean sum of square	Expectations of mean squares
G.C.A.	p-1	S _g	M _g	$\sigma_e^2 + (p + 2) \left[\frac{1}{p-1} \right] \sum_{x=1}^p g_x^2$
S.C.A.	p(p-1)/2	S _s	M _s	$\sigma_e^2 + \left(\frac{2}{p(p-1)} \right) \sum_{i=1}^p \sum_{j=1}^p S_{ij}^2$
Error	(r-1)(t-1)	S _e	M _e	σ_e^2

Where,

P = number of parents

$$S_g = \frac{1}{p+2} \left[\sum_{i=1}^p (Y_i + Y_{ii})^2 - \frac{4}{p} Y_{..}^2 \right]$$

$$S_g = \sum_i \leq \sum_j Y_{ij}^2 - \frac{1}{p+2} \sum_{i=1}^p (Y_i + Y_{ii})^2 + \frac{2}{(p+1)(p+2)} Y_{..}^2$$

Y_i = total of the array involving of ith parent

Y_{ii} = mean value of the ith parent of the array

Y_{ij} = mean value of i × jth cross

Y_{..} = total of all the elements in the diallel table without

Reciprocals $\left[\frac{P(P-1)}{2} \right]$ progenies and P parental lines

M_e = error mean square

M_g, M_s and M_e were obtained by dividing each sum of squares by the corresponding degree of freedom. The following 'F' ratios were used for testing the

significance of GCA and SCA effects.

- (i) To test significance of differences among GCA variance of character.

$$F = \frac{M_g}{M_e}$$

The calculated F-value is tested against table F-value at (P-1) vs. error degree of freedom.

- (ii) To test the significance of differences among sca variance of a character.

$$F = \frac{M_s}{M_e}$$

The calculated F-value is tested against table F-value at [P (P-1)/2] vs. error degree of freedom.

The software used for analysis of combining ability (GCA and SCA) was OPSTAT (HAU, Hisar)

3.7.8 Estimation of combining ability effects

When MS_g and MS_s both are significant, they justify the adequacy of calculating general combining ability or GCA (g_i) and specific combining ability or SCA (S_{ij}) effects for each parent and cross, respectively. These were obtained by using the following formulae:

(a) Estimation of GCA effects

$$g_i = \frac{1}{P+2} \left[\sum (Y_i + Y_{ii}) - \frac{2}{P} \right] Y_{..}$$

(b) Estimation of SCA effects

$$g_i = \frac{1}{P+2} \left[\sum (Y_i + Y_{ii}) - \frac{2}{(P+1)(P+2)} \right] Y_{..}$$

Where,

Y_j = total of the array involving j^{th} parent

Standard errors

The standard errors, which are necessary in connection with testing the significance of GCA and SCA effects and differences between various GCA as well as SCA effects were calculated as:

Standard error of combining ability effects

$$SE (g_i) = \left[\frac{P-1}{P(P+2)} \sigma_e^2 \right]^{\frac{1}{2}}$$

$$SE (S_{ij}) = \left[\frac{P-1}{(P+1)(P+2)} \sigma_e^2 \right]^{\frac{1}{2}}$$

To test the significance of each g_i and S_{ij} , 't' values are calculated as follows:

For GCA effect

$$t (g_i) = \frac{g_i}{SE(g_i)}$$

For SCA effect

$$t (S_{ij}) = \frac{S_{ij}}{SE(S_{ij})}$$

The calculated value of ratio is referred to the 't' table for error degree of freedom.

3.7.9 Estimation of genetic components and other genetic parameters for method 2 model I of Griffing (1956).

The genetic variance parameters were estimated as given below:

- i. $\sigma^2g = (MS_g - MS_e)/(p+2)$
- ii. $\sigma^2s = (MS_s - MS_e)$
- iii. $\sigma^2e = MS_e$
- iv. $\sigma^2A = 2\sigma^2g$
- v. $\sigma^2D = \sigma^2s$

Degree of dominance

The additive (D) and dominance (H) genetic variance were used to estimate dominance ratio.

$$\text{Degree of dominance (dominance ratio)} = \sqrt{(\sigma^2D/\sigma^2A)}$$

If dominance ratio is:

- a. 1 show complete dominance
- b. 1 show over dominance
- c. < 1 show partial dominance

3.8 Assessment of Genetic Diversity using SSR Markers

For the study of genetic diversity DNA from selected 36 genotypes of cucumber was extracted from two to three week old seedlings at National Agricultural Innovation Project (NAIP) laboratory, Department of Vegetable Science, G.B. Pant University of Agriculture and Technology, Pantnagar. The detailed procedure for DNA extraction is given below:

The genomic DNA was extracted by CTAB (Cetyl tri-methyl ammonium bromide) method as described by Doyle and Doyle (1990) with some modifications.

3.8.1 Collection of experimental tissues

The genotypes were grown at Vegetable Research Center, Pantnagar, Udham Singh Nagar. 2-3 weeks old fresh leaves were taken for genomic DNA extraction from all the thirty six genotypes and wrapped in aluminium foil. Samples were placed in an ice box and brought to laboratory. One gram of leaf sample was weighed with electronic balance and placed in -20°C refrigerator.

3.8.2 Isolation of genomic DNA

Total genomic DNA was isolated using the CTAB method. The list of buffers and stock solutions is given in Appendix-II. Pre-heat CTAB buffer at 60°C for thirty minutes in a water bath. Take 2.0ml centrifuge tube and mark them from 1 to 8. In each centrifuge tube add 1ml of extraction buffer (2 percent CTAB). Grind the leaf sample to a fine powder in a pre-cooled mortar and pestle using liquid nitrogen. Mix extraction buffer and powdered sample thoroughly. Incubate at 65°C for one hour (cap should be slightly loose). Mix it intermittently at almost 10 minutes interval. After taking tubes out from the water bath, allow it to come to room temperature and add 10ml of chloroform and isoamyl alcohol (24:1) mixture. Swirl the tube gently by moving wrist

in the shape of 8 for approximately 10 minutes. Centrifuge at 15,000 rpm for 15 minutes. Transfer the aqueous phase to a fresh centrifuge tube. Add double amount of iso-propanol. Mix the contents very gently by inverting the tube 10-15 times. Keep the tubes overnight at -20°C. Spool out the DNA thread using a wide-bore tip into a micro-centrifuge tube.

3.8.3 Determination of quality and quantity of isolated DNA

3.8.3.1 Qualitative analysis “agarose gel electrophoresis”

Electrophoresis through Agarose is the standard method used to check the quality of DNA fragments. The technique is simple, rapid to perform and capable of resolving fragments of DNA. Submerged gel electrophoresis unit was used for fractionating genomic DNA on agarose gel.

Procedure

1. The open end of a clean, dry plastic tray supplied with the electrophoresis apparatus was sealed with tape so as to form mold.
2. Agarose gel was prepared by dissolving (boiling) appropriate amount of agarose in 0.5 X TBE buffer (0.8% for genomic DNA). Cool it down to approximately 50°C. 8µl of ethidium bromide was added in this agarose solution and poured it in gel casting plate with already adjusted gel comb.
3. The agarose solution was left to solidify at room temperature for 30-40 minutes.
4. After complete setting of gel the comb was removed carefully with the tape and the gel was mounted in an electrophoresis tank filled with 0.5 X TBE buffer.
5. The DNA loading dye was mixed with DNA sample in 1:6 ratio and loaded in gel along with one sample of known quantity of DNA.
6. Electrophoresis was done by running the gel at 80 volts for 45 minutes.
7. The gel was then visualized on an UV trans illuminator.
8. The photograph of gel was taken in a gel documentation unit.

3.8.3.2 Quantification of genomic DNA

The purified genomic DNA, dissolved in TE buffer was taken for quantification by UV absorbance at 260 nm in a UV spectrophotometer.

To measure the concentration of DNA by using UV spectrophotometer, the blank is set against TE buffer and then after proper rinsing of Quartz cuvette, the sample with appropriate dilution was loaded in cuvette. The optical density (O.D.) was measured at 260nm for estimating the concentration of DNA. The O.D. was also recorded at 280nm to determine protein contamination. The concentration of DNA was calculated by using following equation:

$$\text{Concentration of DNA } (\mu\text{g}/\mu\text{l}) = \text{O.D.} \times 50 \times \text{dilution factor}/1000$$

The ratio of O.D._{260/280} gives the amount of RNA or protein contamination in the preparation. A value of 1.8 is optimum for best DNA preparation. A value of ratio below 1.8 indicates the presence of protein in the preparation and a value above 1.8 indicates RNA contamination in the isolated DNA.

3.8.4 PCR amplification

The polymerase chain reaction (PCR) is a powerful, extremely sensitive technique with application in the field of molecular biology, agricultural diagnostics, forensic analysis and population genetics. It is based on the enzymatic amplification of DNA fragments that are flanked by oligo-nucleotide primer hybridizing to opposite strands of the target sequence. The PCR involves three basic steps which constitute a single cycle:

- (i) Denaturation of the target DNA at 92-94 °C
- (ii) Annealing of the primers to the template DNA
- (iii) Primer extension by addition of nucleotides to the '3' end of the primers by the enzyme DNA polymerase.

As the number of PCR cycle increases, the amount of target DNA synthesized increases exponentially. Availability of thermostable DNA polymerase Taq (from the bacteria *Thermus aquaticus*) has facilitated automation of the PCR (Saiki *et al.*, 1988).

Primer annealing temperature depends on its T_m value which is calculated from the following equation. $T_m (^{\circ}\text{C}) = 4 (G+C) + 2 (A+T) \pm 3$. Where A, T, G and C stand for the number of corresponding nucleotides in the primer. Annealing may fail at a temperature much higher than T_m whereas annealing temperature much below T_m may lead to non-specific amplification. Annealing temperature gradient of range 30-38 $^{\circ}\text{C}$ was applied in case of decamer primers.

3.8.4.1 PCR ingredients

A. Design of primers

The most essential requirement of PCR is the availability of short oligonucleotides called primers having sequence complementary to either end of SSR the target DNA segment called template DNA to be synthesized on large amount. List of primers used is given in Table 3.6.

Table 3.6 List of SSR primers used for DNA amplification

S.No.	Primer code	Forward primer (5'→3')	Reverse primer (3'→5')
1.	SSR 22203	ATAAGAGAAAATGATTGCCGTGA	TCTTGATTTTGTGTTTGTGAGAGG
2.	SSR 13262	TGTCCTTTCCTTCTACTTCTTGC	TGGTGATTAGTAGAGGGTCAAATTC
3.	SSR 11632	TTCAACTCATTATGGATTGGATT	TGAGGTGAAGCGTGAGAAGA
4.	SSR 00607	GCAAACCTGTGGGACGTTTCT	AAGCCACCTCCCTCTCAAT
5.	SSR 52	GGACTAGAAACACAATCCCACG	GTTTGGTTTGTCTCAAGTAGGTTTC
6.	SSR 54	GGGATGGGATCTGGGTTTG	GTGTGGAAATATGTGGAGGGAG
7.	SSR 60	TACACCTCTGCGAAGCACC	GTTTCGCACTCACTCTTACCG
8.	SSR 61	GCACATTCAAATTTACTTGGGAG	GCTTTAAGTTTGATGGTAGGGTAG
9.	SSR 65	GTGAAGAAATGAGTTGGCAAGTC	GGAGGGAATGTTGGATCAGC
10.	SSR69	TGCTTGAAGTTTGTCTCTGTC	GGTTTATTGGATGATGGGTC

B. Template DNA: The genomic DNA isolated from eight samples was suitably diluted and its 100 ng per PCR tube was used as a template in PCR amplification.

C. Taq DNA polymerase: Taq DNA polymerase is a 94 kD thermostable enzyme which has 5'→3' polymerase activity. It is highly active at temperature around 72 $^{\circ}\text{C}$. The enzyme used in the reaction was obtained from Himedia.

The concentration of enzyme was 3 Unit per μl . One unit of Taq DNA polymerase is defined as the amount of enzyme which incorporates 10nm of total deoxyribo nucleoside triphosphate into acid precipitable DNA in 30 minutes at 75°C under optimal assay conditions.

D. dNTPs

The dNTPs used in this reaction was obtained from Himedia as 2.5 mM each (dATP, dGTP, dCTP, dTTP).

E. Taq assay buffer (10X) A

The 10X assay buffer for the enzyme was also obtained from Himedia. Assay buffers contained 100mM Tris-HCl (pH 9.0), 15mM MgCl_2 , 500mM KCl and 0.1% gelatin. One vial of 25mM MgCl_2 was also supplied along with Taq polymerase for making MgCl_2 gradient.

F. Molecular biology grade water:

Molecular biology grade water obtained from Himedia was used in master-mix.

3.8.4.2 Standardization of the polymerase chain reaction (PCR conditions)

There are number of variables in a PCR which have to be optimized to give the target amplification. These parameters are:

- Denaturation temperature and time
- Annealing temperature and time
- Amounts of template and primer
- Concentration of MgCl_2 in the assay buffer
- The number of cycles

After repeated PCR reactions a reaction mixture was standardized for eight cucumber genotypes which gave strong amplifications. The reaction mixture is presented in Table 3.7. Gradient PCR was used for standardizing the PCR reactions for 10 primers with all the thirty six genotypes. Final reaction that gave good result and clear bands are presented in Table 3.8.

PCR procedure:

- (i) 2µl of the sample (50ng/µl) was added to the master- mixture (Table 3.7) given above from different cucumber samples which would act as template.
- (ii) The tubes were vortexed for proper mixing of template in the cocktail.
- (iii) Tubes were placed in a thermal cycler (Eppendorf Master Cycler Gradient).
- (iv) The cycler was programmed to perform the temperature shift as given in Table 3.8.
- (v) After completion of PCR cycles, sub-samples of the amplicons were analysed by agarose gel electrophoresis just to check PCR amplification.

3.8.4.3 SSR PCR amplification

PCR amplification was undertaken by the procedure as given below. Amplifications were performed in 15 µl volume containing the following components:

Table 3.7: Reagents with their concentration and quantity used for single PCR reaction

S. No.	Reagent	Single tube (µl)
1	DNA template (50ng/µl)	2.0
2	Primer (50ng/µl)	2.0
4	dNTPs mix (2.5mM each)	0.8
5	Taq buffer A (10X)	4.0
6	Taq polymerase (3U/µl)	0.6
7	Triple distilled water	5.6
Total		15 µl

Table 3.8 PCR amplification protocol for SSR primers

Cycles	Denaturation		Annealing		Polymerization	
	Temp.	Time	Temp.	Time	Temp.	Time
First cycle	94°C	5 min	-	-	-	-
35 cycles	94°C	1 min	54-59°C	1 min	72°C	1 min
Last cycle	-	-	-	-	72°C	7 min

3.8.5 Analysis of amplicons (PCR products): Agarose gel electrophoresis

Horizontal electrophoresis assembly was used for fractioning amplified product on agarose gel. Agarose gel (2.5%) was prepared in 100ml of 0.5 X TBE buffer dissolving 1.5g and 2.5g agarose, respectively. For each well, DNA sample and DNA loading dye were mixed in 10:1 ratio and loaded with a micropipette. Electrophoresis was done at 60 V for 2.5 hrs in 0.5 X TBE electrophoresis buffer. The gel was then visualized on an UV Tran illuminator. The photograph of gel was taken in a gel documentation unit and saved.

3.8.6 Scoring of Bands

The SSR-PCR bands were examined under ultra violet trans illuminator and photographed under gel documentation unit. The SSR bands were counted and scored as 1 for their presence or 0 for their absence. The sizes of the bands were estimated by using 100bp standard marker. The presence and absence of bands in all genotypes for 10 primers were used to generate Binomial data using excel sheet. Bands were marked as present only if the DNA amplification produced the fragment of a particular sequence and absent if the DNA amplification lacked that fragment. The banding patterns of all genotypes against each primer were compared. Bands present in one genotype and absent in another genotype were regarded as variable and used to score for polymorphism. In order to check the informativeness and discriminatory power of SSR primers utilized in this study, certain parameters like polymorphism percentage, polymorphic information content and number of alleles were calculated

(a) Percentage Polymorphism

It was calculated by dividing the polymorphic bands by the total number of scored bands:

$$= \frac{\text{Number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

(b) Polymorphism Information Content (PIC value)

The markers with more alleles have larger polymorphism information content. It was calculated as proposed by Roldan-Ruiz *et al.* (2000).

$$\text{PIC} = 2f_i (1-f_i)$$

where,

f_i = frequency of bands present

$1-f_i$ = frequency of bands absent

3.8.7 Diversity Analysis

The collected data were aligned for the construction of cluster analysis and similarity matrix. The cluster analysis of 36 genotypes was constructed with the help of NTSYS software based on Unweighted paired group of arithmetic mean average (UPGMA). A tree like dendrogram was constructed using NTSYS software. Genotypes were divided in various clusters, sub-cluster and sub-sub clusters based on genetic diversity among them and linkage distance was calculated.



*Results
and
Discussion*



The present investigation on “**Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.)**” was carried out at V.R.C., Pantnagar (Uttarakhand). The results obtained in respect of various aspects of the present investigation are described under the following heads

- 4.1 Analysis of variance (ANOVA)
- 4.2 Genetic variability for different yield related traits
- 4.3 To estimate the extent of heterosis over its parents
- 4.4 Estimation of combining ability.
- 4.5 To screen the parents and F₁ hybrids of cucumber against downy mildew (*Pseudoperonospora cubensis*)
- 4.6 To assess the molecular diversity of cucumber genotypes.

4.1 Analysis of Variance (ANOVA)

Mean data of 14 yield related traits were subjected to Analysis of variance (ANOVA) for Randomized Block Design (RBD) is presented in Table 4.1. The mean sum of square due to treatments was found highly significant for yield related traits under study at 1% and 5% level of significance, which revealed that considerable amount of variability, were present in the genotypes included in the study. Hence, there is ample scope for selection of promising genotypes in breeding programme for yield related characters. These findings are also in accordance with the findings of Joshi *et al.* (1980), Chaudhary *et al.* (1985), Saikia *et al.* (1995), Gulam *et al.* (2006), Kumar *et al.* (2008), Yadav *et al.* (2009), Golabadi *et al.* (2012) and Kumar *et al.* (2013) in cucumber.

Table 4.1: Analysis of variances for fourteen yield related traits in cucumber

S. N.	Characters	df	Mean sum of squares		
			Replication	Genotypes	Error
			2	36	72
1	Days to first male flower	0.10	21.93**	2.31	
2	Node number to first male flower	0.10	16.49**	1.08	
3	Days to first female flower	2.009	22.34**	7.19	
4	Node number to first female flower	3.97	14.31**	1.35	
5	Days to first harvest	3.21	16.70**	6.54	
6	Days to last harvest	1.94	79.81**	9.99	
7	Internodal length (cm)	2.07	2.84**	1.22	
8	Plant height (m)	0.004	0.55**	0.02	
9	Fruit length (cm)	1.63	12.69**	2.27	
10	Average fruit diameter (cm)	0.06	0.75**	0.14	
11	Number of fruits per plant	0.079	11.50**	0.26	
12	Average fruit weight (g)	18.24	2553.59**	39.87	
13	Fruit yield per plant (kg)	0.002	0.86**	0.005	
14	Fruit yield (q/ha)	40.29	15426.62**	95.63	

*Significant at 5% level of probability, **Significant at 1% level of probability

4.2 Genetic variability for different characters

4.2.1 Mean performance of parents and F₁ hybrids

4.2.1.1 Yield and its contributing traits

The *per se* performance of parents and 28 F₁ hybrids for yield related characters were observed and presented in Table 4.2. The character wise description of yield and its contributing characters are as follows:

4.2.1.1.1 Days to first male flower

A perusal of data revealed that days to first male flower ranged between 37.67 to 48.33 days with an average value 41.68 days. Among the different parents studied, PCPGR-51 (39.33) and PCPGR-83 (39.33) exhibited minimum days to first male flower. However, maximum days to first male flower were observed in PCPGR-126 (45.00) and PCPGR-112 (41.33). Among the crosses, minimum days to first male flower were observed in PCPGR-138 × PCPGR-149 (37.67), PCPGR-112 × PCPGR-138 (38.00) and PCPGR-51 × PCPGR-138 (38.33) whereas, maximum values for days to first male flower were obtained in PCPGR-50 × PCPGR-149 (48.33), PCPGR-51 × PCPGR-126 (46.33) and PCPGR-59 × PCPGR-126 (46.33).

Amongst all the hybrids, seventeen hybrid combinations *viz.*, PCPGR-138 × PCPGR-149 (37.67), PCPGR-112 × PCPGR-138 (38.00), PCPGR-51 × PCPGR-138 (38.33), PCPGR-51 × PCPGR-112 (39.00), PCPGR-51 × PCPGR-59 (39.33), PCPGR-59 × PCPGR-112 (39.33), PCPGR-112 × PCPGR-149 (39.33), PCPGR-112 × PCPGR-126 (39.67), PCPGR-83 × PCPGR-112 (39.67), PCPGR-50 × PCPGR-59 (40.00), PCPGR-50 × PCPGR-138 (40.00), PCPGR-50 × PCPGR-112 (40.33), PCPGR-126 × PCPGR-138 (40.67), PCPGR-59 × PCPGR-83 (41.00), PCPGR-59 × PCPGR-138 (41.00), PCPGR-83 × PCPGR-138 (41.67), and PCPGR-50 × PCPGR-51 (42.33) resulted in early first male flower appearance than the check cultivars Pant Khira-1 (43.00).

4.2.1.1.2 Node number to first male flower

Perusal of data pertaining to mean values for node number to first male flower ranged from 2.00 to 10.00 with an average of 5.51. Among the parents, PCPGR-50 (2.00) and PCPGR-149 (2.33) found minimum mean values for node number bearing

first male flower whereas, maximum values were observed in PCPGR-138 (8.00) and PCPGR-51 (7.00). Among the crosses, minimum values for same character were noticed in PCPGR-112 × PCPGR-126 (2.33), PCPGR-50 × PCPGR-59 (3.00), PCPGR-50 × PCPGR-138 (3.00) and PCPGR-51 × PCPGR-59 (3.00). However, maximum mean values were recorded in PCPGR-59 × PCPGR-83 (10.00), PCPGR-50 × PCPGR-126 (9.00), PCPGR-59 × PCPGR-126 (9.00), PCPGR-126 × PCPGR-138 (9.00) and PCPGR-50 × PCPGR-149 (9.00).

Amongst all the hybrids, fifteen hybrid combinations *viz.*, PCPGR-112 × PCPGR-126 (2.33), PCPGR-50 × PCPGR-59 (3.00), PCPGR-50 × PCPGR-138 (3.00), PCPGR-51 × PCPGR-59 (3.00), PCPGR-51 × PCPGR-112 (3.00), PCPGR-59 × PCPGR-138 (3.00), PCPGR-51 × PCPGR-138 (4.00), PCPGR-112 × PCPGR-138 (4.00), PCPGR-126 × PCPGR-149 (4.00), PCPGR-59 × PCPGR-112 (4.33), PCPGR-83 × PCPGR-112 (4.33), PCPGR-50 × PCPGR-83 (5.00), PCPGR-50 × PCPGR-112 (5.00), PCPGR-112 × PCPGR-149 (5.00) and PCPGR-59 × PCPGR-149 (5.33), resulted in early male flower appearance at lower node than the checks Pant Khira-1 (6.00).

4.2.1.1.3 Days to first female flower

It is explicit from data regarding mean values for days to first female flower ranged between 45.00 to 58.00 days with an average value 49.82 days. Among the parents, PCPGR-149 (47.33) and PCPGR-59 (48.00) exhibited minimum days to first female flower appearance. However, maximum days to first female flower appearance were observed in PCPGR-126 (53.00) and PCPGR-112 (50.33). Among the crosses, minimum days to first male flower appearance were found in PCPGR-50 × PCPGR-59 (45.00), PCPGR-51 × PCPGR-59 (46.33), PCPGR-51 × PCPGR-138 (46.67) and PCPGR-112 × PCPGR-138 (46.67) whereas, maximum values for days to first female flower appearance were noticed in PCPGR-83 × PCPGR-138 (58.00), PCPGR-59 × PCPGR-83 (54.00), PCPGR-51 × PCPGR-126 (53.33) and PCPGR-126 × PCPGR-138 (53.33).

Amongst all the hybrids tested, fifteenth hybrid combinations *viz.*, PCPGR-50 × PCPGR-59 (45.00), PCPGR-51 × PCPGR-59 (46.33), PCPGR-51 × PCPGR-138 (46.67), PCPGR-112 × PCPGR-138 (46.67), PCPGR-51 × PCPGR-112 (47.00), PCPGR-59 × PCPGR-112 (47.00), PCPGR-112 × PCPGR-149 (47.00), PCPGR-138

× PCPGR-149 (47.00), PCPGR-50 × PCPGR-138 (47.33), PCPGR-50 × PCPGR-112 (47.67), PCPGR-83 × PCPGR-112 (48.67), PCPGR-59 × PCPGR-138 (49.00), PCPGR-59 × PCPGR-126 (49.33), PCPGR-83 × PCPGR-149 (49.33) and PCPGR-50 × PCPGR-149 (49.67) resulted in early first female flower appearance than the check cultivars Pant Khira-1 (50.33).

4.2.1.1.4 Node number to first female flower

A Perusal of data showed that mean values for node number to first female flower ranged from 3.00 to 11.33 with an average of 6.11. Among the parents studied, PCPGR-59 (3.00) recorded minimum mean values for node number bearing first male flower whereas, maximum values were recorded in PCPGR-50 (8.00) and PCPGR-83 (7.33). Among the crosses, minimum values for same character were noticed in PCPGR-59 × PCPGR-112 (3.00), PCPGR-51 × PCPGR-59 (3.33), PCPGR-112 × PCPGR-149 (3.67) and PCPGR-50 × PCPGR-112 (3.67). However, maximum mean values were recorded in PCPGR-51 × PCPGR-126 (11.33), PCPGR-5 × PCPGR-83 (10.67) and PCPGR-126 × PCPGR-138 (10.00). Amongst all the hybrids, nineteen hybrid combinations *viz.*, PCPGR-59 × PCPGR-112 (3.00), PCPGR-51 × PCPGR-59 (3.33), PCPGR-112 × PCPGR-149 (3.67), PCPGR-50 × PCPGR-112 (3.67), PCPGR-50 × PCPGR-149 (4.00), PCPGR-83 × PCPGR-112 (4.00), PCPGR-59 × PCPGR-83 (4.00), PCPGR-112 × PCPGR-138 (4.33), PCPGR-50 × PCPGR-51 (4.67), PCPGR-50 × PCPGR-59 (5.00), PCPGR-51 × PCPGR-112 (5.00), PCPGR-83 × PCPGR-126 (5.00), PCPGR-112 × PCPGR-126 (5.00), PCPGR-138 × PCPGR-149 (5.00), PCPGR-59 × PCPGR-126 (5.33), PCPGR-51 × PCPGR-138 (6.00), PCPGR-83 × PCPGR-149 (6.00), PCPGR-83 × PCPGR-138 (6.33), PCPGR-51 × PCPGR-149 (6.67) resulted in early female flower appearance at lower node than the checks Pant Khira-1 (7.00).

4.2.1.1.5 Days to first harvest

The result of this trait revealed that mean value ranged between 57.20 to 68.67 days with an average value 61.69 days. Among the parents, PCPGR-138 (57.20) and PCPGR-59 (60.20) were earliest in days to first harvest. However, maximum days to first harvest was observed in PCPGR-126 (64.33) and PCPGR-50 (63.40). Among the crosses, minimum days to first harvest were recorded in PCPGR-50 × PCPGR-59

(57.73) and PCPGR-51 × PCPGR-112 (58.40) whereas, maximum values for days to first harvest were found in PCPGR-83 × PCPGR-138 (68.67) and PCPGR-59 × PCPGR-83 (65.53).

Amongst all the hybrids, seven hybrid combinations *viz.*, PCPGR-50 × PCPGR-59 (57.73), PCPGR-51 × PCPGR-112 (58.40), PCPGR-50 × PCPGR-112 (59.13), PCPGR-112 × PCPGR-149 (59.27) PCPGR-112 × PCPGR-138 (59.47), PCPGR-59 × PCPGR-112 (59.73), PCPGR-51 × PCPGR-59 (59.73) and PCPGR-59 × PCPGR-126 (59.80) resulted in early first harvest than the check cultivars Pant Khira-1 (60.53).

4.2.1.1.6 Days to last harvest

The data pertaining mean values for days to last harvest ranged between 94.13 to 115.47 days with an average value 106.87days. Among the parents, PCPGR-138 (94.13) and PCPGR-83 (95.47) exhibited the minimum days to last harvest. However, maximum days to last harvest were observed in PCPGR-59 (109.87) and PCPGR-50 (106.47). Among the crosses, minimum days to first harvest were found in PCPGR-50 × PCPGR-149 (100.60), PCPGR-51 × PCPGR-112 (101.67) and PCPGR-59 × PCPGR-112 (101.93) whereas, maximum days to last harvest were found in PCPGR-112 × PCPGR-149 (115.47) and PCPGR-83 × PCPGR-126 (114.53). All the hybrids found significant over check Pant Khira-1 for days to last harvest except PCPGR-112 × PCPGR-149, PCPGR-83 × PCPGR-126 and PCPGR-83 × PCPGR-138.

4.2.1.1.7 Inter nodal length (cm)

The data regarding inter nodal length showed significant variation under different parents and hybrids studied. Mean values for inter nodal length ranged between 8.61(cm) to 12.09 (cm) with an average value 10.50 cm. Among the parents, PCPGR-59 (8.24 cm) and PCPGR-149 (9.20 cm) exhibited the minimum inter nodal length while PCPGR-138 (11.84 cm) and PCPGR-83 (11.54 cm) exhibited maximum inter nodal length. Among the crosses, minimum inter nodal length were observed in PCPGR-83 × PCPGR-149 (8.61 cm), PCPGR-126 × PCPGR-149 (8.82 cm) and PCPGR-51 × PCPGR-112 (9.00 cm) whereas, maximum inter nodal length were observed in PCPGR-59 × PCPGR-112 (12.09 cm), PCPGR-50 × PCPGR-138 (11.78 cm) and PCPGR-50 × PCPGR-149 (11.41 cm).

4.2.1.1.8 Plant height (m)

The mean values for plant height ranged from 1.85 m to 3.33 m with an estimated mean value 2.81 m. Among the parents, PCPGR-83 (1.86 m) and PCPGR-138 (2.18 m) exhibited the minimum plant height while PCPGR-51 (2.88 m) and PCPGR-59 (2.77 m) showed maximum plant height. Among the crosses, minimum plant height was found in PCPGR-112 × PCPGR-126 (1.85 m), PCPGR-126 × PCPGR-149 (2.10 m) and PCPGR-50 × PCPGR-83 (2.15 m) and maximum plant height were found in PCPGR-51 × PCPGR-83 (3.33 m), PCPGR-51 × PCPGR-112 (3.31 m) and PCPGR-50 × PCPGR-149 (3.28 m).

Amongst all the crosses, six cross combinations, viz., PCPGR-51 × PCPGR-83 (3.33 m), PCPGR-51 × PCPGR-112 (3.31m), PCPGR-50 × PCPGR-149 (3.28 m), PCPGR-51 × PCPGR-138 (3.28 m), PCPGR-51 × PCPGR-149 (3.21 m) and PCPGR-112 × PCPGR-138 (3.16 m) experienced higher plant height than the check Pant Khira-1 (3.15 m).

4.2.1.1.9 Fruit length (cm)

It is explicit from data regarding mean values for fruit length ranged from 14.12 cm to 23.42 cm and the average value was 18.08 cm. Among the parents, PCPGR-138 (14.12 cm) and PCPGR-51 (15.44 cm) were recorded the minimum fruit length whereas, maximum fruit length were recorded in PCPGR-83 (19.38 cm), PCPGR-50 (19.36 cm) and PCPGR-59 (17.46 cm). Among the crosses, minimum fruit length was observed in PCPGR-50 × PCPGR-149 (14.15 cm), PCPGR-50 × PCPGR-83 (15.40 cm) and PCPGR-59 × PCPGR-149 (15.49 cm). However, PCPGR-51 × PCPGR-138 (23.42 cm), PCPGR-50 × PCPGR-138 (22.71 cm), PCPGR-59 × PCPGR-138 (21.56 cm) and PCPGR-51 × PCPGR-59 (20.68 cm) showed maximum fruit length which is higher than the check Pant Khira-1 (20.30 cm).

4.2.1.1.10 Average fruit diameter (cm)

The mean values for fruit diameter ranged from 3.44 cm to 5.51 cm and the average value was 4.65 cm. Among the parents, minimum fruit diameter was observed in PCPGR-83 (3.44 cm) and PCPGR-149 (3.53 cm) whereas, maximum fruit diameter were recorded in PCPGR-112 (4.76 cm) and PCPGR-51 (4.46 cm). Among the crosses, minimum fruit diameter was recorded in PCPGR-138 ×

PCPGR-149 (4.23 cm), PCPGR-50 × PCPGR-59 (4.33 cm) and PCPGR-83 × PCPGR-138 (4.33 cm) while, maximum fruit diameter were recorded in PCPGR-50 × PCPGR-138 (5.51 cm), PCPGR-112 × PCPGR-138 (5.36 cm) and PCPGR-112 × PCPGR-149 (5.25 cm). Amongst all the hybrids, nineteen hybrid combinations exhibited higher fruit diameter than the check Pant Khira-1 (4.64 cm).

4.2.1.1.11 Number of fruits per plant

A Perusal of data pertaining to mean values for number of fruits per plant ranged from 4.13 to 12.13 with an estimated mean value 7.85. Among the parents, PCPGR-126 (6.13) and PCPGR-149 (7.66) exhibited the minimum number of fruits per plant and PCPGR-50 (8.94), and PCPGR-51 (8.73) showed maximum number of fruits per plant. Among the crosses, minimum number of fruits per plant was recorded in PCPGR-126 × PCPGR-149 (4.13), PCPGR-59 × PCPGR-149 (4.4) and PCPGR-50 × PCPGR-149 (4.73). Whereas, Maximum number of fruits per plant were recorded in PCPGR-138 × PCPGR-149 (12.13), PCPGR-59 × PCPGR-138 (11.26) and PCPGR-50 × PCPGR-112 (10.73). Amongst all the hybrids, eleven hybrid combinations, viz., PCPGR-138 × PCPGR-149 (12.13), PCPGR-59 × PCPGR-138 (11.26), PCPGR-50 × PCPGR-112 (10.73), PCPGR-51 × PCPGR-138 (10.60), PCPGR-83 × PCPGR-112 (10.2), PCPGR-50 × PCPGR-59 (9.80), PCPGR-51 × PCPGR-59 (9.80), PCPGR-51 × PCPGR-112 (9.53), PCPGR-112 × PCPGR-149 (9.33), PCPGR-50 × PCPGR-138 (8.80) and PCPGR-59 × PCPGR-112 (8.73) experienced higher number of fruits per plant than the check Pant Khira-1 (8.26).

4.2.1.1.12 Average fruit weight (g)

It is apparent from data regarding average fruit weight revealed that significant variation was found among thirty seven treatments which ranged from 167.11g to 280.91g with an average of 215.96 g. Among the parents, PCPGR-51 (167.11) and PCPGR-126 (181.43) exhibited the minimum average fruit weight while, PCPGR-83 (211.25), and PCPGR-59 (209.75) exhibited maximum average fruit weight. Among the different crosses, minimum average fruit weight was recorded in PCPGR-59 × PCPGR-149 (179.2), PCPGR-59 × PCPGR-126 (182.65) and PCPGR-51 × PCPGR-83 (183.72) whereas, maximum average fruit weight were recorded in PCPGR-112 × PCPGR-138 (280.91), PCPGR-59 × PCPGR-112 (278.88) and PCPGR-50 × PCPGR-59 (265.29).

Table 4.2: Mean performance of cucumber genotypes for different yield and its contributing traits

S.N.	Genotypes	Days to first male flower	Node number to first male flower	Days to first female flower	Node number to first female flower	Days to first harvest	Days to last harvest	Internodal length (cm)	Plant height (m)	Fruit length (cm)	Average fruit diameter (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (kg)	Fruit yield (q/ha)
1.	PCPGR-50	40.67	2.00	50.00	8.00	63.40	106.47	11.14	2.54	19.36	3.56	8.94	190.8	1.70	227.47
2.	PCPGR-51	39.33	7.00	49.00	7.00	60.67	99.40	9.50	2.88	15.44	4.46	8.73	167.11	1.46	194.39
3.	PCPGR-59	41.00	3.00	48.00	3.00	60.20	109.87	8.24	2.77	17.46	4.24	8.08	209.75	1.69	226.01
4.	PCPGR-83	39.33	6.00	50.00	7.33	60.40	95.47	11.54	1.86	19.38	3.44	8.15	211.25	1.72	229.42
5.	PCPGR-112	41.33	4.33	50.33	5.00	61.33	104.73	9.87	2.61	16.31	4.76	8.26	192.27	1.59	211.65
6.	PCPGR-126	45.00	3.00	53.00	6.67	64.33	100.27	10.08	2.72	16.99	4.22	6.13	181.43	1.11	148.32
7.	PCPGR-138	40.00	8.00	49.00	5.00	57.20	94.13	11.84	2.18	14.12	3.97	8.6	188.84	1.62	216.26
8.	PCPGR-149	39.67	2.33	47.33	5.00	61.40	104.40	9.20	2.48	16.37	3.53	7.66	202.41	1.55	206.85
9.	PCPGR-50 × PCPGR-51	42.33	8.00	50.33	4.67	61.87	106.93	10.21	2.17	17.23	4.70	7.06	188.21	1.33	177.27
10.	PCPGR-50 × PCPGR-59	40.00	3.00	45.00	5.00	57.73	107.80	10.86	3.14	19.75	4.33	9.80	265.29	2.59	346.46
11.	PCPGR-50 × PCPGR-83	45.33	5.00	50.33	8.67	64.33	104.73	10.24	2.15	15.40	5.23	6.46	218.62	1.41	188.22
12.	PCPGR-50 × PCPGR-112	40.33	5.00	47.67	3.67	59.13	106.40	10.50	2.90	16.18	4.73	10.73	222.56	2.38	318.27
13.	PCPGR-50 × PCPGR-126	44.67	9.00	51.67	8.00	62.40	106.33	11.38	3.06	19.56	5.25	5.53	240.23	1.32	176.62
14.	PCPGR-50 × PCPGR-138	40.00	3.00	47.33	7.00	61.20	110.27	11.78	3.15	22.71	5.51	8.80	255.94	2.25	300.16
15.	PCPGR-50 × PCPGR-149	48.33	9.00	49.67	4.00	60.67	100.60	11.41	3.28	14.15	4.37	4.73	216.65	1.02	136.39
16.	PCPGR-51 × PCPGR-59	39.33	3.00	46.33	3.33	59.73	103.27	10.74	3.15	20.68	5.20	9.80	231.91	2.27	302.76
17.	PCPGR-51 × PCPGR-83	43.00	8.33	50.67	10.67	61.60	107.00	9.19	3.33	18.36	4.86	7.96	183.72	1.46	195.06
18.	PCPGR-51 × PCPGR-112	39.00	3.00	47.00	5.00	58.40	101.67	9.00	3.31	19.78	4.66	9.53	242.76	2.31	308.21
19.	PCPGR-51 × PCPGR-126	46.33	6.00	53.33	11.33	64.47	105.00	11.31	3.15	15.5	4.72	5.26	193.82	1.01	135.92
20.	PCPGR-51 × PCPGR-138	38.33	4.00	46.67	6.00	61.80	105.27	10.30	3.28	23.42	5.33	10.6	242.10	2.56	341.56
21.	PCPGR-51 × PCPGR-149	45.00	7.00	53.00	6.67	63.47	109.93	10.63	3.21	17.35	4.93	7.73	194.60	1.50	200.47

Table 4.2 Contd...

S.N.	Genotypes	Days to first male flower	Node number to first male flower	Days to first female flower	Node number to first female flower	Days to first harvest	Days to last harvest	Internodal length (cm)	Plant height (m)	Fruit length (cm)	Average fruit diameter (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (kg)	Fruit yield (q/ha)
22	PCPGR-59 × PCPGR-83	41.00	10.00	54.00	4.00	65.53	109.67	11.27	3.08	18.32	4.72	5.26	220.50	1.16	154.67
23	PCPGR-59 × PCPGR-112	39.33	4.33	47.00	3.00	59.73	101.93	12.09	3.13	17.87	4.96	8.73	278.88	2.43	324.29
24	PCPGR-59 × PCPGR-126	46.33	9.00	49.33	5.33	59.80	106.60	10.88	2.73	16.85	5.19	6.53	182.65	1.19	158.71
25	PCPGR-59 × PCPGR-138	41.00	3.00	49.00	9.00	61.40	110.53	9.95	3.01	21.56	4.43	11.26	217.87	2.45	327.20
26	PCPGR-59 × PCPGR-149	43.33	5.33	52.67	9.33	64.00	113.40	11.08	2.83	15.49	4.68	4.40	179.2	0.78	104.60
27	PCPGR-83 × PCPGR-112	39.67	4.33	48.67	4.00	62.80	113.27	11.23	2.44	20.31	4.63	10.20	241.02	2.45	327.62
28	PCPGR-83 × PCPGR-126	44.33	8.33	53.00	5.00	64.07	114.53	11.18	2.96	17.23	4.57	7.20	212.56	1.53	203.78
29	PCPGR-83 × PCPGR-138	41.67	6.00	58.00	6.33	68.67	114.40	10.34	3.01	16.26	4.33	6.13	186.55	1.14	152.47
30	PCPGR-83 × PCPGR-149	43.33	8.00	49.33	6.00	60.00	107.47	8.61	3.05	17.26	4.82	7.66	208.06	1.59	212.47
31	PCPGR-112 × PCPGR-126	39.67	2.33	50.67	5.00	61.73	112.40	10.37	1.85	17.56	4.59	6.40	239.93	1.53	204.71
32	PCPGR-112 × PCPGR-138	38.00	4.00	46.67	4.33	59.47	108.53	12.02	3.16	20.33	5.36	7.93	280.91	2.22	296.84
33	PCPGR-112 × PCPGR-149	39.33	5.00	47.00	3.67	59.27	115.47	11.00	2.96	20.11	5.25	9.33	252.39	2.35	313.60
34	PCPGR-126 × PCPGR-138	40.67	9.00	53.33	10.00	64.60	104.40	10.17	2.18	18.33	5.02	6.33	184.47	1.16	155.37
35	PCPGR-126 × PCPGR-149	45.33	4.00	51.67	8.00	63.07	106.00	8.82	2.10	16.90	4.51	4.13	238.41	0.98	131.20
36	PCPGR-138 × PCPGR-149	37.67	6.33	47.00	5.00	62.07	111.67	10.13	3.06	18.83	4.23	12.13	204.25	2.47	330.24
37	Pant Khira-1	43.00	6.00	50.33	7.00	60.53	114.07	10.57	3.15	20.30	4.64	8.26	222.46	1.84	244.93
	GM	41.68	5.51	49.82	6.11	61.69	106.87	10.50	2.81	18.08	4.65	7.85	215.96	1.70	227.85
	Sem	0.88	0.58	1.55	0.67	1.48	1.83	0.68	0.08	0.86	0.21	0.29	3.64	0.04	5.64
	C.D. (5%)	2.47	1.63	4.37	1.89	4.16	5.15	1.92	0.23	2.44	0.59	0.84	10.27	0.11	15.91
	C.D. (1%)	3.28	2.17	5.79	2.51	5.53	6.83	2.55	0.31	3.24	0.79	1.12	13.64	0.15	21.12
	C.V.	3.65	18.58	5.38	19.04	4.15	2.96	11.28	5.22	8.37	7.78	6.61	2.92	4.28	4.29
	Range	37.67-48.33	2.00-10.00	45.00-58.00	3.00-11.33	57.20-68.67	94.13-115.47	8.61-12.09	1.85-3.33	14.12-23.42	3.9-5.51	4.13-12.13	167.11-280.91	0.78-2.59	104.6-346.46

Amongst all the hybrids, thirteen hybrid combinations, viz., PCPGR-112 × PCPGR-138 (280.91), PCPGR-59 × PCPGR-112 (278.88), PCPGR-50 × PCPGR-59 (265.29), PCPGR-50 × PCPGR-138 (255.94), PCPGR-112 × PCPGR-149 (252.39), PCPGR-51 × PCPGR-112 (242.76), PCPGR-51 × PCPGR-138 (242.1), PCPGR-83 × PCPGR-112 (241.02), PCPGR-50 × PCPGR-126 (240.23), PCPGR-112 × PCPGR-126 (239.93), PCPGR-126 × PCPGR-149 (238.41), PCPGR-51 × PCPGR-59 (231.91) and PCPGR-50 × PCPGR-112 (222.56) showed higher average fruit weight than the check Pant Khira-1 (222.46).

4.2.1.1.13 Fruit yield per plant (kg)

The mean values for fruit yield per plant was ranged from 0.78 kg to 2.59 kg and the average value was 1.70 kg. Among the parents, PCPGR-126 (1.11) and PCPGR-51 (1.46) exhibited the minimum fruit yield per plant while, PCPGR-83 (1.72) and PCPGR-50 (1.70) exhibited maximum fruit yield per plant. Among the crosses, minimum fruit yield per plant was observed in PCPGR-59 × PCPGR-149 (0.78), PCPGR-126 × PCPGR-149 (0.98), PCPGR-50 × PCPGR-149 (1.02) and PCPGR-51 × PCPGR-126 (1.01) whereas, maximum fruit yield per plant were observed in PCPGR-50 × PCPGR-59 (2.59), and PCPGR-51 × PCPGR-138 (2.56).

Amongst all the hybrids, twelve hybrid combinations, viz., PCPGR-50 × PCPGR-59 (2.59), PCPGR-51 × PCPGR-138 (2.56), PCPGR-138 × PCPGR-149 (2.47), PCPGR-59 × PCPGR-138 (2.45), PCPGR-83 × PCPGR-112 (2.45), PCPGR-59 × PCPGR-112 (2.43), PCPGR-50 × PCPGR-112 (2.38), PCPGR-112 × PCPGR-149 (2.35), PCPGR-51 × PCPGR-112 (2.31), PCPGR-51 × PCPGR-59 (2.27), PCPGR-50 × PCPGR-138 (2.25) and PCPGR-112 × PCPGR-138 (2.22) resulted in higher fruit yield per plant than the check Pant Khira-1 (1.84).

4.2.1.1.14 Fruit yield (q/ha)

It is evident from data regarding mean values for fruit yield ranged between 104.6 to 346.46 q/ha and the average value was 227.85 q/ha. Among the parents, PCPGR-126 (148.32) and PCPGR-51 (194.39) were recorded the minimum fruit yield while maximum fruit yield were recorded in PCPGR-83 (229.42) and PCPGR-50 (227.47). Among the crosses, minimum fruit yield was noticed in PCPGR-59 × PCPGR-149 (104.6), PCPGR-126 × PCPGR-149 (131.20), PCPGR-50 × PCPGR-149

(136.39) and PCPGR-51 × PCPGR-126 (135.92) and maximum fruit yield were recorded in PCPGR-50 × PCPGR-59 (346.46) and PCPGR-51 × PCPGR-138 (341.56).

Amongst all the hybrids, twelve hybrid combinations, *viz.*, PCPGR-50 × PCPGR-59 (346.46), PCPGR-51 × PCPGR-138 (341.56), PCPGR-138 × PCPGR-149 (330.24), PCPGR-59 × PCPGR-138 (327.20), PCPGR-83 × PCPGR-112 (327.62), PCPGR-59 × PCPGR-112 (324.29), PCPGR-50 × PCPGR-112 (318.27), PCPGR-112 × PCPGR-149 (313.6), PCPGR-51 × PCPGR-112 (308.21), PCPGR-51 × PCPGR-59 (302.76), PCPGR-50 × PCPGR-138 (300.16) and PCPGR-112 × PCPGR-138 (296.84) experienced higher fruit yield than the check Pant Khira-1 (244.93).

The difference in reproductive behaviour occurs due to change in environmental condition. That might be the reason for such varying yield and yield attributing traits. Environmental factors that affect cucumber production are temperature and humidity. Cucumber grows best under conditions of high temperature, low humidity, moderate light intensity and good soil structure with an uninterrupted supply of water and nutrients (Papadopoulos, 1994). Optimum temperature for cucumber growth is between 20°C to 25°C, with growth reduction occurring below 16°C and above 30°C (Hector *et al.*, 1993). Joshi *et al.* (1980), Chaudhary *et al.* (1985), Saikia *et al.* (1995), Gulam *et al.* (2006), Kumar *et al.* (2008), Yadav *et al.* (2009), Golabadi *et al.* (2012) and Kumar *et al.* (2013) have also reported good amount of variability among germplasm for different traits in cucumber.

4.2.1.2 Coefficient of variation

Information on genetic variability of yield and quality components is of vital importance in crop improvement programme. Plant breeding is mainly the exploitation of genetic variation and in view of the possible decline of variation breeders should always examine means of conserving variability and creating new germplasm. The extent of genotypic variability indicates the amenability of given character for its improvement (Burton, 1953). The estimate of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance for 14 yield and yield contributing characters are presented in Table 4.3.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are the best criteria to measure available variability. Heritability of a character is important in determining its response to selection. Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an effective breeding program. The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960). It is generally expressed in percentage. Assessment of variability parameters revealed that there is lot of variation present among the genotypes studied. In general, the value of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters.

4.2.1.2.1 Genotypic coefficient of variation (GCV)

Genotypic coefficient of variation values for different characters are presented in Table 4.3. GCV was found highest for node number to first male flower (41.11%) followed by node number to first female flower (34.02%), fruit yield per hectare (31.37%), fruit yield per plant (31.36%) and number of fruits per plant (24.63%) whereas, moderate GCV was observed for plant height (14.97%), average fruit weight (13.40%) and fruit length (10.41%). However, average fruit diameter (9.70%), days to first male flower (6.13%), inter nodal length (6.98%), days to last harvest (4.51%), days to first female flower (4.51%) and days to first harvest (2.98%) were low in GCV.

4.2.1.2.2 Phenotypic coefficient of variation (PCV)

Phenotypic coefficient of variation values for different characters are presented in Table 4.3. PCV was found highest for node number to first male flower (45.22%) followed by node number to first female flower (38.99%), fruit yield per hectare (31.66%), fruit yield per plant (31.65%) and number of fruits per plant (25.51%) whereas, moderate PCV was observed for plant height (15.86%), average fruit weight (13.71%), fruit length (13.39%), average fruit diameter (12.67%) and inter nodal length (12.63%). However, days to first male flower (7.13%), days to first female flower (7.02%), days to last harvest (5.39%), and days to first harvest (5.10%) were low in PCV.

Table 4.3: Estimation of coefficient of variance and other genetic parameters for different yield and its contributing traits in cucumber

S.N.	Characters	Range	General Mean	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	GA as% of mean 5%	GA as% of mean 1%
1.	Days to first male flower	37.67-48.33	41.68	6.13	7.13	3.64	73.9	10.86	13.92
2.	Node number to first male flower	2.00-10.00	5.40	41.11	45.22	18.85	82.6	76.97	98.65
3.	Days to first female flower	45.00-58.00	49.82	4.51	7.02	5.38	41.2	5.96	7.64
4.	Node number to first female flower	3.00-11.33	6.11	34.03	38.99	19.04	76.2	61.18	78.40
5.	Days to first harvest	57.20-68.67	61.69	2.98	5.10	4.14	34.1	3.58	4.59
6.	Days to last harvest	94.13-115.47	106.87	4.51	5.39	2.95	69.9	7.77	9.96
7.	Inter nodal length (cm)	8.61-12.09	10.45	6.98	12.63	10.52	30.6	7.96	10.20
8.	Plant height (m)	1.85-3.33	2.81	14.97	15.86	5.22	89.2	29.12	37.33
9.	Fruit length (cm)	14.12-23.42	17.94	10.41	13.39	8.42	60.5	16.68	21.38
10.	Average fruit diameter (cm)	3.9-5.51	4.69	9.70	12.67	8.14	58.7	15.32	19.63
11.	Number of fruits per plant	4.13-12.13	7.85	24.63	25.51	6.61	93.3	49.02	62.82
12.	Average fruit weight (g)	167.11-280.91	215.96	13.40	13.71	2.92	95.5	26.97	34.57
13.	Fruit yield per plant (kg)	0.78-2.59	1.70	31.36	31.65	4.28	98.2	64.01	82.04
14.	Fruit yield (q/ha)	104.6-346.46	227.85	31.37	31.66	4.29	98.2	64.03	82.06

Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Rastogi and Arya (1990), Saikia *et al.* (1995), Karuppiah *et al.* (2002), Kumar *et al.* (2008), Mehdi and Khan (2009), Kumar *et al.* (2013) and Krishna Reddy (2014) reported that the coefficients of genotypic and phenotypic variability were moderate to high for different characters in cucumber.

4.2.1.2.3 Heritability (h^2) and Genetic Advance

The broad sense heritability estimate provides information on relative magnitude of genetic and environmental variation in germplasm pool (Dudley and Moll, 1969). Estimates on broad sense heritability ranged from 30.60 per cent (Inter nodal length) to 98.2 per cent (Fruit yield per hectare). Fruit yield per plant (kg) and fruit yield q/ha exhibited maximum heritability (98.2%) followed by average fruit weight (95.5%), number of fruits per plant (93.3%), plant height (89.2%), node number to first male flower (82.60%) and node number to first female flower (76.2%). The moderate heritability recorded for days to first male flower (73.9%) followed by days to last harvest (69.9%), fruit length (60.50%), average fruit diameter (58.70%). Low heritability recorded for days to first female flower (41.2%), days to first harvest (34.1%) and inter nodal length (30.60%).

The heritability estimates for these traits implies that these characters are least influence by the environment. Saikia *et al.* (1995) recorded high heritability for fruit yield per vine and node to first female flower. Kumar *et al.* (2008) observed high heritability for days to first female flower, number of fruit per plant, fruit length, fruit weight and fruit yield per hectare. Further, Kumar *et al.* (2013) reported high heritability for yield per plot.

Low to high estimates of broad sense heritability indicates that these characters are greatly influenced by environmental effects. Due to the masking effect of the environment on genotypes, genetic improvement through selection in these traits is difficult.

High value of genetic advance was observed for node number to first male flower (98.65) followed by fruit yield (82.06), fruit yield per plant (82.04), node

number to first female flower (78.40) and number of fruits per plant (62.82) plant height (37.33), average fruit weight (34.57) and fruit length (21.38). Moderate value of genetic advance was observed for average fruit diameter (19.63), days to first male flower (13.92) and Inter nodal length (10.20). Low value of genetic advance was observed for days to last harvest (9.96), days to first female flower (7.64) and days to first harvest (4.59).

High heritability along with high genetic advance indicate that mostly the heritability is due to additive gene effects and selection may be effective. Similarly, High estimate of heritability along with genetic advance for all traits studied revealed that these characters are controlled by additive gene action (Kumar *et al.*, 2008), Mehdi and Khan (2009). In contrast, Yadav *et al.* (2009) observed high heritability and genetic advance for some of the traits.

4.3 Heterosis

The estimates of relative heterosis, (mid-parent) heterobeltiosis (better parent) and standard heterosis (standard parent) for all the 14 traits have been presented in Table 4.4 - 4.17. The negative heterosis was considered to be desirable for days to first male flower, days to first female flower, node number of first male flower, node number of first female flower and days to first harvest as it indicates earliness. The genotype Pant Khira-1 was used as a standard parent for standard heterosis.

4.3.1 Days to first male flower

The estimates of relative heterosis, heterobeltiosis and standard heterosis for days to first male flower are presented in Table 4.4. A perusal of data revealed that heterosis over mid parent, better parent and over check value ranged from -8.11 to 20.33 per cent, -11.85 to 18.85 and -12.40 to 12.40 per cent, respectively. Out of twenty eight crosses, twelve crosses exhibited significant relative heterosis, eight hybrids showed significant heterobeltiosis and fifteen hybrids showed significant standard heterosis for days to first male flower.

For relative heterosis, two cross combinations *viz.*, PCPGR-112 × PCPGR-126 (-8.11%) and PCPGR-112 × PCPGR-138 (-6.56%) exhibited significant desirable negative relative heterosis. However, out of all crosses, three crosses showed significant

Table 4.4 Heterosis for days to first male flower

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	42.33	5.83*	4.10	-1.55
2.	PCPGR-50 × PCPGR-59	40	-2.04	-2.44	-6.98*
3.	PCPGR-50 × PCPGR-83	45.33	13.33**	11.48**	5.43
4.	PCPGR-50 × PCPGR-112	40.33	-1.63	-2.42	-6.20*
5.	PCPGR-50 × PCPGR-126	44.67	4.28	-0.74	3.88
6.	PCPGR-50 × PCPGR-138	40	-0.83	-1.64	-6.98*
7.	PCPGR-50 × PCPGR-149	48.33	20.33**	18.85**	12.40**
8.	PCPGR-51 × PCPGR-59	39.33	-2.07	-4.07	-8.53**
9.	PCPGR-51 × PCPGR-83	43	9.32**	9.32**	0
10.	PCPGR-51 × PCPGR-112	39	-3.31	-5.65	-9.30**
11.	PCPGR-51 × PCPGR-126	46.33	9.88**	2.96	7.75**
12.	PCPGR-51 × PCPGR-138	38.33	-3.36	-4.17	-10.85**
13.	PCPGR-51 × PCPGR-149	45	13.92**	13.45**	4.65
14.	PCPGR-59 × PCPGR-83	41	2.07	0.00	-4.65
15.	PCPGR-59 × PCPGR-112	39.33	-4.45	-4.84	-8.53**
16.	PCPGR-59 × PCPGR-126	46.33	7.75**	2.96	7.75**
17.	PCPGR-59 × PCPGR-138	41	1.23	0.00	-4.65
18.	PCPGR-59 × PCPGR-149	43.33	7.44**	5.69	0.78
19.	PCPGR-83 × PCPGR-112	39.67	-1.65	-4.03	-7.75**
20.	PCPGR-83 × PCPGR-126	44.33	5.14	-1.48	3.1
21.	PCPGR-83 × PCPGR-138	41.67	5.04	4.17	-3.1
22.	PCPGR-83 × PCPGR-149	43.33	9.70**	9.24**	0.78
23.	PCPGR-112 × PCPGR-126	39.67	-8.11**	-11.85**	-7.75**
24.	PCPGR-112 × PCPGR-138	38	-6.56*	-8.06**	-11.63**
25.	PCPGR-112 × PCPGR-149	39.33	-2.88	-4.84	-8.53**
26.	PCPGR-126 × PCPGR-138	40.67	-4.31	-9.63**	-5.43
27.	PCPGR-126 × PCPGR-149	45.33	7.09**	0.74	5.43
28.	PCPGR-138 × PCPGR-149	37.67	-5.44	-5.83	-12.40**
Range	Minimum	38.00	-8.11	-11.85	-12.40
	Maximum	48.33	20.33	18.85	12.40

negative heterobeltiosis *viz.*, PCPGR-112 × PCPGR-126 (-11.85%), PCPGR-126 × PCPGR-138 (-9.63%) and PCPGR-112 × PCPGR-138 (-8.06%). Looking to standard heterosis, among the crosses, twelve cross combinations showed significant negative standard heterosis in desirable direction for this particular trait. Top seven crosses which showed maximum negative heterosis over check for days to first male flower were PCPGR-138 × PCPGR-149 (-12.40%), PCPGR-112 × PCPGR-138 (-11.63%), PCPGR-51 × PCPGR-138 (-10.85%), PCPGR-51 × PCPGR-112 (-9.30%) and PCPGR-51 × PCPGR-59 (-8.53%).

4.3.2 Node number to first male flower

A perusal of estimates of relative heterosis, heterobeltiosis and standard heterosis for node number to first male flower presented in Table 4.5. It is clear from data that heterosis over mid parent, better parent and over check value ranged from -47.06 to 315.38 per cent, -62.50 to 285.71 and -61.11 to 66.67 per cent, respectively. Out of twenty eight crosses, twenty crosses exhibited significant relative heterosis, seventeen hybrids showed significant heterobeltiosis and eighteen hybrids showed significant standard heterosis for node number to first male flower.

For relative heterosis, seven cross combinations *viz.*, PCPGR-51 × PCPGR-112 (-47.07%), PCPGR-51 × PCPGR-138 (-46.67%), PCPGR-59 × PCPGR-138 (-45.45%), PCPGR-50 × PCPGR-138 (-40.00%), PCPGR-51 × PCPGR-59 (-40.00%), PCPGR-112 × PCPGR-126 (-36.36%) and PCPGR-112 × PCPGR-138 (-35.14%) exhibited significant desirable negative relative heterosis for node number to first male flower. However, out of all crosses, nine crosses showed significant negative heterobeltiosis, *viz.*, PCPGR-50 × PCPGR-138 (-62.50%), PCPGR-59 × PCPGR-138 (-62.50%), PCPGR-51 × PCPGR-59 (-57.14%), PCPGR-51 × PCPGR-112 (-57.14%), PCPGR-51 × PCPGR-138 (-50.00%), PCPGR-112 × PCPGR-138 (-50.00%), PCPGR-112 × PCPGR-126 (-46.15%), PCPGR-83 × PCPGR-112 (-27.78%) and PCPGR-83 × PCPGR-138 (-25.00%). For standard heterosis, among the crosses, nine cross combinations showed significant negative standard heterosis in desirable direction for this particular trait. Top six crosses that showed maximum negative standard heterosis over check for node number to first male flower were PCPGR-112 × PCPGR-126 (-61.11%), PCPGR-50 × PCPGR-59 (-50.00%), PCPGR-50 × PCPGR-138 (-50.00%), PCPGR-51 × PCPGR-59 (-50.00%), PCPGR-51 × PCPGR-112 (-50.00%) and PCPGR-59 × PCPGR-138 (-50.00%).

Table 4.5 Heterosis for node number to first male flower

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	8	77.78**	14.29	33.33*
2.	PCPGR-50 × PCPGR-59	3	20	0	-50.00**
3.	PCPGR-50 × PCPGR-83	5	25	-16.67	-16.67
4.	PCPGR-50 × PCPGR-112	5	57.89*	15.38	-16.67
5.	PCPGR-50 × PCPGR-126	9	260.00**	200.00**	50.00**
6.	PCPGR-50 × PCPGR-138	3	-40.00**	-62.50**	-50.00**
7.	PCPGR-50 × PCPGR-149	9	315.38**	285.71**	50.00**
8.	PCPGR-51 × PCPGR-59	3	-40.00**	-57.14**	-50.00**
9.	PCPGR-51 × PCPGR-83	8.33	28.21*	19.05	38.89**
10.	PCPGR-51 × PCPGR-112	3	-47.06**	-57.14**	-50.00**
11.	PCPGR-51 × PCPGR-126	6	20	-14.29	0
12.	PCPGR-51 × PCPGR-138	4	-46.67**	-50.00**	-33.33*
13.	PCPGR-51 × PCPGR-149	7	50.00**	0	16.67
14.	PCPGR-59 × PCPGR-83	10	122.22**	66.67**	66.67**
15.	PCPGR-59 × PCPGR-112	4.33	18.18	0	-27.78
16.	PCPGR-59 × PCPGR-126	9	200.00**	200.00**	50.00**
17. ×	PCPGR-59 × PCPGR-138	3	-45.45**	-62.50**	-50.00**
18.	PCPGR-59 × PCPGR-149	5.33	100.00**	77.78**	-11.11
19.	PCPGR-83 × PCPGR-112	4.33	-16.13	-27.78*	-27.78
20.	PCPGR-83 × PCPGR-126	8.33	85.19**	38.89**	38.89**
21.	PCPGR-83 × PCPGR-138	6	-14.29	-25.00*	0
22.	PCPGR-83 × PCPGR-149	8	92.00**	33.33*	33.33*
23.	PCPGR-112 × PCPGR-126	2.33	-36.36**	-46.15*	-61.11**
24.	PCPGR-112 × PCPGR-138	4	-35.14**	-50.00**	-33.33*
25.	PCPGR-112 × PCPGR-149	5	50.00*	15.38	-16.67
26.	PCPGR-126 × PCPGR-138	9	63.64**	12.5	50.00**
27.	PCPGR-126 × PCPGR-149	4	50	33.33*	-33.33*
28.	PCPGR-138 × PCPGR-149	6.33	22.58	-20.83	5.56
Range	Minimum	2.33	-47.06	-62.50	-61.11
	Maximum	10.00	315.38	285.71	66.67

4.3.3 Days to first female flower

A critical examination of data presented in Table 4.6 revealed that the range of heterosis for Days to first female flower was -8.16 to 17.17 per cent for relative heterosis, -10.00 to 16.00 per cent for heterobeltiosis and -10.60 to 15.23 per cent for standard heterosis.

Out of twenty eight crosses, five crosses exhibited significant relative heterosis, three hybrids showed significant heterobeltiosis and two hybrids showed significant standard heterosis for days to first female flower. For relative heterosis, PCPGR-50 × PCPGR-59 (-8.16%) exhibited significant desirable negative relative heterosis. However, out of all crosses, one crosses, PCPGR-50 × PCPGR-59 (-10.00%) exhibited significant negative heterobeltiosis. In case of standard heterosis, PCPGR-50 × PCPGR-59 exhibited significant negative standard heterosis (-10.60%) over check for days to first female flower. Cizov (1945) found considerable heterosis under polyhouse for earliness. Further, Vijayakumari *et al.* (1991) reported that the gynoeocious and monoecious hybrids were promising for earliness.

4.3.4 Node number to first female flower

It is explicit from data presented in the Table 4.7 revealed that heterosis over mid parent, better parent and over check parent for number of flowers per cluster ranged from -43.59 to 133.33 per cent, -54.17 to 86.67per cent and -57.14 to 61.90 per cent, respectively. For node number to first female flower out of all cross combinations, eleven crosses showed significant relative heterosis, fifteen hybrids showed significant heterobeltiosis and ninteen hybrids exhibited significant standard heterosis.

Out of twenty eight cross combinations, six crosses showed desirable significant negative relative heterosis for node number to first female flower *viz.*, PCPGR-50 × PCPGR-112 (-43.59%), PCPGR-50 × PCPGR-149 (-38.46%), PCPGR-50 × PCPGR-51(-37.78%), PCPGR-83 × PCPGR-112 (-35.14%) PCPGR-51 × PCPGR-59 (-33.33%) and PCPGR-83 × PCPGR-126 (-28.57%) while, ten cross combinations showed significant negative heterosis over better parent for same traits. Top five cross combinations that showed desirable significant heterosis over better parents were PCPGR-50 × PCPGR-112 (-54.17%), PCPGR-51 × PCPGR-59(-52.38%), PCPGR-50 × PCPGR-149 (-50.00%), PCPGR-59 × PCPGR-83 (-45.45%) and PCPGR-83 × PCPGR-112 (-45.45%). In case of standard heterosis, fourteen crosses exhibited

Table 4.6: Heterosis for days to first female flower

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	50.33	1.68	0.67	0.00
2.	PCPGR-50 × PCPGR-59	45.00	-8.16*	-10.00*	-10.60*
3.	PCPGR-50 × PCPGR-83	50.33	0.67	0.67	0.00
4.	PCPGR-50 × PCPGR-112	47.67	-4.98	-5.30	-5.30
5.	PCPGR-50 × PCPGR-126	51.67	0.32	-2.52	2.65
6.	PCPGR-50 × PCPGR-138	47.33	-4.38	-5.33	-5.96
7.	PCPGR-50 × PCPGR-149	49.67	2.05	-0.67	-1.32
8.	PCPGR-51 × PCPGR-59	46.33	-4.47	-5.44	-7.95
9.	PCPGR-51 × PCPGR-83	50.67	2.36	1.33	0.66
10.	PCPGR-51 × PCPGR-112	47.00	-5.37	-6.62	-6.62
11.	PCPGR-51 × PCPGR-126	53.33	4.58	0.63	5.96
12.	PCPGR-51 × PCPGR-138	46.67	-4.76	-4.76	-7.28
13.	PCPGR-51 × PCPGR-149	53.00	10.03*	8.16	5.30
14.	PCPGR-59 × PCPGR-83	54.00	10.20*	8.00	7.28
15.	PCPGR-59 × PCPGR-112	47.00	-4.41	-6.62	-6.62
16.	PCPGR-59 × PCPGR-126	49.33	-2.31	-6.92	-1.99
17.	PCPGR-59 × PCPGR-138	49.00	1.03	0.00	-2.65
18.	PCPGR-59 × PCPGR-149	52.67	10.49*	9.72*	4.64
19.	PCPGR-83 × PCPGR-112	48.67	-2.99	-3.31	-3.31
20.	PCPGR-83 × PCPGR-126	53.00	2.91	0.00	5.30
21.	PCPGR-83 × PCPGR-138	58.00	17.17**	16.00**	15.23**
22.	PCPGR-83 × PCPGR-149	49.33	1.37	-1.33	-1.99
23.	PCPGR-112 × PCPGR-126	50.67	-1.94	-4.40	0.66
24.	PCPGR-112 × PCPGR-138	46.67	-6.04	-7.28	-7.28
25.	PCPGR-112 × PCPGR-149	47.00	-3.75	-6.62	-6.62
26.	PCPGR-126 × PCPGR-138	53.33	4.58	0.63	5.96
27.	PCPGR-126 × PCPGR-149	51.67	2.99	-2.52	2.65
28.	PCPGR-138 × PCPGR-149	47.00	-2.42	-4.08	5.56
Range	Minimum	45.00	-8.16	-10.00	-10.60
	Maximum	58.00	17.17	16.00	15.23

Table 4.7: Heterosis for node number to first female flower

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	4.670	-37.78**	-41.67**	-33.33*
2.	PCPGR-50 × PCPGR-59	5.000	-9.090	-37.50**	-28.57*
3.	PCPGR-50 × PCPGR-83	8.670	13.040	8.330	23.810
4.	PCPGR-50 × PCPGR-112	3.670	-43.59**	-54.17**	-47.62**
5.	PCPGR-50 × PCPGR-126	8.000	9.090	0.000	14.290
6.	PCPGR-50 × PCPGR-138	7.000	7.690	-12.500	0.000
7.	PCPGR-50 × PCPGR-149	4.000	-38.46**	-50.00**	-42.86**
8.	PCPGR-51 × PCPGR-59	3.330	-33.33*	-52.38**	-52.38**
9.	PCPGR-51 × PCPGR-83	10.670	48.84**	45.45**	52.38**
10.	PCPGR-51 × PCPGR-112	5.000	-16.670	-28.57*	-28.57*
11.	PCPGR-51 × PCPGR-126	11.330	65.85**	61.90**	61.90**
12.	PCPGR-51 × PCPGR-138	6.000	0.000	-14.290	-14.290
13.	PCPGR-51 × PCPGR-149	6.670	11.110	-4.760	-4.760
14.	PCPGR-59 × PCPGR-83	4.000	-22.580	-45.45**	-42.86**
15.	PCPGR-59 × PCPGR-112	3.000	-25.000	-40.00*	-57.14**
16.	PCPGR-59 × PCPGR-126	5.330	10.340	-20.000	-23.810
17.	PCPGR-59 × PCPGR-138	9.000	125.00**	80.00**	28.57*
18.	PCPGR-59 × PCPGR-149	9.330	133.33**	86.67**	33.33*
19.	PCPGR-83 × PCPGR-112	4.000	-35.14*	-45.45**	-42.86**
20.	PCPGR-83 × PCPGR-126	5.000	-28.57*	-31.82*	-28.57*
21.	PCPGR-83 × PCPGR-138	6.330	2.700	-13.640	-9.520
22.	PCPGR-83 × PCPGR-149	6.000	-2.700	-18.180	-14.290
23.	PCPGR-112 × PCPGR-126	5.000	-14.290	-25.000	-28.57*
24.	PCPGR-112 × PCPGR-138	4.330	-13.330	-13.330	-38.10**
25.	PCPGR-112 × PCPGR-149	3.670	-26.670	-26.670	-47.62**
26.	PCPGR-126 × PCPGR-138	10.000	71.43**	50.00**	42.86**
27.	PCPGR-126 × PCPGR-149	8.000	37.14*	20.000	14.290
28.	PCPGR-138 × PCPGR-149	5.000	0.000	0.000	-28.57*
Range	Minimum	3.000	-43.59	-54.17	-57.14
	Maximum	11.330	133.33	86.67	61.90

significant negative heterosis over standard checks out of 28 cross combinations. Top five cross combinations that showed desirable significant heterosis over standard check were PCPGR-59 × PCPGR-112 (-57.14%), PCPGR-51 × PCPGR-59(-52.38%), PCPGR-50 × PCPGR-112 (-47.62%), PCPGR-112 × PCPGR-149 (-47.62%), PCPGR-50 × PCPGR-149 (-42.86%), PCPGR-59 × PCPGR-83 (-42.86%) and PCPGR-83 × PCPGR-112 (-42.86%).

4.3.5 Days to first harvest

The estimates of relative heterosis, heterobeltiosis and standard heterosis for days to first harvest are presented in Table 4.8 revealed that heterosis over mid parent, better parent and over check parent for number of flowers per cluster ranged from -6.58 to 16.78 per cent, -8.94 to 13.69 cent and -4.63 to 13.44 per cent, respectively. For days to first harvest, out of all cross combinations, four hybrids showed significant relative heterosis, four crosses showed significant heterobeltiosis while other two hybrids exhibited significant standard heterosis.

Out of twenty eight cross combinations PCPGR-50 × PCPGR-59 (-6.58%) exhibited desirable significant negative relative heterosis for days to first harvest while, two cross combinations *viz.*, PCPGR-50 × PCPGR-59 (-8.94%) and PCPGR-59 × PCPGR-126 (-7.05%) showed desirable positive heterosis over better parent whereas, none of the cross combination observed significant negative heterosis in case of standard heterosis out of twenty eight cross combinations. Singh *et al.* (2010) and Singh *et al.* (2016) reported higher significant heterosis in desirable direction for days to first fruit harvest.

4.3.6 Days to last harvest

A perusal estimates of relative heterosis, heterobeltiosis and standard heterosis for days to last harvest presented in Table 4.9 revealed that heterosis over mid parent, better parent and over check parent for days to last harvest ranged from -5.00 to 20.68 per cent, -7.22 to 19.83 cent and -11.81 to 1.23 per cent, respectively. For days to last harvest, nineteen crosses showed significant relative heterosis, twelve hybrids showed significant heterobeltiosis and seventeen hybrids showed significant standard heterosis out of all cross combinations.

Table 4.8 Heterosis for days to first

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	61.870	-0.270	-2.420	2.200
2.	PCPGR-50 × PCPGR-59	57.730	-6.58*	-8.94**	-4.630
3.	PCPGR-50 × PCPGR-83	64.330	3.930	1.470	6.280
4.	PCPGR-50 × PCPGR-112	59.130	-5.180	-6.730	-2.310
5.	PCPGR-50 × PCPGR-126	62.400	-2.300	-3.010	3.080
6.	PCPGR-50 × PCPGR-138	61.200	1.490	-3.470	1.100
7.	PCPGR-50 × PCPGR-149	60.670	-2.780	-4.310	0.220
8.	PCPGR-51 × PCPGR-59	59.730	-1.160	-1.540	-1.320
9.	PCPGR-51 × PCPGR-83	61.600	1.760	1.540	1.760
10.	PCPGR-51 × PCPGR-112	58.400	-4.260	-4.780	-3.520
11.	PCPGR-51 × PCPGR-126	64.470	3.150	0.210	6.500
12.	PCPGR-51 × PCPGR-138	61.800	4.860	1.870	2.090
13.	PCPGR-51 × PCPGR-149	63.470	3.990	3.370	4.850
14.	PCPGR-59 × PCPGR-83	65.530	8.68**	8.50*	8.26*
15.	PCPGR-59 × PCPGR-112	59.730	-1.700	-2.610	-1.320
16.	PCPGR-59 × PCPGR-126	59.800	-3.960	-7.05*	-1.210
17.	PCPGR-59 × PCPGR-138	61.400	4.600	1.990	1.430
18.	PCPGR-59 × PCPGR-149	64.000	5.260	4.230	5.730
19.	PCPGR-83 × PCPGR-112	62.800	3.180	2.390	3.740
20.	PCPGR-83 × PCPGR-126	64.070	2.730	-0.410	5.840
21.	PCPGR-83 × PCPGR-138	68.670	16.78**	13.69**	13.44**
22.	PCPGR-83 × PCPGR-149	60.000	-1.480	-2.280	-0.880
23.	PCPGR-112 × PCPGR-126	61.730	-1.750	-4.040	1.980
24.	PCPGR-112 × PCPGR-138	59.470	0.340	-3.040	-1.760
25.	PCPGR-112 × PCPGR-149	59.270	-3.420	-3.470	-2.090
26.	PCPGR-126 × PCPGR-138	64.600	6.31*	0.410	6.720
27.	PCPGR-126 × PCPGR-149	63.070	0.320	-1.970	4.190
28.	PCPGR-138 × PCPGR-149	62.070	4.670	1.090	2.530
Range	Minimum	57.730	-6.58	-8.94	-4.630
	Maximum	68.670	16.78	13.69	13.44

Table 4.9: Heterosis for days to last harvest

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	106.930	3.890	0.440	-6.25**
2.	PCPGR-50 × PCPGR-59	107.800	-0.340	-1.880	-5.49*
3.	PCPGR-50 × PCPGR-83	104.730	3.730	-1.630	-8.18**
4.	PCPGR-50 × PCPGR-112	106.400	0.760	-0.060	-6.72**
5.	PCPGR-50 × PCPGR-126	106.330	2.870	-0.130	-6.78**
6.	PCPGR-50 × PCPGR-138	110.270	9.94**	3.570	-3.330
7.	PCPGR-50 × PCPGR-149	100.600	-4.58*	-5.51*	-11.81**
8.	PCPGR-51 × PCPGR-59	103.270	-1.310	-6.01*	-9.47**
9.	PCPGR-51 × PCPGR-83	107.000	9.82**	7.65**	-6.20**
10.	PCPGR-51 × PCPGR-112	101.670	-0.390	-2.930	-10.87**
11.	PCPGR-51 × PCPGR-126	105.000	5.18*	4.720	-7.95**
12.	PCPGR-51 × PCPGR-138	105.270	8.78**	5.90*	-7.71**
13.	PCPGR-51 × PCPGR-149	109.930	7.88**	5.30*	-3.620
14.	PCPGR-59 × PCPGR-83	109.670	6.82**	-0.180	-3.860
15.	PCPGR-59 × PCPGR-112	101.930	-5.00*	-7.22**	-10.64**
16.	PCPGR-59 × PCPGR-126	106.600	1.460	-2.970	-6.55**
17.	PCPGR-59 × PCPGR-138	110.530	8.37**	0.610	-3.100
18.	PCPGR-59 × PCPGR-149	113.400	5.85**	3.220	-0.580
19.	PCPGR-83 × PCPGR-112	113.270	13.15**	8.15**	-0.700
20.	PCPGR-83 × PCPGR-126	114.530	17.03**	14.23**	0.410
21.	PCPGR-83 × PCPGR-138	114.400	20.68**	19.83**	0.290
22.	PCPGR-83 × PCPGR-149	107.470	7.54**	2.940	-5.79*
23.	PCPGR-112 × PCPGR-126	112.400	9.66**	7.32**	-1.460
24.	PCPGR-112 × PCPGR-138	108.530	9.15**	3.630	-4.85*
25.	PCPGR-112 × PCPGR-149	115.470	10.42**	10.25**	1.230
26.	PCPGR-126 × PCPGR-138	104.400	7.41**	4.120	-8.47**
27.	PCPGR-126 × PCPGR-149	106.000	3.580	1.530	-7.07**
28.	PCPGR-138 × PCPGR-149	111.670	12.49**	6.96**	-2.100
Range	Minimum	100.600	-5.00	-7.22	-11.81
	Maximum	115.470	20.68	19.83	1.230

Out of twenty eight crosses, seventeen cross combinations showed desirable significant positive relative heterosis for days to last harvest among them top three were PCPGR-83 × PCPGR-138 (20.68%), PCPGR-83 × PCPGR-126 (17.03%), PCPGR-83 × PCPGR-112 (13.15%). In case of heterosis over better parent, nine cross combinations showed significant positive heterosis. Among them top five were PCPGR-83 × PCPGR-138 (19.83%), PCPGR-83 × PCPGR-126 (14.23%), PCPGR-112 × PCPGR-149 (10.25%), PCPGR-83 × PCPGR-112 (8.15%) and PCPGR-51 × PCPGR-83 (7.65%). In case of standard heterosis, none of the crosses have shown significant positive heterosis over standard checks out of twenty eight cross combinations. Singh *et al.* (2010) reported significant heterosis for days to last fruit harvest.

4.3.7 Inter nodal length (cm)

The estimates of relative heterosis, heterobeltiosis and standard heterosis for inter nodal length presented in Table 4.10. A perusal of data revealed that heterosis over mid parent, better parent and over check value ranged from -16.95 to 33.49 per cent, -25.38 to 22.49 and -18.49 to 14.42 per cent, respectively. Out of twenty eight crosses, five crosses exhibited significant relative heterosis, five hybrids showed significant heterobeltiosis and one hybrids showed significant standard heterosis for inter nodal length.

For relative heterosis, one cross combinations *viz.*, PCPGR-83 × PCPGR-149 (-16.95%), exhibited significant desirable negative relative heterosis. However, out of all crosses, three crosses *viz.*, PCPGR-83 × PCPGR-149 (-25.38%), PCPGR-51 × PCPGR-83 (-20.42%), and PCPGR-59 × PCPGR-138 (-15.99%) showed significant negative heterobeltiosis. For standard heterosis, only one cross combinations exhibited significant negative standard heterosis in desirable direction for this particular trait namely PCPGR-83 × PCPGR-149 (-15.99%). Hanchinamani and Patil (2009) reported significant heterosis for inter nodal length over better parent.

Table 4.10: Heterosis for internodal length (cm)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	10.21	-1	-8.29	-3.34
2.	PCPGR-50 × PCPGR-59	10.86	12.11	-2.45	2.81
3.	PCPGR-50 × PCPGR-83	10.24	-9.73	-11.32	-3.12
4.	PCPGR-50 × PCPGR-112	10.50	-0.03	-5.72	-0.63
5.	PCPGR-50 × PCPGR-126	11.38	7.31	2.21	7.73
6.	PCPGR-50 × PCPGR-138	11.78	2.52	-0.53	11.48
7.	PCPGR-50 × PCPGR-149	11.41	12.18	2.42	7.95
8.	PCPGR-51 × PCPGR-59	10.74	21.12*	13.13	1.67
9.	PCPGR-51 × PCPGR-83	9.19	-12.67	-20.42**	-13.06
10.	PCPGR-51 × PCPGR-112	9.00	-7.06	-8.81	-14.83
11.	PCPGR-51 × PCPGR-126	11.31	15.55	12.2	7.03
12.	PCPGR-51 × PCPGR-138	10.30	-3.5	-13.06	-2.56
13.	PCPGR-51 × PCPGR-149	10.63	13.71	11.93	0.6
14.	PCPGR-59 × PCPGR-83	11.27	13.88	-2.4	6.62
15.	PCPGR-59 × PCPGR-112	12.09	33.49**	22.49*	14.42
16.	PCPGR-59 × PCPGR-126	10.88	18.79*	7.97	3
17.	PCPGR-59 × PCPGR-138	9.95	-0.93	-15.99*	-5.84
18.	PCPGR-59 × PCPGR-149	11.08	27.04**	20.43*	4.86
19.	PCPGR-83 × PCPGR-112	11.23	4.92	-2.69	6.31
20.	PCPGR-83 × PCPGR-126	11.18	3.38	-3.18	5.77
21.	PCPGR-83 × PCPGR-138	10.34	-11.57	-12.69	-2.15
22.	PCPGR-83 × PCPGR-149	8.61	-16.95*	-25.38**	-18.49*
23.	PCPGR-112 × PCPGR-126	10.37	3.93	2.84	-1.89
24.	PCPGR-112 × PCPGR-138	12.02	10.72	1.49	13.75
25.	PCPGR-112 × PCPGR-149	11.00	15.4	11.48	4.13
26.	PCPGR-126 × PCPGR-138	10.17	-7.25	-14.16	-3.79
27.	PCPGR-126 × PCPGR-149	8.82	-8.54	-12.53	-16.56
28.	PCPGR-138 × PCPGR-149	10.13	-3.69	-14.44	-4.1
Range	Minimum	8.61	-16.95	-25.38	-18.49
	Maximum	12.09	33.49	22.49	14.42

4.3.8 Plant height (m)

The estimates of relative heterosis, heterobeltiosis and standard heterosis for plant height presented in Table 4.11. A perusal of data revealed that heterosis over mid parent, better parent and over check value ranged from -30.63 to 49.09 per cent, -32.03 to 37.96 and -33.33 to 5.71 per cent, respectively. Out of twenty eight crosses, twenty four crosses exhibited significant relative heterosis, twenty three hybrids showed significant heterobeltiosis and eight hybrids showed significant standard heterosis for plant height.

In case of relative heterosis, twenty cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-83 × PCPGR-138 (49.09%), PCPGR-51 × PCPGR-83 (40.51%), PCPGR-83 × PCPGR-149 (40.34%), PCPGR-50 × PCPGR-138 (33.10%) and PCPGR-59 × PCPGR-83 (33.09%). However, out of all crosses, eighteen crosses showed significant positive heterobeltiosis. Among them top five were PCPGR-83 × PCPGR-138 (37.96%), PCPGR-50 × PCPGR-149 (28.93%), PCPGR-50 × PCPGR-138 (23.69%), PCPGR-138 × PCPGR-149 (23.32%) and PCPGR-83 × PCPGR-149 (22.65%). For standard heterosis, none of the cross combinations have shown significant positive standard heterosis in desirable direction for this particular trait. Present findings are in conformity with the findings of Singh *et al.* (2010) and Mule *et al.* (2012). Lower *et al.* (1982) recorded significant heterosis for plant height over better parent.

4.3.9 Fruit length (cm)

A perusal of estimates of relative heterosis, heterobeltiosis and standard heterosis for fruit length are presented in Table 4.12. It is apparent from data that heterosis over mid parent, better parent and over check value ranged from -20.81 to 36.53 per cent, -26.91 to 24.67 and -30.30 to 15.36 per cent, respectively. Out of twenty eight crosses, eleven crosses exhibited significant relative heterosis, twelve hybrids showed significant heterobeltiosis and fourteen hybrids showed significant standard heterosis for fruit length.

Table 4.11: Heterosis for plant height (m)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	2.17	-20.02**	-24.65**	-31.11**
2.	PCPGR-50 × PCPGR-59	3.14	18.17**	13.34**	-0.21
3.	PCPGR-50 × PCPGR-83	2.15	-2.27	-15.45**	-31.64**
4.	PCPGR-50 × PCPGR-112	2.91	12.59**	11.08*	-7.72
5.	PCPGR-50 × PCPGR-126	3.06	16.18**	12.35**	-2.75
6.	PCPGR-50 × PCPGR-138	3.15	33.10**	23.69**	0
7.	PCPGR-50 × PCPGR-149	3.28	30.46**	28.93**	4.23
8.	PCPGR-51 × PCPGR-59	3.15	11.44**	9.37*	0
9.	PCPGR-51 × PCPGR-83	3.33	40.51**	15.62**	5.71
10.	PCPGR-51 × PCPGR-112	3.32	20.68**	15.16**	5.29
11.	PCPGR-51 × PCPGR-126	3.15	12.37**	9.37*	0
12.	PCPGR-51 × PCPGR-138	3.28	29.61**	14.00**	4.23
13.	PCPGR-51 × PCPGR-149	3.22	19.88**	11.69**	2.12
14.	PCPGR-59 × PCPGR-83	3.08	33.09**	11.18*	-2.12
15.	PCPGR-59 × PCPGR-112	3.13	16.26**	12.98**	-0.53
16.	PCPGR-59 × PCPGR-126	2.73	-0.61	-1.44	-13.23**
17.	PCPGR-59 × PCPGR-138	3.02	21.64**	8.77	-4.23
18.	PCPGR-59 × PCPGR-149	2.83	7.73	2.16	-10.05*
19.	PCPGR-83 × PCPGR-112	2.45	9.31	-6.5	-22.33**
20.	PCPGR-83 × PCPGR-126	2.97	29.36**	8.8	-5.82
21.	PCPGR-83 × PCPGR-138	3.02	49.09**	37.96**	-4.23
22.	PCPGR-83 × PCPGR-149	3.05	40.34**	22.65**	-3.17
23.	PCPGR-112 × PCPGR-126	1.85	-30.63**	-32.03**	-41.16**
24.	PCPGR-112 × PCPGR-138	3.17	31.85**	21.02**	0.53
25.	PCPGR-112 × PCPGR-149	2.97	16.26**	13.38**	-5.82
26.	PCPGR-126 × PCPGR-138	2.18	-11.13*	-19.93**	-30.69**
27.	PCPGR-126 × PCPGR-149	2.1	-19.44**	-22.98**	-33.33**
28.	PCPGR-138 × PCPGR-149	3.07	31.24**	23.32**	-2.65
Range	Minimum	1.85	-30.63	-32.03	-31.64
	Maximum	3.33	49.09	37.96	5.71

Table 4.12: Heterosis for fruit length (cm)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	17.24	-0.96	-10.97	-15.09*
2.	PCPGR-50 × PCPGR-59	19.75	7.28	2.03	-2.69
3.	PCPGR-50 × PCPGR-83	15.4	-20.49**	-20.53**	-24.12**
4.	PCPGR-50 × PCPGR-112	16.18	-9.26	-16.41*	-20.28**
5.	PCPGR-50 × PCPGR-126	19.57	7.66	1.07	-3.61
6.	PCPGR-50 × PCPGR-138	22.72	35.68**	17.34**	11.9
7.	PCPGR-50 × PCPGR-149	14.15	-20.81**	-26.91**	-30.30**
8.	PCPGR-51 × PCPGR-59	20.68	25.68**	18.42*	1.89
9.	PCPGR-51 × PCPGR-83	18.37	5.46	-5.25	-9.52
10.	PCPGR-51 × PCPGR-112	19.79	24.61**	21.32**	-2.53
11.	PCPGR-51 × PCPGR-126	15.5	-4.43	-8.77	-23.65**
12.	PCPGR-51 × PCPGR-138	23.42	58.45**	51.68**	15.36*
13.	PCPGR-51 × PCPGR-149	17.35	9.04	5.94	-14.53*
14.	PCPGR-59 × PCPGR-83	18.32	-0.55	-5.47	-9.74
15.	PCPGR-59 × PCPGR-112	17.87	5.81	2.31	-11.97
16.	PCPGR-59 × PCPGR-126	16.85	-2.2	-3.53	-17.00**
17.	PCPGR-59 × PCPGR-138	21.57	36.53**	23.47**	6.24
18.	PCPGR-59 × PCPGR-149	15.49	-8.46	-11.32	-23.69**
19.	PCPGR-83 × PCPGR-112	20.32	13.84*	4.82	0.08
20.	PCPGR-83 × PCPGR-126	17.23	-5.24	-11.09	-15.11*
21.	PCPGR-83 × PCPGR-138	16.26	-2.93	-16.10*	-19.89**
22.	PCPGR-83 × PCPGR-149	17.26	-3.47	-10.95	-14.98*
23.	PCPGR-112 × PCPGR-126	17.57	5.51	3.39	-13.46*
24.	PCPGR-112 × PCPGR-138	20.33	33.61**	24.67**	0.16
25.	PCPGR-112 × PCPGR-149	20.12	23.09**	22.84**	-0.9
26.	PCPGR-126 × PCPGR-138	18.33	17.81*	7.89	-9.7
27.	PCPGR-126 × PCPGR-149	16.9	1.3	-0.53	-16.75**
28.	PCPGR-138 × PCPGR-149	18.83	23.48**	15	-7.22
Range	Minimum	14.15	-20.81	-26.91	-30.30
	Maximum	23.42	36.53	24.67	11.90

For relative heterosis, ten cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-51 × PCPGR-138 (58.45%), PCPGR-59 × PCPGR-138 (36.53%), PCPGR-50 × PCPGR-138 (35.68%), PCPGR-112 × PCPGR-138 (33.61%) and PCPGR-51 × PCPGR-59 (25.68%), However, out of all crosses, seven crosses, PCPGR-51 × PCPGR-138 (51.68%), PCPGR-112 × PCPGR-138 (24.67%), PCPGR-59 × PCPGR-138 (23.47%) PCPGR-112 × PCPGR-149 (22.84%), PCPGR-51 × PCPGR-112 (21.32%), PCPGR-51 × PCPGR-59 (18.42%) and PCPGR-50 × PCPGR-138 (17.34%), showed significant positive heterobeltiosis. In case of standard heterosis, one cross combinations exhibited significant positive standard heterosis in desirable direction for this particular trait namely PCPGR-51 × PCPGR-138 (15.36%). Significant heterosis for fruit length had also been reported by Singh *et al.* (2010), Airina *et al.* (2013) and Munshi *et al.* (2005).

4.3.10 Average fruit diameter (cm)

The estimates of relative heterosis, heterobeltiosis and standard heterosis for average fruit diameter presented in Table 4.13. It is clear from data that heterosis over mid parent, better parent and over check value ranged from 1.12 to 49.31 per cent, -3.64 to 46.73 and -8.76 to 18.74 per cent, respectively. Out of twenty eight crosses, twenty crosses exhibited significant relative heterosis, nine hybrids showed significant heterobeltiosis and three hybrids showed significant standard heterosis for average fruit diameter.

In case of relative heterosis, twenty cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-50 × PCPGR-83 (49.31%), PCPGR-50 × PCPGR-138 (46.18%), PCPGR-83 × PCPGR-149 (38.17%), PCPGR-50 × PCPGR-126 (34.85%) and PCPGR-112 × PCPGR-149 (26.64%), However, nine crosses showed significant positive heterobeltiosis, among them top five were PCPGR-50 × PCPGR-83 (46.73%), PCPGR-50 × PCPGR-138 (38.64%) PCPGR-83 × PCPGR-149 (36.42%), PCPGR-50 × PCPGR-126 (24.41%) and PCPGR-50 × PCPGR-149 (22.62%) showed significant positive heterobeltiosis. For standard heterosis, three cross combinations namely PCPGR-50 × PCPGR-138 (18.74%), PCPGR-112 × PCPGR-138 (15.58%), PCPGR-51 × PCPGR-138 (14.79%) exhibited significant positive standard heterosis in desirable direction for this particular trait. Singh *et al.* (2010) and Airina *et al.* (2013) also observed significant heterosis for fruit diameter.

Table 4.13: Heterosis for average fruit diameter (cm)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%) (20)	Heterobeltiosis (%) (9)	Standard heterosis (%) (3)
1.	PCPGR-50 × PCPGR-51	4.71	17.18*	5.37	1.36
2.	PCPGR-50 × PCPGR-59	4.33	11.02	2.2	-6.68
3.	PCPGR-50 × PCPGR-83	5.23	49.31**	46.73**	12.71
4.	PCPGR-50 × PCPGR-112	4.73	13.65*	-0.63	1.94
5.	PCPGR-50 × PCPGR-126	5.25	34.85**	24.41**	13.07
6.	PCPGR-50 × PCPGR-138	5.51	46.18**	38.64**	18.74**
7.	PCPGR-50 × PCPGR-149	4.37	23.19**	22.62*	-5.81
8.	PCPGR-51 × PCPGR-59	5.21	19.60**	16.57*	12.13
9.	PCPGR-51 × PCPGR-83	4.87	23.05**	8.96	4.81
10.	PCPGR-51 × PCPGR-112	4.67	1.12	-2.03	0.50
11.	PCPGR-51 × PCPGR-126	4.73	8.83	5.82	1.79
12.	PCPGR-51 × PCPGR-138	5.33	26.25**	19.33**	14.79*
13.	PCPGR-51 × PCPGR-149	4.93	23.33**	10.45	6.25
14.	PCPGR-59 × PCPGR-83	4.72	22.95**	11.4	1.72
15.	PCPGR-59 × PCPGR-112	4.96	10.18	4.13	6.82
16.	PCPGR-59 × PCPGR-126	5.19	22.77**	22.48**	11.84
17.	PCPGR-59 × PCPGR-138	4.43	7.83	4.48	-4.59
18.	PCPGR-59 × PCPGR-149	4.69	20.58**	10.53	0.93
19.	PCPGR-83 × PCPGR-112	4.63	12.84	-2.8	-0.29
20.	PCPGR-83 × PCPGR-126	4.57	19.36**	8.37	-1.51
21.	PCPGR-83 × PCPGR-138	4.33	16.71*	8.89	-6.75
22.	PCPGR-83 × PCPGR-149	4.82	38.17**	36.42**	3.80
23.	PCPGR-112 × PCPGR-126	4.59	2.19	-3.64	-1.15
24.	PCPGR-112 × PCPGR-138	5.37	22.81**	12.67	15.58*
25.	PCPGR-112 × PCPGR-149	5.25	26.64**	10.29	13.14
26.	PCPGR-126 × PCPGR-138	5.02	22.57**	19.04*	8.18
27.	PCPGR-126 × PCPGR-149	4.52	16.51*	7.03	-2.73
28.	PCPGR-138 × PCPGR-149	4.24	12.83	6.54	-8.76
Range	Minimum	4.24	1.12	-3.64	-8.76
	Maximum	5.51	49.31	46.73	18.74s

4.3.11 Number of fruit per plant

The estimates of relative heterosis, heterobeltiosis and standard heterosis for number of fruit per plant presented in Table 4.14. A perusal of data revealed that heterosis over mid parent, better parent and over check value ranged from -44.31 to 49.18 per cent, -47.09 to 41.09 and -50.00 to 46.77 per cent, respectively. Out of twenty eight crosses, twenty crosses exhibited significant relative heterosis, twenty one hybrids showed significant heterobeltiosis and twenty two hybrids showed significant standard heterosis for number of fruit per plant.

In case of relative heterosis, nine cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-138 × PCPGR-149 (49.18%), PCPGR-59 × PCPGR-138 (35.06%), PCPGR-50 × PCPGR-112 (24.71%), PCPGR-83 × PCPGR-112 (24.26%) and PCPGR-51 × PCPGR-138 (22.31%), However, out of all crosses, seven crosses, PCPGR-138 × PCPGR-149 (41.09%), PCPGR-59 × PCPGR-138 (31.01%) PCPGR-83 × PCPGR-112 (23.39%), PCPGR-51 × PCPGR-138 (21.37%) and PCPGR-50 × PCPGR-112 (19.97%) showed significant positive heterobeltiosis. On the other hand for standard heterosis, nine cross combinations exhibited significant positive standard heterosis over check in desirable direction for this particular trait. Among them top five were PCPGR-138 × PCPGR-149 (46.77%), PCPGR-59 × PCPGR-138 (36.29%), PCPGR-50 × PCPGR-112 (29.84%), PCPGR-51 × PCPGR-138 (28.23%) and PCPGR-83 × PCPGR-112 (23.39%). Significant heterosis over better parent and check for number of fruits per plant was also reported by Om *et al.* (1978), Pandey *et al.* (2005), Hanchinamani and Patil (2009) and Airina *et al.* (2013).

4.3.12 Average fruit weight (g)

A perusal of estimates of relative heterosis, heterobeltiosis and standard heterosis for average fruit weight presented in Table 4.15. It is apparent from data that heterosis over mid parent, better parent and over check value ranged from -13.04 to 47.41 per cent, -14.56 to 46.10 and -19.45 to 26.27 per cent, respectively. Out of twenty eight crosses, twenty four crosses exhibited significant relative heterosis, fifteen hybrids showed significant heterobeltiosis and twenty one hybrids showed significant standard heterosis for average fruit weight.

Table 4.14: Heterosis for number of fruits per plant

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	7.07	-20.06**	-21.01**	-14.52**
2.	PCPGR-50 × PCPGR-59	9.8	15.09**	9.54	18.55**
3.	PCPGR-50 × PCPGR-83	6.47	-24.35**	-27.72**	-21.77**
4.	PCPGR-50 × PCPGR-112	10.73	24.71**	19.97**	29.84**
5.	PCPGR-50 × PCPGR-126	5.53	-26.61**	-38.15**	-33.06**
6.	PCPGR-50 × PCPGR-138	8.8	0.3	-1.64	6.45
7.	PCPGR-50 × PCPGR-149	4.73	-43.02**	-47.09**	-42.74**
8.	PCPGR-51 × PCPGR-59	9.8	16.55**	12.21*	18.55**
9.	PCPGR-51 × PCPGR-83	7.97	-5.63	-8.78	-3.63
10.	PCPGR-51 × PCPGR-112	9.53	12.16**	9.16	15.32**
11.	PCPGR-51 × PCPGR-126	5.27	-29.15**	-39.69**	-36.29**
12.	PCPGR-51 × PCPGR-138	10.6	22.31**	21.37**	28.23**
13.	PCPGR-51 × PCPGR-149	7.73	-5.69	-11.45*	-6.45
14.	PCPGR-59 × PCPGR-83	5.27	-35.11**	-35.38**	-36.29**
15.	PCPGR-59 × PCPGR-112	8.73	6.83	5.65	5.65
16.	PCPGR-59 × PCPGR-126	6.53	-8.09	-19.18**	-20.97**
17.	PCPGR-59 × PCPGR-138	11.27	35.06**	31.01**	36.29**
18.	PCPGR-59 × PCPGR-149	4.4	-44.13**	-45.57**	-46.77**
19.	PCPGR-83 × PCPGR-112	10.2	24.26**	23.39**	23.39**
20.	PCPGR-83 × PCPGR-126	7.2	0.82	-11.66*	-12.90*
21.	PCPGR-83 × PCPGR-138	6.13	-26.77**	-28.68**	-25.81**
22.	PCPGR-83 × PCPGR-149	7.67	-3.06	-5.93	-7.26
23.	PCPGR-112 × PCPGR-126	6.4	-11.11*	-22.58**	-22.58**
24.	PCPGR-112 × PCPGR-138	7.93	-5.93	-7.75	-4.03
25.	PCPGR-112 × PCPGR-149	9.33	17.15**	12.90*	12.90*
26.	PCPGR-126 × PCPGR-138	6.33	-14.03**	-26.36**	-23.39**
27.	PCPGR-126 × PCPGR-149	4.13	-40.10**	-46.09**	-50.00**
28.	PCPGR-138 × PCPGR-149	12.13	49.18**	41.09**	46.77**
Range	Minimum	4.13	-44.13	-47.09	-50.00
	Maximum	12.13	49.18	41.09	46.77

Table 4.15: Heterosis for average fruit weight (g)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	188.210	5.17*	-1.360	-15.40**
2.	PCPGR-50 × PCPGR-59	265.290	32.46**	26.48**	19.25**
3.	PCPGR-50 × PCPGR-83	218.630	8.76**	3.490	-1.730
4.	PCPGR-50 × PCPGR-112	222.560	16.20**	15.75**	0.040
5.	PCPGR-50 × PCPGR-126	240.240	29.08**	25.91**	7.99**
6.	PCPGR-50 × PCPGR-138	255.940	34.83**	34.14**	15.05**
7.	PCPGR-50 × PCPGR-149	216.660	10.20**	7.03**	-2.610
8.	PCPGR-51 × PCPGR-59	231.910	23.07**	10.56**	4.240
9.	PCPGR-51 × PCPGR-83	183.730	-2.880	-13.03**	-17.41**
10.	PCPGR-51 × PCPGR-112	242.760	35.10**	26.26**	9.12**
11.	PCPGR-51 × PCPGR-126	193.820	11.22**	6.83*	-12.88**
12.	PCPGR-51 × PCPGR-138	242.100	36.03**	28.20**	8.83**
13.	PCPGR-51 × PCPGR-149	194.610	5.33*	-3.860	-12.52**
14.	PCPGR-59 × PCPGR-83	220.500	4.75*	4.380	-0.880
15.	PCPGR-59 × PCPGR-112	278.890	38.74**	32.96**	25.36**
16.	PCPGR-59 × PCPGR-126	182.650	-6.61**	-12.92**	-17.90**
17.	PCPGR-59 × PCPGR-138	217.870	9.32**	3.870	-2.070
18.	PCPGR-59 × PCPGR-149	179.200	-13.04**	-14.56**	-19.45**
19.	PCPGR-83 × PCPGR-112	241.030	19.46**	14.10**	8.34**
20.	PCPGR-83 × PCPGR-126	212.560	8.26**	0.620	-4.450
21.	PCPGR-83 × PCPGR-138	186.550	-6.75**	-11.69**	-16.14**
22.	PCPGR-83 × PCPGR-149	208.060	0.590	-1.510	-6.48**
23.	PCPGR-112 × PCPGR-126	239.940	28.41**	24.79**	7.85**
24.	PCPGR-112 × PCPGR-138	280.910	47.41**	46.10**	26.27**
25.	PCPGR-112 × PCPGR-149	252.400	27.90**	24.69**	13.45**
26.	PCPGR-126 × PCPGR-138	184.470	-0.360	-2.310	-17.08**
27.	PCPGR-126 × PCPGR-149	238.410	24.22**	17.78**	7.17**
28.	PCPGR-138 × PCPGR-149	204.250	4.410	0.910	-8.19**
Range	Minimum	179.200	-13.04	-14.56	-19.45
	Maximum	278.890	47.41	46.10	26.27

For relative heterosis, twenty two cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-112 × PCPGR-138 (47.41%), PCPGR-59 × PCPGR-112 (38.74%), PCPGR-51 × PCPGR-138 (36.03%), PCPGR-51 × PCPGR-112 (35.10%) and PCPGR-50 × PCPGR-138 (34.83%), However, out of all crosses, fifteen crosses, showed significant positive heterobeltiosis, among them top five were PCPGR-112 × PCPGR-138 (46.10%), PCPGR-50 × PCPGR-138 (34.14%), PCPGR-59 × PCPGR-112 (32.96%), PCPGR-51 × PCPGR-138 (28.20%) and PCPGR-50 × PCPGR-59 (26.48%). In case of standard heterosis, ten cross combinations exhibited significant positive standard heterosis over check in desirable direction for this particular trait, among them top five were PCPGR-112 × PCPGR-138 (26.27%), PCPGR-59 × PCPGR-112 (25.36%), PCPGR-50 × PCPGR-59 (19.25%), PCPGR-50 × PCPGR-138 (15.05%) and PCPGR-112 × PCPGR-149 (13.45%). Bairagi *et al.* (2005) also found superior hybrids showing heterosis over better parent and check for fruit weight. Similar findings were also reported by Dogra and Kanwar (2011) and Singh *et al.* (2016).

4.3.13 Fruit yield per plant (kg)

The estimates of relative heterosis, heterobeltiosis and standard heterosis for fruit yield per plant are presented in Table 4.16. A critical examination of data revealed that heterosis over mid parent, better parent and over check value ranged from -51.49 to 66.45 per cent, -53.54 to 58.23 and -57.25 to 41.12 per cent, respectively. Out of twenty eight crosses, twenty five crosses exhibited significant relative heterosis, twenty six hybrids showed significant heterobeltiosis and all hybrids showed significant standard heterosis for fruit yield per plant.

In case of relative heterosis, fourteen cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-51 × PCPGR-138 (66.45%), PCPGR-138 × PCPGR-149 (56.26%), PCPGR-50 × PCPGR-59 (52.75%), PCPGR-51 × PCPGR-112 (51.69%) and PCPGR-112 × PCPGR-149 (49.68%), However, out of all crosses, twelve crosses, showed significant positive heterobeltiosis, including top five *viz.*, PCPGR-51 × PCPGR-138 (58.23%), PCPGR-138 × PCPGR-149 (52.88%), PCPGR-50 × PCPGR-59 (52.15%), PCPGR-112 × PCPGR-149 (47.80%) and PCPGR-51 × PCPGR-112 (45.49%).

Table 4.16: Heterosis for fruit yield per plant (kg)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	1.33	-16.00**	-22.07**	-27.72**
2.	PCPGR-50 × PCPGR-59	2.6	52.75**	52.15**	41.12**
3.	PCPGR-50 × PCPGR-83	1.41	-17.51**	-17.83**	-23.19**
4.	PCPGR-50 × PCPGR-112	2.38	44.59**	39.65**	29.53**
5.	PCPGR-50 × PCPGR-126	1.33	-5.91	-22.27**	-27.90**
6.	PCPGR-50 × PCPGR-138	2.25	35.47**	32.03**	22.46**
7.	PCPGR-50 × PCPGR-149	1.02	-37.15**	-40.04**	-44.38**
8.	PCPGR-51 × PCPGR-59	2.27	44.19**	34.25**	23.55**
9.	PCPGR-51 × PCPGR-83	1.46	-7.97*	-14.92**	-20.47**
10.	PCPGR-51 × PCPGR-112	2.31	51.69**	45.49**	25.72**
11.	PCPGR-51 × PCPGR-126	1.02	-20.98**	-30.37**	-44.75**
12.	PCPGR-51 × PCPGR-138	2.56	66.45**	58.23**	39.31**
13.	PCPGR-51 × PCPGR-149	1.51	0.11	-2.8	-18.12**
14.	PCPGR-59 × PCPGR-83	1.16	-32.03**	-32.56**	-36.96**
15.	PCPGR-59 × PCPGR-112	2.43	48.02**	43.50**	32.07**
16.	PCPGR-59 × PCPGR-126	1.19	-15.20**	-29.72**	-35.33**
17.	PCPGR-59 × PCPGR-138	2.46	48.29**	45.08**	33.51**
18.	PCPGR-59 × PCPGR-149	0.79	-51.49**	-53.54**	-57.25**
19.	PCPGR-83 × PCPGR-112	2.46	48.44**	42.83**	33.51**
20.	PCPGR-83 × PCPGR-126	1.53	8.00*	-11.05**	-16.85**
21.	PCPGR-83 × PCPGR-138	1.14	-31.74**	-33.72**	-38.04**
22.	PCPGR-83 × PCPGR-149	1.59	-2.55	-7.36*	-13.41**
23.	PCPGR-112 × PCPGR-126	1.53	13.44**	-3.56	-16.67**
24.	PCPGR-112 × PCPGR-138	2.23	38.73**	37.45**	21.01**
25.	PCPGR-112 × PCPGR-149	2.35	49.68**	47.80**	27.72**
26.	PCPGR-126 × PCPGR-138	1.16	-14.88**	-28.19**	-36.78**
27.	PCPGR-126 × PCPGR-149	0.99	-25.91**	-36.34**	-46.38**
28.	PCPGR-138 × PCPGR-149	2.48	56.26**	52.88**	34.60**
Range	Minimum	0.79	-51.49	-53.54	-57.25
	Maximum	2.56	66.45	58.23	41.12

For standard heterosis, twelve cross combinations exhibited significant positive standard heterosis over check in desirable direction for this particular trait including top five *viz.*, PCPGR-50 × PCPGR-59 (41.12%), PCPGR-51 × PCPGR-138 (39.31%), PCPGR-138 × PCPGR-149 (34.60%), PCPGR-83 × PCPGR-112 (33.51%) and PCPGR-59 × PCPGR-138 (33.51%). Significant heterosis for yield per plant had also been reported by Bairagi *et al.* (2005), Dogra and Kanwar (2011), Samant (2014), Singh *et al.* (2014) and Singh *et al.* (2016).

4.3.14 Fruit yield (q/ha)

The estimates of relative heterosis, heterobeltiosis and standard heterosis for fruit yield are presented in Table 4.17. A perusal of data revealed that heterosis over mid parent, better parent and over check value ranged from -51.67 to 66.35 per cent, -53.72 to 57.94 and -57.29 to 41.45 per cent, respectively. Out of twenty eight crosses, twenty five crosses exhibited significant relative heterosis, twenty six hybrids showed significant heterobeltiosis and all hybrids showed significant standard heterosis for fruit yield.

For relative heterosis, fourteen cross combinations exhibited significant desirable positive relative heterosis. Among them top five were PCPGR-51 × PCPGR-138 (66.35%), PCPGR-138 × PCPGR-149 (56.10%), PCPGR-50 × PCPGR-59 (52.80%), PCPGR-51 × PCPGR-112 (51.81%) and PCPGR-112 × PCPGR-149 (49.87%), However, out of all crosses, twelve crosses showed significant positive heterobeltiosis including top five *viz.*, PCPGR-51 × PCPGR-138 (57.94%), PCPGR-138 × PCPGR-149 (52.70%), PCPGR-50 × PCPGR-59 (52.31%), PCPGR-112 × PCPGR-149 (48.17%) and PCPGR-51 × PCPGR-112 (45.62%). For standard heterosis, twelve cross combinations exhibited significant positive standard heterosis over check in desirable direction for this particular trait including top five *viz.*, PCPGR-50 × PCPGR-59 (41.45%), PCPGR-51 × PCPGR-138 (39.45%), PCPGR-138 × PCPGR-149 (34.83%), PCPGR-83 × PCPGR-112 (33.76%) and PCPGR-59 × PCPGR-138 (33.59%). Hormuzdi and Moore (1990), Vijayakumari *et al.* (1991), Singh *et al.* (1999), Bairagi *et al.* (2002), Kumbhar *et al.* (2005), Yadav *et al.* (2009), Mule *et al.* (2012) and Kaur and Dhall (2017) also reported promising heterosis for fruit yield and yield contributing traits in cucumber.

Table 4.17: Heterosis for fruit yield (q/ha)

S.N	F ₁ hybrid	<i>Per se</i> performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	PCPGR-50 × PCPGR-51	177.28	-15.95**	-22.07**	-27.62**
2.	PCPGR-50 × PCPGR-59	346.46	52.80**	52.31**	41.45**
3.	PCPGR-50 × PCPGR-83	188.22	-17.61**	-17.96**	-23.15**
4.	PCPGR-50 × PCPGR-112	318.27	44.96**	39.92**	29.94**
5.	PCPGR-50 × PCPGR-126	176.62	-6.0	-22.35**	-27.89**
6.	PCPGR-50 × PCPGR-138	300.16	35.29**	31.96**	22.55**
7.	PCPGR-50 × PCPGR-149	136.4	-37.19**	-40.04**	-44.31**
8.	PCPGR-51 × PCPGR-59	302.76	44.03**	33.96**	23.61**
9.	PCPGR-51 × PCPGR-83	195.06	-7.95*	-14.98**	-20.36**
10.	PCPGR-51 × PCPGR-112	308.21	51.81**	45.62**	25.84**
11.	PCPGR-51 × PCPGR-126	135.92	-20.68**	-30.08**	-44.51**
12.	PCPGR-51 × PCPGR-138	341.56	66.35**	57.94**	39.45**
13.	PCPGR-51 × PCPGR-149	200.48	-0.07	-3.08	-18.15**
14.	PCPGR-59 × PCPGR-83	154.67	-32.08**	-32.58**	-36.85**
15.	PCPGR-59 × PCPGR-112	324.29	48.19**	43.48**	32.40**
16.	PCPGR-59 × PCPGR-126	158.71	-15.20**	-29.78**	-35.20**
17.	PCPGR-59 × PCPGR-138	327.2	47.96**	44.77**	33.59**
18.	PCPGR-59 × PCPGR-149	104.6	-51.67**	-53.72**	-57.29**
19.	PCPGR-83 × PCPGR-112	327.63	48.56**	42.81**	33.76**
20.	PCPGR-83 × PCPGR-126	203.79	7.90*	-11.17**	-16.80**
21.	PCPGR-83 × PCPGR-138	152.48	-31.58**	-33.54**	-37.75**
22.	PCPGR-83 × PCPGR-149	212.48	-2.59	-7.39*	-13.25**
23.	PCPGR-112 × PCPGR-126	204.71	13.74**	-3.28	-16.42**
24.	PCPGR-112 × PCPGR-138	296.85	38.74**	37.26**	21.20**
25.	PCPGR-112 × PCPGR-149	313.6	49.87**	48.17**	28.04**
26.	PCPGR-126 × PCPGR-138	155.37	-14.77**	-28.16**	-36.56**
27.	PCPGR-126 × PCPGR-149	131.2	-26.12**	-36.57**	-46.43**
28.	PCPGR-138 × PCPGR-149	330.24	56.10**	52.70**	34.83**
Range	Minimum	104.6	-51.67	-53.72	-57.29
	Maximum	346.46	66.35	57.94	41.45

For yield related traits most promising heterotic crosses with respect to each character in desired direction are presented in Table 4.18 based on the significance test of relative heterosis, heterobeltiosis and standard heterosis as well as the *per se* performance of the cross combinations, the most promising heterotic hybrids are identified and depicted in tabular form with respect to each character.

For days to first male flower, cross PCPGR-112 × PCPGR-138 showed desirable significant negative heterosis over mid parent, better parent and standard check while, PCPGR-112 × PCPGR-126 showed desirable significant negative heterosis over mid parent and better parent. In case of node number to first male flower PCPGR-59 × PCPGR-138 exhibited desirable significant negative heterosis over mid parent and better parent, PCPGR-50 × PCPGR-138 showed desirable significant negative heterosis over better parent and standard parent for node number to first male flower. For days to first female flower cross PCPGR-50 × PCPGR-59 exhibited desirable significant negative heterosis over all three cases. For node number to first female flower cross PCPGR-50 × PCPGR-112 showed desirable significant negative heterosis over mid parent, better parent and standard check while, PCPGR-50 × PCPGR-149 showed desirable negative heterosis over mid parent and better parent, PCPGR-51 × PCPGR-59 exhibited desirable significant negative heterosis over better parent and standard check. For days to first fruit harvest PCPGR-50 × PCPGR-59 exhibited desirable significant negative relative heterosis and heterobeltiosis. For days to last harvest PCPGR-83 × PCPGR-138 and PCPGR-83 × PCPGR-126 exhibited desirable significant positive heterosis over mid parent and better parent. PCPGR-83 × PCPGR-149 exhibited desirable significant negative heterosis over mid parent, better parent and standard check for intermodal length. PCPGR-83 × PCPGR-138 showed desirable significant positive heterosis over mid parent, and better parent for plant height. For fruit length PCPGR-59 × PCPGR-138 and PCPGR-112 × PCPGR-138 showed desirable significant positive relative heterosis and heterobeltiosis. PCPGR-50 × PCPGR-138 showed desirable significant positive heterosis over mid parent, better parent and standard parent while, PCPGR-50 × PCPGR-83 and PCPGR-83 × PCPGR-149 revealed significant positive heterosis over mid parent and better parent for average fruit diameter. For number of fruits per plant PCPGR-138 × PCPGR-149 and PCPGR-59 × PCPGR-138 exhibited desirable significant positive heterosis over

Table 4.18: Summary table showing top three promising heterotic crosses with respect to each yield and its contributing traits in desired direction

S.N.	Characters	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1.	Days to first male flower	PCPGR-112 × PCPGR-126 PCPGR-112 × PCPGR-138	PCPGR-112 × PCPGR-126 PCPGR-126 × PCPGR-138 PCPGR-112 × PCPGR-138	PCPGR-138 × PCPGR-149 PCPGR-112 × PCPGR-138 PCPGR-51 × PCPGR-138
2.	Node number to first male flower	PCPGR-51 × PCPGR-112 PCPGR-51 × PCPGR-138 PCPGR-59 × PCPGR-138	PCPGR-50 × PCPGR-138 PCPGR-59 × PCPGR-138 PCPGR-51 × PCPGR-59	PCPGR-112 × PCPGR-126 PCPGR-50 × PCPGR-59 PCPGR-50 × PCPGR-138
3.	Days to first female flower	PCPGR-50 × PCPGR-59	PCPGR-50 × PCPGR-59	PCPGR-50 × PCPGR-59
4.	Node number to first female flower	PCPGR-50 × PCPGR-112 PCPGR-50 × PCPGR-149 PCPGR-50 × PCPGR-51	PCPGR-50 × PCPGR-112 PCPGR-51 × PCPGR-59 PCPGR-50 × PCPGR-149	PCPGR-59 × PCPGR-112 PCPGR-51 × PCPGR-59 PCPGR-50 × PCPGR-112
5.	Days to first harvest	PCPGR-50 × PCPGR-59	PCPGR-50 × PCPGR-59 PCPGR-50 × PCPGR-126	-
6.	Days to last harvest	PCPGR-83 × PCPGR-138 PCPGR-83 × PCPGR-126 PCPGR-83 × PCPGR-112	PCPGR-83 × PCPGR-138 PCPGR-83 × PCPGR-126 PCPGR-112 × PCPGR-149	-
7.	Inter nodal length (cm)	PCPGR-83 × PCPGR-149	PCPGR-83 × PCPGR-149 PCPGR-51 × PCPGR-83 PCPGR-59 × PCPGR-138	PCPGR-83 × PCPGR-149
8.	Plant height (m)	PCPGR-83 × PCPGR-138 PCPGR-51 × PCPGR-83 PCPGR-83 × PCPGR-149	PCPGR-83 × PCPGR-138 PCPGR-50 × PCPGR-149 PCPGR-50 × PCPGR-138	-
9.	Fruit length (cm)	PCPGR-59 × PCPGR-138 PCPGR-50 × PCPGR-138 PCPGR-112 × PCPGR-138	PCPGR-112 × PCPGR-138 PCPGR-59 × PCPGR-138 PCPGR-112 × PCPGR-149	PCPGR-51 × PCPGR-138
10.	Average fruit diameter (cm)	PCPGR-50 × PCPGR-83 PCPGR-50 × PCPGR-138 PCPGR-83 × PCPGR-149	PCPGR-50 × PCPGR-83 PCPGR-50 × PCPGR-138 PCPGR-83 × PCPGR-149	PCPGR-50 × PCPGR-138 PCPGR-112 × PCPGR-138 PCPGR-51 × PCPGR-138
11.	Number of fruits per plant	PCPGR-138 × PCPGR-149 PCPGR-59 × PCPGR-138 PCPGR-50 × PCPGR-112	PCPGR-138 × PCPGR-149 PCPGR-59 × PCPGR-138 PCPGR-83 × PCPGR-112	PCPGR-138 × PCPGR-149 PCPGR-59 × PCPGR-138 PCPGR-50 × PCPGR-112
12.	Average fruit weight (g)	PCPGR-112 × PCPGR-138 PCPGR-59 × PCPGR-112 PCPGR-51 × PCPGR-138	PCPGR-112 × PCPGR-138 PCPGR-50 × PCPGR-138 PCPGR-59 × PCPGR-112	PCPGR-112 × PCPGR-138 PCPGR-59 × PCPGR-112 PCPGR-50 × PCPGR-59
13.	Fruit yield per plant (kg)	PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149 PCPGR-50 × PCPGR-59	PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149 PCPGR-50 × PCPGR-59	PCPGR-50 × PCPGR-59 PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149
14.	Fruit yield (q/ha)	PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149 PCPGR-50 × PCPGR-59	PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149 PCPGR-50 × PCPGR-59	PCPGR-50 × PCPGR-59 PCPGR-51 × PCPGR-138 PCPGR-138 × PCPGR-149

mid parent, better parent and standard check while, PCPGR-50 × PCPGR-112 showed desirable significant positive heterosis over mid parent and standard check. For average fruit weight PCPGR-112 × PCPGR-138 and PCPGR-59 × PCPGR-112 showed desirable significant positive heterosis over mid parent, better parent and standard check. For fruit yield per plant and fruit yield per hectare cross PCPGR-51 × PCPGR-138, PCPGR-138 × PCPGR-149 and PCPGR-50 × PCPGR-59 exhibited desirable significant positive heterosis over mid parent, better parent and standard check.

4.4. Combining ability analysis

The concept of combining ability as a measure of gene action was given by Sprague and Tatum (1942). The parents differ in their general combining ability and use of good general combining parents in hybridization is expected to give useful transgressive segregants in segregating generations. In the same way, superior cross combinations can be discriminated with the help of their specific combining ability (SCA) effects. Thus, information regarding the combining ability of the parents for various yield and yield contributing traits is necessary for devising an effective and efficient breeding methodology. Selection of suitable parents is the most crucial aspect of any crop breeding programme. Information on the relative importance of general combining ability (GCA) and specific combining ability (SCA) is of immense value in breeding programme for species, which are amenable to the development of F_i hybrid cultivars. In vegetable crops for breeding of high-yielding varieties breeder faces problem in selection of parental lines and F_1 crosses. The selection of suitable parental lines and cross combinations is essential for genetic improvement of cucumber. For the development of superior hybrids, estimates of GCA of parents and SCA of the crosses help in proper selection of parents for hybridization programme. Therefore, the objective is to estimate the GCA and SCA of yield and its contributing characters in parental lines and hybrids derived from diallel crosses. Basic information on combining ability in cucumber would help in developing improved cultivars. The common approach and choosing the parents on the basis of performance, adaptation and genetic variability does not necessarily lead to useful results because the differential ability of the parent. This ability of the parent depends upon the complex interaction among the genes and hence cannot be judged by *per se* performance alone (Allard, 1960).

Therefore, it is important to assess the general and specific combining ability effects in the selection of the parents and the formulation of an appropriate crossing plan. Among the various breeding methods diallel mating design (method 2) excluding reciprocals (Griffing, 1956) has been used in the present study to evaluate 8 parents and their 28 crosses with standard check. The result are presented and discussed as follows:

4.4.1 Analysis of variance for combining ability

Analysis of variance for combining ability with respect to different yield related traits presented in Table 4.19. The total variability among F₁ hybrids was further partitions into different component and there significant was tasted. It is evident from the data presented in table that mean some of squares due to parent and crosses was significant for all fourteen yield related traits studied.

Table 4.19: Analysis of variance for combining ability in cucumber genotypes for yield and its contributing traits

S. N.	Characters	df	Mean sum of squares		
			GCA	SCA	Error
			7	28	70
1	Days to first male flower		17.396***	4.987***	0.784
2	Node number to first male flower		5.752***	5.621***	0.360
3	Days to first female flower		14.117***	6.037 **	2.415
4	Node number to first female flower		8.101***	4.081***	0.459
5	Days to first harvest		7.777 **	5.165 **	2.216
6	Days to last harvest		14.292***	28.732***	3.408
7	Inter nodal length (cm)		1.038 *	0.957 **	0.386
8	Plant height (m)		0.170***	0.191***	0.007
9	Fruit length (cm)		2.265 **	4.662***	0.767
10	Average fruit diameter (cm)		0.194 **	0.275***	0.049
11	Number of fruits per plant		7.479***	3.053***	0.089
12	Average fruit weight (g)		1064.002***	826.841***	13.337
13	Fruit yield per plant (kg)		0.585***	0.225***	0.002
14	Fruit yield (q/ha)		10413.620***	3997.302***	31.246

4.4.2 Combining ability effects for yield related traits

In the present investigation, the general combining ability (GCA) effects and specific combining ability (SCA) effects of hybrids for fourteen yield related traits evaluation are represented in Table 4.20 and Table 4.21, respectively. The results obtained are discussed as below

4.4.2.1 Days to first male flower

The estimates of GCA and SCA effects for days to first male flower are presented in Table 4.20 and Table 4.21 respectively. The GCA effect ranged from -1.74 to 0.75 per cent. Out of eight parents, five parents exhibited significant GCA effect for days to first male flower and two parents namely PCPGR-138 (-1.742%) and PCPGR-112 (-1.675%) exhibited significant negative GCA effects.

A perusal of data revealed that range of SCA effects for days to first male flower was -2.92 to 5.24. Out of 28 crosses, nine cross combinations exhibited significant SCA effect for same trait. Desirable significant negative SCA effects was recorded in four crosses namely PCPGR-138 × PCPGR-149 (-2.92%), PCPGR-112 × PCPGR-126 (-2.55%), PCPGR-50 × PCPGR-59 (-2.15%) and PCPGR-51 × PCPGR-59 (-1.78%).

4.4.2.2 Node number to first male flower

The estimates of GCA effects for node number to first male flower ranges from -1.28 to 1.25. Among all parent, five parents showed significant GCA effect for same trait, while other two parents *viz.*, PCPGR-112 (-1.28%) and PCPGR-59 (-0.58%) exhibited desirable significant negative GCA effect for node number to first male flower.

It is clear from data presented in Table 4.21 that SCA effects for node number to first male flower range from -2.33 to 3.86. Among all the crosses, significant SCA effects for same traits was observed in twenty one cross combinations. Desirable significant negative SCA effects for node number to first male flower were observed in ten crosses Top five crosses exhibited significant negative SCA effects were PCPGR-50 × PCPGR-138 (-2.33%), PCPGR-112 × PCPGR-126 (-2.30%), PCPGR-51 × PCPGR-59(-2.30%), PCPGR-59 × PCPGR-138 (-2.10%) and PCPGR-51 × PCPGR-138 (-2.06%).

4.4.2.3 Days to first female flower

A perusal of data revealed that range of GCA effect for days to first female flower was -1.29 to 2.07. Out of all eight parents, three parents exhibited significant GCA effect for same traits and only single parent *viz.*, PCPGR-112 (-1.29%) exhibited significant negative GCA effect for days to first female flower.

Data regarding SCA effect for days to first female flower revealed that range was observed from -3.28 to 6.84. Out of all crosses significant SCA effects for same trait was observed in five crosses and only one cross combination namely PCPGR-50 × PCPGR-59 (-3.28%) showed desirable negative SCA effect.

4.4.2.4 Node number to first female flower

The estimates of GCA and SCA effects regarding node number to first female flower are presented in Table 4.20 and Table 4.21, respectively. The GCA effect ranged from -1.60 to 1.12 per cent. Out of eight parents, five parents showed significant GCA effect for node number to first female flower while two parents PCPGR-112 (-1.60%) and PCPGR-59 (-0.97%) exhibited significant negative GCA effects.

The perusal of data revealed that range of SCA effects for node number to first female flower was -2.66 to 4.43. Out of twenty eight crosses, eleven cross combinations exhibited significant SCA effect for same trait. Desirable significant negative SCA effects was found in five crosses namely PCPGR-83 × PCPGR-126 (-2.66%), PCPGR-51 × PCPGR-59 (-2.46%), PCPGR-50 × PCPGR-51 (-2.33%), PCPGR-50 × PCPGR-149 (-2.10%) and PCPGR-59 × PCPGR-83 (-1.56%).

4.4.2.5 Days to first harvest

The estimates of GCA and SCA effects for days to first harvest are presented in Table 4.20 and Table 4.21, respectively. The GCA effect ranged from -1.22 to 1.33 per cent. Out of eight parents, three parents showed significant GCA effect for days to first harvest whereas only single parent namely PCPGR-112 (-0.122%) exhibited significant negative GCA effects which was. Similar finding also reported by Reddy *et al.* (2014) and Jat *et al.* (2015).

The perusal of data revealed that range of SCA effects for days to first harvest was -3.13 to 5.90. Out of twenty eight crosses, five cross combinations exhibited significant SCA effect for same trait. Desirable significant negative SCA effects was observed in two crosses namely PCPGR-50 × PCPGR-59 (-3.13%) and PCPGR-83 × PCPGR-138 (-2.93%). Similar findings were also reported by Reddy *et al.* (2014) and Pati *et al.* (2015) for days to first fruit harvest.

4.4.2.6 Days to last harvest

The estimates of GCA and SCA effects for days to last harvest are presented in Table 4.20 and Table 4.21, respectively. The GCA effect ranged from -2.21 to 1.32 per cent. Out of eight parents, three parents showed significant GCA effect for days to last harvesting and one parent *viz.*, PCPGR-51 (-2.21%) exhibited significant negative GCA.

The perusal of data revealed that range of SCA effects for days to last harvest was -6.99 to 8.20. Out of twenty eight crosses, twelve cross combinations exhibited significant SCA effect for same trait. Desirable significant negative SCA effects was found in three crosses namely PCPGR-50 × PCPGR-149 (-26.99%), PCPGR-59 × PCPGR-112 (-6.93%) and PCPGR-51 × PCPGR-112 (-13.69%).

4.4.2.7 Inter nodal length (cm)

A critical examination of data presented in the Table 4.29 revealed that GCA effect for inter nodal length range from -0.44 to 0.41. Among all parent, four parents showed significant GCA effect for same traits. Desirable significant negative GCA effects were observed among two parents *viz.*, PCPGR-149 (-0.44%) and PCPGR-51 (-0.41%).

Data regarding SCA effects revealed that SCA effects for inter nodal length ranged from -1.50 to 1.56. Among all crosses significant SCA effects for same traits was observed in five cross combinations. Desirable significant negative SCA effects for inter nodal length were observed in three crosses namely PCPGR-83 × PCPGR-149 (-1.50%), PCPGR-51 × PCPGR-112 (-1.23%) and PCPGR-126 × PCPGR-149 (-1.21%).

Table 4.20: General combining ability effect of parents for different yield and its contributing traits in cucumber

S.N.	Name of genotypes	Characters													
		DFMF	NFMF	DFFF	NFFF	DFH	DLH	IL	PH	FL	AFD	NFPP	AFW	FYPP	FYQH
1.	PCPGR-50	0.758 **	-0.350	-0.625	0.225	-0.135	-0.405	0.413 *	-0.029	0.330	-0.058	0.046	4.712***	0.039 **	5.195 **
2.	PCPGR-51	-0.275	0.383 *	-0.292	0.692***	-0.282	-2.218***	-0.415 *	0.212***	-0.431	0.152 *	0.486***	-13.064***	0.004	0.365
3.	PCPGR - 59	-0.242	-0.583 **	-0.892	-0.975***	-0.715	1.288 *	-0.116	0.139***	0.504	0.016	0.140	5.380***	0.093***	12.433***
4.	PCPGR-83	0.225	1.250***	1.575 **	0.458 *	1.232 **	0.195	0.061	-0.149***	0.150	-0.179 **	-0.337***	-4.846***	-0.115***	-15.324***
5.	PCPGR-112	-1.675***	-1.283***	-1.292 **	-1.608***	-1.228 **	0.908	0.143	-0.023	0.436	0.187 **	0.883***	20.103***	0.352***	47.046***
6.	PCPGR-126	2.258***	0.417 *	2.075***	1.125***	1.332 **	-0.425	-0.026	-0.175***	-0.450	0.046	-1.690***	-8.705***	-0.438***	-58.343***
7.	PCPGR-138	-1.742***	0.183	-0.225	0.292	-0.188	-0.672	0.385 *	0.000	0.217	0.033	0.983***	0.778	0.217***	28.999***
8.	PCPGR-149	0.692 *	-0.017	-0.325	-0.208	-0.015	1.328 *	-0.444 *	0.024	-0.758 **	-0.197 **	-0.510***	-4.359***	-0.153***	-20.370***
	CD 1%	0.916	0.621	1.609	0.702	1.541	1.911	0.643	0.089	0.907	0.228	0.308	3.780	0.043	5.786
	CD 5%	0.619	0.419	1.087	0.474	1.041	1.291	0.435	0.060	0.613	0.154	0.208	2.554	0.029	3.910

DFMF - Days to first male flower, **NFMF** –Node number to first male flower, **DFFF** -Days to first female flower, **DFH** –Days to first harvest, **DLH** – Days to last harvest, **IL** - Inter nodal length PH-Plant height, FL-Fruit length, AFD-Average fruit diameter, NFPP- Number of fruits per plant, , AFW-Average fruit weight, FYPP-Fruit yield per plant and FYH-Fruit yield per hectare.

Table 4.21: Estimation of specific combining ability effects for different yield and its contributing traits in F₁'s of diallel cross of cucumber

S.N.	Name of crosses	Characters													
		DFMF	NFMF	DFFF	NFFF	DFH	DLH	IL	PH	FL	AFD	NFPP	AFW	FYPP	FYQH
1.	PCPGR-50 × PCPGR-51	0.211	2.467***	1.444	-2.333***	0.563	2.884	-0.287	-0.819***	-0.488	-0.038	-1.306***	-19.214***	-0.418***	-55.661***
2.	PCPGR-50 × PCPGR-59	-2.156 *	-1.567 **	-3.289 *	-0.333	-3.137 *	0.244	0.064	0.228 **	1.094	-0.275	1.774***	39.419***	0.759***	101.455***
3.	PCPGR-50 × PCPGR-83	2.711 **	-1.400 *	-0.422	1.900 **	1.516	-1.729	-0.741	-0.475***	-2.903 **	0.820***	-1.083***	2.981	-0.216***	-29.025***
4.	PCPGR-50 × PCPGR-112	-0.389	1.133 *	-0.222	-1.033	-1.224	-0.776	-0.559	0.153	-2.409 **	-0.047	1.964***	-18.031***	0.286***	38.652***
5.	PCPGR-50 × PCPGR-126	0.011	3.433***	0.411	0.567	-0.517	0.491	0.494	0.461***	1.861 *	0.611 **	-0.663 *	28.451***	0.020	2.390
6.	PCPGR-50 × PCPGR-138	-0.656	-2.333***	-1.622	0.400	-0.197	4.671 **	0.479	0.373***	4.344***	0.888***	-0.070	34.674***	0.292***	38.589***
7.	PCPGR-50 × PCPGR-149	5.244***	3.867***	0.811	-2.100 **	-0.904	-6.996***	0.935	0.483***	-3.248***	-0.023	-2.643***	0.525	-0.569***	-75.806***
8.	PCPGR-51 × PCPGR-59	-1.789 *	-2.300***	-2.289	-2.467***	-0.990	-2.476	0.772	-0.007	2.784 **	0.389	1.333***	23.815***	0.471***	62.588***
9.	PCPGR-51 × PCPGR-83	1.411	1.200 *	-0.422	3.433***	-1.070	2.351	-0.962	0.460***	0.821	0.244	-0.024	-14.143***	-0.131 **	-17.356 **
10.	PCPGR-51 × PCPGR-112	-0.689	-1.600 **	-1.222	-0.167	-1.810	-3.696 *	-1.230 *	0.321***	1.955 *	-0.323	0.323	19.945***	0.252***	33.421***
11.	PCPGR-51 × PCPGR-126	2.711 **	-0.300	1.744	3.433***	1.696	0.971	1.249 *	0.307***	-1.445	-0.121	-1.370***	-0.190	-0.255***	-33.477***
12.	PCPGR-51 × PCPGR-138	-1.289	-2.067***	-2.622	-1.067	0.550	1.484	-0.176	0.265 **	-1.306	0.495 *	1.290***	38.606***	0.637***	84.818***
13.	PCPGR-51 × PCPGR-149	2.944 **	1.133 *	3.811 *	0.100	2.043	4.151 *	0.987	0.175 *	0.713	0.328	-0.084	-3.750	-0.050	-6.897
14.	PCPGR-59 × PCPGR-83	-0.622	3.833***	3.511 *	-1.567 *	3.296 *	1.511	0.819	0.287***	-0.157	0.236	-2.377***	4.187	-0.523***	-69.817***
15.	PCPGR-59 × PCPGR-112	-0.389	0.700	-0.622	-0.500	-0.044	-6.936***	1.561 **	0.212 *	-0.896	0.106	-0.130	37.625***	0.279***	37.434***
16.	PCPGR-59 × PCPGR-126	2.678 **	3.667***	-1.656	-0.900	-2.537	-0.936	0.523	-0.036	-1.029	0.481 *	0.243	-29.801***	-0.171***	-22.754***
17.	PCPGR-59 × PCPGR-138	1.344	-2.100***	0.311	3.600***	0.583	3.244	-0.821	0.072	3.020***	-0.269	2.303***	-4.067	0.441***	58.394***
18.	PCPGR-59 × PCPGR-149	1.244	0.433	4.078 **	4.433***	3.010 *	4.111 *	1.138	-0.135	-2.082 *	0.217	-3.070***	-37.600***	-0.859***	-114.841***
19.	PCPGR-83 × PCPGR-112	-0.522	-1.133 *	-1.422	-0.933	1.076	5.491 **	0.526	-0.188 *	1.904 *	-0.029	1.813***	9.990 **	0.514***	68.527***
20.	PCPGR-83 × PCPGR-126	0.211	1.167 *	-0.456	-2.667***	-0.217	8.091***	0.639	0.484***	-0.292	0.056	1.386***	10.332 **	0.377***	50.075***
21.	PCPGR-83 × PCPGR-138	1.544	-0.933	6.844***	-0.500	5.903***	8.204***	-0.609	0.359***	-1.930 *	-0.174	-2.354***	-25.158***	-0.667***	-88.576***
22.	PCPGR-83 × PCPGR-149	0.778	1.267 *	-1.722	-0.333	-2.937 *	-0.729	-1.507 *	0.369***	0.042	0.545 *	0.673 *	1.486	0.156***	20.792***
23.	PCPGR-112 × PCPGR-126	-2.556 **	-2.300***	0.078	-0.600	-0.090	5.244 **	-0.253	-0.755***	-0.245	-0.294	-0.634 *	12.760***	-0.087 *	-11.367 *
24.	PCPGR-112 × PCPGR-138	-0.222	-0.400	-1.622	-0.433	-0.837	1.624	0.990	0.383***	1.854 *	0.496 *	-1.774***	44.253***	-0.048	-6.576
25.	PCPGR-112 × PCPGR-149	-1.322	0.800	-1.189	-0.600	-1.210	6.558***	0.802	0.160 *	2.612 **	0.612 **	1.120***	20.874***	0.445***	59.546***
26.	PCPGR-126 × PCPGR-138	-1.489	2.900***	1.678	2.500***	1.736	-1.176	-0.695	-0.448***	0.737	0.294	-0.800 **	-23.379***	-0.322***	-42.661***
27.	PCPGR-126 × PCPGR-149	0.744	-1.900 **	0.111	1.000	0.030	-1.576	-1.216 *	-0.555***	0.282	0.017	-1.507***	35.698***	-0.129 **	-17.462 **
28.	PCPGR-138 × PCPGR-149	-2.922 **	0.667	-2.256	-1.167	0.550	4.338 *	-0.310	0.237 **	1.548	-0.250	3.820***	-7.945 *	0.707***	94.236***
	CD 1%	2.224	1.506	3.904	1.703	3.740	4.638	1.561	0.215	2.200	0.554	0.748	9.175	0.105	14.044
	CD 5%	1.647	1.116	2.891	1.261	2.769	3.435	1.156	0.159	1.629	0.410	0.554	6.795	0.078	10.400

DFMF - Days to first male flower, NFMF -Node number to first male flower, DFFF -Days to first female flower, DFH -Days to first harvest, DLH - Days to last harvest, IL - Inter nodal length PH-Plant height, FL-Fruit length, AFD-Average fruit diameter, NFPP- Number of fruits per plant, AFW-Average fruit weight, FYPP-Fruit yield per plant and FYH-Fruit yield per hectare.

4.4.2.8 Plant height (m)

The estimates of GCA effects for plant height ranged from -0.17 to 0.21. Out of eight parents, four parents exhibited significant GCA effect for same trait and two parents namely PCPGR-51 (0.21%) and PCPGR-59 (0.13%) showed desirable significant positive GCA effect for plant height. Significant GCA effects for plant height were also reported by Singh *et al.* (2010) and Mule *et al.* (2012).

A critical examination of data for SCA effects revealed that range of SCA for plant height ranged from -0.819 to 0.484. Out of all crosses, twenty three crosses exhibited significant SCA effect for same trait whereas, significant positive effects were observed among sixteen crosses. Top five hybrids showed desirable significant positive SCA effects for plant height were PCPGR-83 × PCPGR-126 (0.484%), PCPGR-50 × PCPGR-149 (0.483%), PCPGR-50 × PCPGR-126 (0.461%), PCPGR-51 × PCPGR-83 (0.460%) and PCPGR-112 × PCPGR-138 (0.38%). Singh *et al.* (2011) and Bairagi *et al.* (2013) also found significant SCA effects for plant height.

4.4.2.9 Fruit length (cm)

It is evident from data presented in Table 4.20 that GCA effects for fruit length ranged from -0.75 to 0.50. Out of all parents, significant GCA effect was observed for only one parent and none of the parents found desirable significant positive effect for fruit length.

The read-through of data for SCA effects revealed that SCA for fruit length ranged from -3.24 to 4.344. Out of all crosses, thirteen cross combinations exhibited significant SCA effect for same trait whereas, significant positive effects were observed among eight crosses. Top five hybrids showed desirable significant positive SCA effects for fruit length were PCPGR-50 × PCPGR-138 (4.34%), PCPGR-59 × PCPGR-138 (3.02%), PCPGR-51 × PCPGR-59 (2.78%), PCPGR-112 × PCPGR-149 (2.61%) and PCPGR-51 × PCPGR-112 (1.95%). Sarkar and Sirohi (2010) and Mule *et al.* (2012) also observed significant SCA effects for fruit length.

4.4.2.10 Average fruit diameter (cm)

A perusal of data presented in Table 4.20 revealed that GCA effects for average fruit diameter ranged from -0.197 to 0.187. Out of all parents, significant GCA effect

was observed for four parents and two parents namely PCPGR-112 (0.187%) and PCPGR-51 (0.152%) exhibited desirable significant positive effect for average fruit diameter. Significant GCA effects for fruit diameter were also reported by Sarkar and Sirohi (2010), Bairagi *et al.* (2013) and Vidhya and Kumar (2014).

A critical examination of data for SCA effects revealed that SCA for average fruit diameter ranged from 0.481 to 0.888. Out of all crosses, eight cross combinations exhibited significant positive SCA effect for same trait. Top five hybrids showed desirable significant positive SCA effects for average fruit diameter were PCPGR-50 × PCPGR-138 (0.888%), PCPGR-50 × PCPGR-83 (0.820%), PCPGR-112 × PCPGR-149 (0.612%), PCPGR-50 × PCPGR-126 (0.611%) and PCPGR-83 × PCPGR-149 (0.545%). Significant positive SCA result for average fruit diameter were also reported by Mule *et al.* (2012), Reddy *et al.* (2014) and Pati *et al.* (2015).

4.4.2.11 Number of fruits per plant

A perusal of data revealed that range of GCA effect for number per plant was -1.69 to 0.983. Among all eight parent, significant GCA effect was observed for six parent and among these, three parents namely PCPGR-138 (0.98%), PCPGR-112 (0.88%) and PCPGR-51 (0.48%) exhibited desirable significant positive GCA effect for number of fruits per plant. Similar findings were also reported by Singh *et al.* (2011), Bairagi *et al.* (2013) and Pati *et al.* (2015).

The estimates of SCA effects for number of fruits per plant ranged from -3.07 to 3.82. Out of twenty eight crosses, significant SCA effects for same traits were observed in twenty two cross combinations whereas, among them ten crosses exhibited desirable significant positive SCA effect for number of fruits per plant. Top five hybrids showed desirable significant positive SCA effects for number of fruits per plant were PCPGR-138 × PCPGR-149 (3.82%), PCPGR-59 × PCPGR-138 (2.30%), PCPGR-50 × PCPGR-112 (1.96%), PCPGR-83 × PCPGR-112 (1.81%) and PCPGR-50 × PCPGR-59 (1.77%). Similar findings were also reported by Sarkar and Sirohi (2010), Vidhya and Kumar (2014) and Jat *et al.* (2015).

4.4.2.12 Average fruit weight (g)

The estimates of GCA effects for average fruit weight ranged from -13.06 to 20.10. Out of eight parents, seven parents exhibited significant GCA effect for same

trait and among them three parents *viz.*, PCPGR-112 (20.10%), PCPGR-59 (5.38%) and PCPGR-50 (4.71%) showed desirable significant positive GCA effect for average fruit weight. Significant general combining ability effects for various characters were also reported by Sarkar and Sirohi (2010), Singh *et al.* (2011) and Pati *et al.* (2015.)

It is apparent from data presented in Table 4.21 that SCA effects for average fruit weight per range from -37.60 to 44.25. Among all crosses significant SCA effects for same traits was observed in twenty one cross combinations while, desirable significant positive SCA effects for average fruits weight were observed in thirteen crosses. Top five cross combinations exhibited desirable significant positive SCA effect for average fruits weight were PCPGR-112x PCPGR-138 (44.25%), PCPGR-50 × PCPGR-59 (39.41%), PCPGR-51 × PCPGR-138 (38.60%), PCPGR-59 × PCPGR-112 (37.62%) and PCPGR-126 × PCPGR-149 (35.69%). Significant SCA effects for fruit weight were also observed by Singh *et al.* (2010), Rabou and Hamed (2011) and Reddy *et al.* (2014).

4.4.2.13 Fruit yield per plant (kg)

It is evident from data presented in the Table 4.20 revealed that GCA effect for fruit yield per plant ranged from -0.43 to 0.35. Among all parents, seven parents showed significant GCA effect for same trait. Desirable significant positive GCA effects were observed among four parents namely PCPGR-112 (0.35%), PCPGR-138 (0.21%), PCPGR-59 (0.093%) and PCPGR-50 (0.039%). Significant GCA effects for yield per plant were also observed by Singh *et al.* (2010), Mule *et al.* (2012), Bairagi *et al.* (2013), Pati *et al.* (2015) and Jat *et al.* (2015).

The estimates of SCA effects for fruit yield per plant ranged from -0.85 to 0.75. Out of twenty eight crosses, significant SCA effects for same traits observed in twenty five cross combinations whereas, thirteen crosses among them exhibited significant positive SCA effect for fruit yield per plant. Top five cross combinations exhibited desirable significant positive SCA effects for fruit yield per plant were PCPGR-50 × PCPGR-59 (0.76%), PCPGR-138 × PCPGR-149 (0.70%), PCPGR-51 × PCPGR-138 (0.63%), PCPGR-83 × PCPGR-112 (0.51%) and PCPGR-51 × PCPGR-59(0.47%). Sarkar and Sirohi (2010), Singh *et al.* (2010), Bairagi *et al.* (2013) and Pati *et al.* (2015) had also reported significant sca effects for yield per plant.

4.4.2.14 Fruit yield (q/ha)

The estimates of GCA effects for fruit yield ranged from -58.34 to 47.04. Out of eight parents, seven parents exhibited significant GCA effect for same trait and among them four parents namely PCPGR-112 (47.04%), PCPGR-138 (29.00%), PCPGR-59 (12.43%) and PCPGR-50 (5.19%) exhibited desirable significant positive GCA effect for fruit yield.

The estimates of SCA effects for fruit yield per plant ranged from -114.84 to 101.45. Out of twenty eight crosses, significant SCA effects for same traits observed in twenty five cross combinations whereas, thirteen crosses among them showed desirable exhibited significant positive SCA effect for fruit yield. Top five cross combinations exhibited desirable significant positive SCA effects for fruit yield were PCPGR-50 × PCPGR-59 (101.45%), PCPGR-138 × PCPGR-149 (94.23%), PCPGR-51 × PCPGR-138 (84.81%), PCPGR-83 × PCPGR-112 (68.52%) and PCPGR-51 × PCPGR-59(62.58%).

The ranking of genotypes for yield related traits were made as per the general combining ability and specific combining ability of diallel cross (excluding reciprocal) and presented in Table 22. PCPGR-112 was found as a best general combiner for maximum number of traits *viz.*, days to first male flower, node number to first male flower, days to first female flower, node to first female flower, days to first harvest, average fruit diameter, number of fruits per plant, average fruit weight, fruit yield per plant and fruit yield per hectare followed by PCPGR-59 (node number to first male flower, node number to first female flower, plant height, average fruit weight, fruit yield per plant, and fruit yield per hectare. PCPGR-138 (For days to first male flower, number of fruits per plant, fruit yield per plant, and fruit yield per hectare), PCPGR-51 (for days to last harvest, intermodal length, plant height and number of fruits per plant) and PCPGR-50 (for average fruit weight and fruit yield per hectare). The general combining ability is primarily the function of additive and additive × additive gene action. According to Gilbert (1967), the additive parental effects have more practical use to the breeders compare to non-allelic interaction, if these are exploited through conventional selection methods. Rojas and Sprague (1942) also pointed out that GCA effects would be more stable as compared to SCA effects.

Table 4.22: Best general and specific combiner for different traits in cucumber

S.N.	Characters	Best general combiners	Best specific combiners
1.	Days to first male flower	PCPGR-138 PCPGR-112	PCPGR-138 × PCPGR-149 PCPGR-112 × PCPGR-126 PCPGR-50 × PCPGR-59 PCPGR-51 × PCPGR-59
2.	Node number to first male flower	PCPGR-112 PCPGR-59	PCPGR-50 × PCPGR-138 PCPGR-112 × PCPGR-126 PCPGR-51 × PCPGR-59 PCPGR-59 × PCPGR-138
3.	Days to first female flower	PCPGR-112	PCPGR-50 × PCPGR-59
4.	Node number to first female flower	PCPGR-112 PCPGR-59	PCPGR-83 × PCPGR-126 PCPGR-51 × PCPGR-59 PCPGR-50 × PCPGR-51 PCPGR-50 × PCPGR-149
5.	Days to first harvest	PCPGR-112	PCPGR-50 × PCPGR-59 PCPGR-83 × PCPGR-138
6.	Days to last harvest	PCPGR-51	PCPGR-50 × PCPGR-149 PCPGR-59 × PCPGR-112 PCPGR-51 × PCPGR-112
7.	Inter nodal length (cm)	PCPGR-149 PCPGR-51	PCPGR-83 × PCPGR-149 PCPGR-51 × PCPGR-112 PCPGR-126 × PCPGR-149
8.	Plant height (m)	PCPGR-51 PCPGR-59	PCPGR-83 × PCPGR-126 PCPGR-50 × PCPGR-149 PCPGR-50 × PCPGR-126 PCPGR-51 × PCPGR-83
9.	Fruit length (cm)	-	PCPGR-50 × PCPGR-138 PCPGR-59 × PCPGR-138 PCPGR-51 × PCPGR-59 PCPGR-112 × PCPGR-149
10.	Average fruit diameter (cm)	PCPGR-112 PCPGR-51	PCPGR-50 × PCPGR-138 PCPGR-50 × PCPGR-83 PCPGR-112 × PCPGR-149 PCPGR-50 × PCPGR-126
11.	Number of fruits per plant	PCPGR-138 PCPGR-112 PCPGR-51	PCPGR-138 × PCPGR-149 PCPGR-59 × PCPGR-138 PCPGR-50 × PCPGR-112 PCPGR-83 × PCPGR-112
12.	Average fruit weight (g)	PCPGR-112 PCPGR-59 PCPGR-50	PCPGR-112 × PCPGR-138 PCPGR-50 × PCPGR-59 PCPGR-51 × PCPGR-138 PCPGR-59 × PCPGR-112
13.	Fruit yield per plant (kg)	PCPGR-112 PCPGR-138 PCPGR-59	PCPGR-50 × PCPGR-59 PCPGR-138 × PCPGR-149 PCPGR-51 × PCPGR-138 PCPGR-83 × PCPGR-112
14.	Fruit yield (q/ha)	PCPGR-112 PCPGR-138 PCPGR-59 PCPGR-50	PCPGR-50 × PCPGR-59 PCPGR-138 × PCPGR-149 PCPGR-51 × PCPGR-138 PCPGR-83 × PCPGR-112

In general, additive effects are mainly due to polygenes producing fixable effects and indicate the capacity of variety in relation to all other varieties, it was crossed with. High GCA effects of a parent is a function of breeding value and hence due to additive gene effect and/or additive x additive interaction effect which represents the fixable components of genetic variance (Griffing, 1956). It is clear that parents have good GCA effects may be presumed to possess more favourable genes for the concerned characters. The results are in conformity with the findings of Masmade and Kale (1986), Horinuzdi and Moore (1989b), Kanobdee *et al.* (1990), Dogra *et al.* (1997b), Quiang *et al.* (1998), Ballui *et al.* (2000) and Munshi *et al.* (2005, 2006) in cucumber. Singh *et al.* (2010) found Peelibheet local, Pant Khira-1 and Patna-3 were good combiner for yield and its contributing traits.

Specific combining ability effects mainly represent dominance, additive × dominance and dominance × dominance type of gene action. The crosses showing SCA effects involving parent with good GCA could be exploited as F₁ hybrid breeding, however, if a cross having high SCA has one of its parent as good general combiner and other as poor or average combiner, such crosses are likely to give some segregants, only if additive genetic system is present in a good general combiner and epistatic effects in the cross act in the same direction so as to maximize the desirable expression of the character in consideration (Whitehouse *et al.*, 1958 and Lonquist, 1961). On the basis of ranking best specific combiner were PCPGR-50 × PCPGR-59 (days to first male flower, days to first female flower, days to first harvest, average fruit weight, fruit yield per plant and fruit yield per hectare), PCPGR-51 × PCPGR-59 (days to first male flower, node number to first male flower, node number to first female flower and fruit length), PCPGR-138 × PCPGR-149 (days to first male flower, number of fruits per plant, fruit yield per plant, and fruit yield per hectare), PCPGR-50 × PCPGR-138 (node number to first male flower, fruit length and average fruit diameter), PCPGR-51 × PCPGR-138 (average fruit weight, fruit yield per plant and fruit yield per hectare), PCPGR-59 × PCPGR-138 (node number to first male flower, fruit length and number of fruits per plant), PCPGR-50 × PCPGR-149 (node number to first female flower, plant height and days to last harvest), PCPGR-83 × PCPGR-112 (number of fruits per plant, fruit yield per plant and fruit yield per hectare), PCPGR-112 × PCPGR-149 (fruit length and average fruit diameter), PCPGR-83 × PCPGR-126 (node number to first

female flower and plant height), PCPGR-112 × PCPGR-126 (days to first male flower and node number to first male flower). Usually the high estimates of SCA effects are obtained from the crosses involving diverse parent. Musmade and Kale (1986) found that both GCA and SCA variances were significant for all the characters studied in cucumber. Baranwal (1995) exhibited high SCA estimates for vine length, fruit length, fruit weight, fruit volume and fruit yield. Ananthan and Pappiah (1997), Bhatnagar (1998) and Munshi *et al.* (2006) found high SCA estimates for most of the characters in cucumber. Dogra and Kanwar (2011) recorded high SCA estimates for yield and number of fruits.

4.5 Screening of parents and F₁ hybrids of cucumber against downy mildew

4.5.1 Symptomatology

Disease symptoms of *P. cubensis* first appeared as small, slightly chlorotic to bright yellow areas on an upper leaf surface. Later, the lesions expanded; they remained chlorotic or yellow or became necrotic and brown. Formation of yellow, more or less angular spots on the upper surface of leaves. The disease is characterized by a ‘downy’ or ‘felt’ appearance which is due to the sporangia found on the abaxial side of the leaf. The lesions can be angular and restricted by the veins of the leaf on *Cucumis sativus* (cucumber) (Savory *et al.*, 2010).

4.5.2 Downy mildew incidence (%)

All eight parents and twenty eight F₁ hybrids were evaluated in three replication with resistant check poinsette. In each replication, downy mildew disease incidence was recorded for all twelve plants. The first symptom of downy mildew was observed on 22 February 2019 five days after post-inoculation of suspension (17 February 2019) in three parents and six hybrids. The results of late blight incidence (%) for all parents and F₁ hybrids presented in Table 4.23. The data revealed significant variable reactions of different parents and F₁ hybrids to the incidence of downy mildew in the current experiment taken at weekly intervals after the onset of observable symptoms at the first planting date for six consecutive weeks. The details of disease incidence are given below:

4.5.2.1 Downy mildew incidence at first week

A perusal of data pertaining mean disease incidence at first week revealed that the incidence of disease among all genotypes ranged from 2.78 to 33.33 per cent and general mean was 16.23 per cent. Six parents with check and twelve crosses had a lower incidence of downy mildew than population mean. Minimum incidence of downy mildew was reported in check variety Poinsette and Crosses PCPGR-112 × PCPGR-138, PCPGR-50 × PCPGR-112 with 2.78% per cent and it was found statistically at par with one parent PCPGR-112 (5.55%) and four hybrids namely PCPGR-51 × PCPGR-112 (5.55%), PCPGR-112 × PCPGR-126 (5.55%), PCPGR-83 × PCPGR-112 (5.55%) and PCPGR-59 × PCPGR-112 (8.33%).

On the other hand, maximum incidence of downy mildew was observed in PCPGR-51 × PCPGR-126 (33.33%) and was statistically at par with two parents *viz.*, PCPGR-59 (27.78%) and PCPGR-83 (27.78%) and fourteen cross combinations namely PCPGR-50 × PCPGR-59 (30.55%), PCPGR-59 × PCPGR-126 (30.55%), PCPGR-126 × PCPGR-138 (27.78%), PCPGR-50 × PCPGR-51 (27.78%), PCPGR-51 × PCPGR-83 (25.00%), PCPGR-83 × PCPGR-126 (25.00%), PCPGR-83 × PCPGR-149 (25.00%), PCPGR-51 × PCPGR-59 (22.22%), PCPGR-51 × PCPGR-149 (22.22%), PCPGR-126 × PCPGR-149 (22.22%), PCPGR-83 × PCPGR-138 (22.22%), PCPGR-138 × PCPGR-149 (19.45%), PCPGR-51 × PCPGR-138 (19.45%), PCPGR-50 × PCPGR-149 (19.45%),

4.5.2.2 Downy mildew incidence at second week

A critical examination of data revealed that mean downy mildew incidence at second week ranged from 11.11 to 41.67 per cent and general mean of incidence was 29.81 per cent. Five parents with check variety and eleven crosses had lower incidence of downy mildew than population mean. Minimum incidence of downy mildew was reported in check variety Poinsette and cross PCPGR-50 × PCPGR-59 with 11.11 per cent. This was found statistically at par with one parent PCPGR-112 (13.89%) and four hybrids namely PCPGR-51 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126 and PCPGR-112 × PCPGR-138 with 16.67 per cent.

On the other hand, maximum incidence of downy mildew was noticed in seven crosses, PCPGR-50 × PCPGR-149, PCPGR-51 × PCPGR-59, PCPGR-51 × PCPGR-83,

PCPGR-51 × PCPGR-126, PCPGR-51 × PCPGR-149, PCPGR-126 × PCPGR-138 and PCPGR-138 × PCPGR-149 with 41.67 per cent incidence. This was found statistically at par with two parents PCPGR-59 (38.89%), PCPGR-83 (36.11%) and seven hybrids namely PCPGR-50 × PCPGR-51 (38.89%), PCPGR-50 × PCPGR-59 (38.89%), PCPGR-83 × PCPGR-126 (38.89%), PCPGR-83 × PCPGR-149 (38.89%), PCPGR-59 × PCPGR-126 (38.89%), PCPGR-126 × PCPGR-149 (36.11%), PCPGR-50 × PCPGR-83 (36.11%). Among all the genotypes under study, one cross namely PCPGR-50 × PCPGR-59, had an equal incidence of downy mildew compared to the control cultivar.

4.5.2.3 Downy mildew incidence at third week

The data regarding mean disease incidence at third week indicated that the incidence of disease among all genotypes ranged from 19.45 to 58.33 per cent and general mean was 42.57 per cent. Five parents with check and thirteen crosses had lower incidence of downy mildew than population mean. Minimum incidence of downy mildew was reported in check variety Poinsette and parents PCPGR-112 with 19.45% per cent and was found statistically at par with six hybrids namely PCPGR-50 × PCPGR-112 (22.22%), PCPGR-112 × PCPGR-138 (22.22%), PCPGR-51 × PCPGR-112 (25.00%), PCPGR-83 × PCPGR-112 (25.00%), PCPGR-112 × PCPGR-126 (25.00%) and PCPGR-59 × PCPGR-112 (27.78%).

Maximum incidence of downy mildew was observed in three crosses, PCPGR-83 × PCPGR-126, PCPGR-83 × PCPGR-149 and PCPGR-126 × PCPGR-138 with 58.33 per cent incidence. This was found statistically at par with two parents PCPGR-83 (52.78%), PCPGR-59 (50.00%) and twelve hybrids namely PCPGR-50 × PCPGR-59 (55.55%), PCPGR-50 × PCPGR-149 (55.55%), PCPGR-51 × PCPGR-59 (55.55%), PCPGR-51 × PCPGR-83 (55.55%), PCPGR-51 × PCPGR-126 (55.55%), PCPGR-51 × PCPGR-149 (55.55%), PCPGR-59 × PCPGR-126 (55.55%) PCPGR-83 × PCPGR-138 (55.55%), PCPGR-126 × PCPGR-149 (55.55%), PCPGR-138 × PCPGR-149 (55.55%), PCPGR-50 × PCPGR-51 (52.78%) and PCPGR-50 × PCPGR-83 (50.00%). Among all the genotypes under study, one parent namely PCPGR-112, had an equal incidence of downy mildew compared to the control cultivar.

Table 4.23: Downy mildew incidence at week interval

S. N.	Genotypes	Incidence (%)					
		1 week	2 week	3 week	4 week	5 week	6 week
1	PCPGR-50	13.89 (21.66)	30.55 (33.51)	44.45 (41.80)	58.33 (49.85)	66.67 (54.85)	75.00 (60.21)
2	PCPGR-51	11.11 (19.22)	22.22 (28.03)	33.33 (35.15)	41.67 (40.15)	58.33 (49.85)	66.67 (54.85)
3	PCPGR - 59	27.78 (31.75)	38.89 (38.55)	50.00 (45.00)	58.33 (49.85)	66.67 (54.85)	72.22 (58.57)
4	PCPGR-83	27.78 (31.75)	36.11 (36.91)	52.78 (46.60)	61.11 (51.45)	69.45 (56.49)	77.78 (61.97)
5	PCPGR-112	5.55 (11.19)	13.89 (21.66)	19.45 (26.07)	27.78 (31.75)	36.11 (36.91)	36.11 (36.91)
6	PCPGR-126	13.89 (21.66)	25.00 (29.79)	33.33 (35.15)	44.45 (41.80)	61.11 (51.45)	69.45 (56.49)
7	PCPGR-138	11.11 (19.22)	25.00 (29.78)	38.89 (38.55)	47.22 (43.40)	50.00 (45.00)	55.56 (48.25)
8	PCPGR-149	8.33 (16.78)	25.00 (29.79)	30.55 (33.51)	38.89 (38.55)	52.78 (46.60)	66.67 (54.85)
9	PCPGR-50 × PCPGR-51	27.78 (31.75)	38.89 (38.55)	52.78 (46.60)	63.89 (53.09)	72.22 (58.25)	80.55 (63.93)
10	PCPGR-50 × PCPGR-59	30.55 (33.51)	38.89 (38.55)	55.55 (48.20)	66.67 (54.85)	75.00 (60.21)	86.11 (68.34)
11	PCPGR-50 × PCPGR-83	16.67 (23.62)	36.11 (36.75)	50.00 (45.00)	61.11 (51.45)	66.67 (54.85)	72.22 (58.25)
12	PCPGR-50 × PCPGR-112	2.78 (5.60)	11.11 (19.22)	22.22 (28.03)	27.78 (31.75)	33.33 (35.15)	36.11 (36.80)
13	PCPGR-50 × PCPGR-126	13.89 (21.65)	27.78 (31.75)	41.67 (40.15)	50.00 (45.00)	61.11 (51.49)	63.89 (53.25)
14	PCPGR-50 × PCPGR-138	13.89 (21.66)	25.00 (29.78)	41.67 (40.15)	49.89 (44.93)	52.67 (46.53)	61.11 (51.49)
15	PCPGR-50 × PCPGR-149	19.45 (26.06)	41.67 (40.15)	55.55 (48.20)	63.89 (53.09)	69.45 (56.49)	77.78 (61.97)
16	PCPGR-51 × PCPGR -59	22.22 (28.03)	41.67 (40.15)	55.55 (48.20)	69.45 (56.49)	77.78 (61.97)	83.33 (66.38)
17	PCPGR-51 × PCPGR-83	25.00 (29.78)	41.67 (40.15)	55.55 (48.20)	63.89 (53.09)	69.45 (56.49)	75.33 (60.42)
18	PCPGR-51 × PCPGR-112	5.55 (11.19)	16.67 (23.62)	25.00 (29.78)	27.78 (31.75)	30.55 (33.51)	36.11 (36.91)
19	PCPGR-51 × PCPGR-126	33.33 (35.15)	41.67 (40.15)	55.55 (48.20)	66.67 (54.85)	75.00 (60.21)	83.33 (66.37)
20	PCPGR-51 × PCPGR-138	19.45 (26.06)	30.55 (33.51)	41.67 (40.15)	52.78 (46.60)	61.11 (51.45)	63.89 (53.09)
21	PCPGR-51 × PCPGR-149	22.22 (28.03)	41.67 (40.15)	55.55 (48.20)	63.89 (53.20)	72.22 (58.25)	80.55 (63.94)

Table 4.23 Contd...

S. N.	Genotypes	Incidence (%)					
		1 week	2 week	3 week	4 week	5 week	6 week
22	PCPGR-59 × PCPGR-83	11.11 (16.06)	25.00 (29.78)	36.11 (36.80)	47.22 (43.40)	52.78 (46.60)	58.33 (50.00)
23	PCPGR-59 × PCPGR-112	8.33 (13.62)	19.45 (26.06)	27.78 (31.75)	30.55 (33.51)	36.11 (36.91)	36.11 (36.91)
24	PCPGR-59 × PCPGR-126	30.55 (33.51)	38.89 (38.55)	55.55 (48.20)	66.67 (54.85)	75.00 (60.21)	88.88 (70.77)
25	PCPGR-59 × PCPGR-138	11.11 (19.22)	30.55 (33.51)	41.67 (40.20)	50.00 (45.00)	55.56 (48.25)	58.33 (50.00)
26	PCPGR-59 × PCPGR-149	13.89 (21.65)	25.00 (29.78)	36.11 (36.80)	47.22 (43.40)	55.64 (48.25)	61.11 (51.45)
27	PCPGR-83 × PCPGR-112	8.33 (13.62)	16.67 (23.62)	25.00 (29.78)	30.55 (33.51)	36.11 (36.91)	38.89 (38.55)
28	PCPGR-83 × PCPGR-126	25.00 (29.78)	38.89 (38.55)	58.33 (49.85)	66.67 (54.85)	75.00 (60.22)	80.55 (63.94)
29	PCPGR-83 × PCPGR-138	22.22 (28.03)	33.33 (35.15)	55.55 (48.20)	69.45 (56.49)	77.78 (61.97)	83.33 (65.91)
30	PCPGR-83 × PCPGR-149	25.00 (29.78)	38.89 (38.55)	58.33 (49.85)	69.45 (56.49)	80.55 (63.94)	86.11 (68.34)
31	PCPGR-112 × PCPGR-126	5.55 (11.19)	16.67 (23.62)	25.00 (29.78)	27.78 (31.75)	30.55 (33.51)	36.11 (36.91)
32	PCPGR-112 × PCPGR-138	2.78 (5.59)	16.67 (24.09)	22.22 (28.03)	27.78 (31.75)	27.78 (31.75)	30.55 (33.51)
33	PCPGR-112 × PCPGR-149	13.89 (21.65)	22.22 (28.03)	33.33 (35.15)	38.89 (38.55)	44.45 (41.80)	47.22 (43.40)
34	PCPGR-126 × PCPGR-138	27.78 (31.54)	41.67 (40.15)	58.33 (49.85)	66.67 (54.85)	77.78 (62.18)	86.11 (68.81)
35	PCPGR-126 × PCPGR-149	22.22 (28.03)	36.11 (36.80)	55.55 (48.20)	66.67 (54.85)	75.00 (60.21)	86.11 (68.34)
36	PCPGR-138 × PCPGR-149	19.45 (26.06)	41.67 (40.15)	55.55 (48.20)	63.89 (53.09)	69.45 (56.49)	77.78 (61.97)
37	Poinsette	2.78 (5.59)	11.11 (19.22)	19.45 (26.06)	22.22 (28.03)	25.00 (29.79)	27.78 (31.75)
	Mean	16.23 (8.32)	29.81 (31.50)	42.57 (42.39)	51.27 (49.16)	58.71 (54.72)	64.95 (59.56)
	CD(0.05)	8.63 (9.66)	9.85 (6.55)	9.64 (5.90)	10.41 (6.28)	11.53 (7.18)	12.33 (8.02)
	± SE(m)	3.06 (3.42)	3.49 (2.32)	3.41 (2.09)	3.68 (2.22)	4.08 (2.54)	4.37 (2.84)

4.5.2.4 Downy mildew incidence at fourth week

It is apparent from disease incidence data that the incidence range was 22.22 to 69.44% and the mean value was 51.27%. Five parents with one resistant check and twelve crosses had lower incidence of downy mildew than population mean. Minimum incidence of downy mildew (19.45% per cent) was reported in check variety Poinsette and was found statistically at par with one parent PCPGR-112 (27.78%) and six hybrids namely PCPGR-50 × PCPGR-112 (27.78%), PCPGR-112 × PCPGR-138 (27.78%), PCPGR-51 × PCPGR-112 (27.78%), PCPGR-112 × PCPGR-126 (27.78%) and PCPGR-59 × PCPGR-112 (30.55%), PCPGR-83 × PCPGR-112 (30.55%).

Moreover, maximum incidence of downy mildew was observed in three crosses, PCPGR-83 × PCPGR-138 and PCPGR-83 × PCPGR-149 and PCPGR-51 × PCPGR-59 with 69.45 per cent incidence. This was found statistically at par with one parent PCPGR-83 (61.11%). and twelve hybrids namely PCPGR-50 × PCPGR-59 (66.67%), PCPGR-51 × PCPGR-126 (66.67%), PCPGR-59 × PCPGR-126 (66.67%), PCPGR-83 × PCPGR-126 (66.67%), PCPGR-126 × PCPGR-138 (66.67%), PCPGR-126 × PCPGR-149 (66.67%), PCPGR-50 × PCPGR-51 (63.89%) PCPGR-50 × PCPGR-149 (63.89%), PCPGR-51 × PCPGR-83 (63.89%), PCPGR-51 × PCPGR-149 (63.89%), PCPGR-138 × PCPGR-149 (63.89%) and PCPGR-50 × PCPGR-83 (61.11%).

4.5.2.5 Downy mildew incidence at five week

The critical data examination of disease incidence revealed that range of incidence was 25.00 to 80.55 per cent and mean value was recorded 58.71 per cent. Four parents with resistant check and eleven crosses gave less downy mildew incidence than population mean. Minimum incidence of downy mildew (25.00 per cent) was reported in check variety Poinsette and was found statistically at par with one parent PCPGR-112 (36.11%) and six hybrids namely PCPGR-112 × PCPGR-138 (27.78%), PCPGR-51 × PCPGR-112 (30.55%), PCPGR-112 × PCPGR-126 (30.55%), PCPGR-50 × PCPGR-112 (33.33%), PCPGR-83 × PCPGR-112 (36.11%) and PCPGR-59 × PCPGR-112 (36.11%).

In addition, maximum incidence of downy mildew was found in cross PCPGR-83 × PCPGR-149 with 80.55 per cent incidence and was found statistically at

par with ten hybrids namely PCPGR-51 × PCPGR-59(77.78%), PCPGR-83 × PCPGR-138 (77.78%), PCPGR-126 × PCPGR-138 (77.78%), PCPGR-50 × PCPGR-59 (75.00%), PCPGR-51 × PCPGR-126 (75.00%), PCPGR-59 × PCPGR-126 (75.00%), PCPGR-83 × PCPGR-126 (75.00%) PCPGR-126 × PCPGR-149 (75.00%), PCPGR-50 × PCPGR-51 (72.22%) and PCPGR-51 × PCPGR-149 (72.22).

4.5.2.6 Downy mildew incidence at sixth w week

A perusal of data pertaining mean disease incidence at sixth week indicated that the range of disease incidence among all genotypes was 27.78 to 88.88 per cent and general mean was 64.95 per cent. Two parents with resistant check and thirteen crosses gave less downy mildew incidence than population mean. Minimum incidence of downy mildew (27.78 per cent) was reported in check variety Poinsette and was found statistically at par with one parent PCPGR-112 (36.11%) and six hybrids namely PCPGR-112 × PCPGR-138 (30.55%), PCPGR-51 × PCPGR-112 (36.11%), PCPGR-112 × PCPGR-126 (36.11%), PCPGR-50 × PCPGR-112 (36.11%), and PCPGR-59 × PCPGR-112 (36.11%), PCPGR-83 × PCPGR-112 (38.89%).

Furthermore, maximum incidence of downy mildew was observed in cross, PCPGR-59 × PCPGR-126 with 88.88 per cent incidence and was found statistically at par with eleven hybrids namely PCPGR-50 × PCPGR-59 (86.11%), PCPGR-83 × PCPGR-149 (86.11%), PCPGR-126 × PCPGR-138 (86.11%), PCPGR-126 × PCPGR-149 (86.11%), PCPGR-51 × PCPGR-59(83.33%), PCPGR-51 × PCPGR-126 (83.33%), PCPGR-83 × PCPGR-138 (83.33%) PCPGR-50 × PCPGR-51 (80.55%), PCPGR-51 × PCPGR-149 (80.55%), PCPGR-83 × PCPGR-126 (80.55) and PCPGR-138 × PCPGR-149 (77.78%).

4.5.3 Downy mildew disease severity in cucumber

All eight parents with resistant check Poinsette and twenty eight F₁ hybrids were evaluated for downy mildew severity (%) in three replications. In each replication five plants were selected and disease severity for downy mildew was recorded. The results of downy mildew severity (%) for all parents and F₁ hybrids are presented in Table 4.50. Data on disease reactions of different parents and F₁ hybrids against downy mildew severity in current experiment taken at weekly interval after the onset of observable symptoms at the first planting date for six consecutive weeks and the details of observations are given below:

4.5.3.1 Downy mildew severity at first week

The data regarding mean disease severity at first week revealed that the disease severity among all genotypes ranged from 0.00 to 6.67 per cent with an average value of 2.78 per cent. Two parents with resistant check and sixteen crosses had less downy mildew severity than population mean. Minimum downy mildew severity (0.00%) was reported in check variety Poinsette and five hybrids namely PCPGR-51 × PCPGR-112, PCPGR-59 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126, PCPGR-112 × PCPGR-149 and was found statistically at par with two parents and six crosses *viz.*, PCPGR-112 (0.74%), PCPGR-126 (1.48), PCPGR-50 × PCPGR-112 (0.74%), PCPGR-59 × PCPGR-149 (0.74%) PCPGR-50 × PCPGR-51 (1.48%), PCPGR-51 × PCPGR-149 (1.48%), PCPGR-126 × PCPGR-149 (1.48) and PCPGR-51 × PCPGR-126 (1.48%).

Moreover, maximum severity of downy mildew (6.67%) was observed in four crosses PCPGR-51 × PCPGR-83, PCPGR-51 × PCPGR-138, PCPGR-59 × PCPGR-138, PCPGR-83 × PCPGR-149. This was found statistically at par with six parents PCPGR-51 (5.18%), PCPGR-138 (5.18%), PCPGR-59 (4.44%), PCPGR-83 (3.70%), PCPGR-50 (2.96%), PCPGR-149 (2.96%) and eight hybrids namely PCPGR-126 × PCPGR-138 (5.18%), PCPGR-59 × PCPGR-126 (4.44%), PCPGR-50 × PCPGR-59 (3.70%), PCPGR-50 × PCPGR-126 (3.70%), PCPGR-59 × PCPGR-83 (3.70%), PCPGR-83 × PCPGR-138 (3.70%), PCPGR-138 × PCPGR-149 (3.70%), PCPGR-50 × PCPGR-83 (2.96%). Five cross combinations observed same severity than check variety.

4.5.3.2 Downy mildew severity at second week

A perusal of data revealed that mean downy mildew severity ranged from 1.48 to 17.04 per cent with a mean severity 8.83 per cent. Three parents with standard check and fourteen crosses had less downy mildew severity than population mean. Minimum downy mildew severity (1.48%) was reported in check variety Poinsette and one hybrid *viz.*, PCPGR-83 × PCPGR-112. This was found statistically at par with two hybrids namely PCPGR-59 × PCPGR-112 (2.22%) and PCPGR-112 × PCPGR-149 (2.22%).

On the other hand, maximum severity of downy mildew (17.04%) was observed in one parent PCPGR-83 and one hybrid namely PCPGR-83 × PCPGR-138. This was found statistically at par with one parent PCPGR-59 (16.30%), and seven hybrids

namely PCPGR-59 × PCPGR-126 (16.30%), PCPGR-83 × PCPGR-149 (15.56%), PCPGR-50 × PCPGR-59 (14.82%), PCPGR-51 × PCPGR-83 (14.07%), PCPGR-126 × PCPGR-138 (13.33%), PCPGR-51 × PCPGR-149(13.33%) and PCPGR-126 × PCPGR-149 (11.85%). One cross combinations observed equal severity than check variety.

4.5.3.3 Downy mildew severity at third week

A perusal of data revealed that mean downy mildew severity ranged from 2.96 to 25.93 per cent with an average value of 16.84 per cent. Four parents with check and ten crosses had less downy mildew severity than population mean. Minimum downy mildew severity was reported in check Poinsette (2.96%) and found statistically at par with three hybrids *i.e.*, PCPGR-59 × PCPGR-112 (3.70%), PCPGR-83 × PCPGR-112 (3.70%) and PCPGR-112 × PCPGR-126 (4.52%).

Furthermore, maximum severity of downy mildew (25.93%) was observed in parents PCPGR-59 and hybrids PCPGR-59 × PCPGR-126 and found statistically at par with one parents PCPGR-83 (24.44%) and four hybrids hybrid namely PCPGR-83 × PCPGR-149 (25.19%), PCPGR-126 × PCPGR-138 (24.44%) PCPGR-83 × PCPGR-138 (23.70%) and PCPGR-138 × PCPGR-149 (22.22%).

4.5.3.4 Downy mildew severity at fourth week

A critical examination of data revealed that mean downy mildew severity ranged from 6.67 to 47.41 per cent with an average value of 26.10 per cent. Two parents with check and seven crosses had less downy mildew severity than population mean. Minimum downy mildew severity (6.67%) was reported in check Poinsette and hybrid PCPGR-59 × PCPGR-112 and was found statistically at par with one hybrid PCPGR-83 × PCPGR-112 (7.04%).

Furthermore, maximum severity of downy mildew (37.04%) was observed in hybrid PCPGR-59 × PCPGR-126 and found statistically at par with one parent PCPGR-83 (36.30%) and six hybrids namely PCPGR-83 × PCPGR-149 (36.29%), PCPGR-50 × PCPGR-51 (34.07%) PCPGR-126 × PCPGR-149 (33.33%) PCPGR-50 × PCPGR-59 (32.59%), PCPGR-51 × PCPGR-126 (32.59%) and PCPGR-126 × PCPGR-138 (32.59%).

4.5.3.5 Downy mildew severity at fifth week

The data pertaining disease severity showed that range of severity at fifth week was 8.15 to 47.41 per cent with average severity of 36.18 per cent. Two parents with check and nine crosses gave less downy mildew severity than population mean. Minimum downy mildew severity was found in check variety Poinsette (8.15%) and none of the parents and hybrids found statistically at par with check parent.

Maximum severity of downy mildew was observed in cross PCPGR-59 × PCPGR-126 with 48.15 per cent and found statistically at par with one parent PCPGR-83 (47.41%) and three hybrids *i.e.*, PCPGR-83 × PCPGR-149 (47.41%), PCPGR-50 × PCPGR-59 (46.66%) and PCPGR-51 × PCPGR-149 (45.18%).

4.5.3.6 Downy mildew severity at sixth week

The read-through of data regarding disease severity revealed that range for severity at sixth week was 15.55 to 57.78 per cent with average severity of 46.03 per cent. Two parents with check and ten crosses gave less downy mildew severity than population mean. Minimum downy mildew severity was reported in check variety Poinsette (15.55%) and none of the parents and hybrids found statistically at par with check parent.

Moreover, maximum severity of downy mildew was observed in cross PCPGR-59 × PCPGR-126 with 57.78 per cent and found statistically at par with six hybrids namely PCPGR-50 × PCPGR-59 (57.04%), PCPGR-51 × PCPGR-126 (56.30%), PCPGR-51 × PCPGR-59(55.56%), PCPGR-83 × PCPGR-126 (55.56%), PCPGR-83 × PCPGR-149 (55.56%) and PCPGR-126 × PCPGR-149 (54.82%).

On the basis of downy mildew severity percentage in F₁ and their parental population with check, they were categorized into different groups stating their susceptible reactions to downy mildew (Table 4.25). Out of all parents and F₁ hybrids only check variety Poinsette exhibited resistant reaction against downy mildew while none of the parents and hybrids showed resistant reaction to downy mildew.

Table 4.24: Downy mildew disease severity at weekly interval

S.N.	Genotypes	1 week	2 week	3 week	4 week	5 week	6 week
1.	PCPGR-50	2.96 (9.77)	11.11 (19.41)	21.48 (27.48)	31.85 (34.34)	44.44 (41.81)	52.59 (46.49)
2.	PCPGR-51	5.18 (13.10)	9.63 (18.06)	15.56 (23.19)	23.70 (29.13)	35.56 (36.60)	46.67 (43.09)
3.	PCPGR - 59	4.44 (11.90)	16.30 (23.80)	25.93 (30.60)	31.11 (33.89)	40.74 (39.66)	51.11(45.64)
4.	PCPGR-83	3.70 (9.05)	17.04 (24.37)	24.44 (29.61)	36.30 (37.04)	47.41 (43.51)	53.33 (46.91)
5.	PCPGR-112	0.74 (2.86)	4.44 (11.90)	6.67 (14.82)	15.56 (23.19)	22.22 (28.11)	33.33 (35.26)
6.	PCPGR-126	1.48 (5.71)	6.67 (14.82)	18.52 (25.43)	28.89 (32.50)	37.78 (37.92)	48.89 (44.36)
7.	PCPGR-138	5.18 (13.10)	8.89 (17.26)	16.30 (23.80)	27.41 (31.56)	37.04 (37.49)	42.22 (40.52)
8.	PCPGR-149	2.96 (9.77)	5.18 (13.10)	16.30 (23.80)	23.70 (29.13)	36.30 (37.05)	47.41 (43.51)
9.	PCPGR-50 × PCPGR-51	1.48 (5.71)	7.41 (15.76)	21.48 (27.57)	34.07 (35.70)	42.22 (40.52)	54.07 (47.34)
10.	PCPGR-50 X PCPGR- 59	3.70 (10.97)	14.82 (22.62)	20.00 (26.54)	32.59 (34.81)	46.66 (43.09)	57.04 (49.05)
11.	PCPGR-50 × PCPGR-83	2.96 (9.77)	7.41 (15.76)	17.78 (24.91)	26.67 (31.08)	40.00 (39.23)	49.63 (44.79)
12.	PCPGR-50 × PCPGR-112	0.74 (2.86)	2.96 (9.77)	13.33 (21.37)	17.78 (24.91)	26.67 (31.08)	35.56 (36.60)
13.	PCPGR-50 × PCPGR-126	3.70 (10.97)	8.15 (16.55)	20.74 (27.09)	27.41 (31.56)	35.56 (36.60)	48.89 (44.36)
14.	PCPGR-50 × PCPGR-138	2.22 (6.91)	5.93 (14.04)	17.04 (24.37)	29.63 (32.97)	42.22 (40.52)	44.44 (41.81)
15.	PCPGR-50 × PCPGR-149	2.22 (6.91)	8.96 (17.33)	16.30 (23.80)	31.11 (33.89)	37.04 (37.49)	53.33 (46.91)
16.	PCPGR-51 × PCPGR -59	2.29 (7.05)	11.11 (19.41)	18.52 (25.48)	28.89 (32.50)	39.26 (38.80)	55.56 (48.19)
17.	PCPGR-51 × PCPGR-83	6.67 (14.83)	14.07 (22.02)	19.26 (26.03)	29.63 (32.97)	40.74 (39.66)	51.11 (45.64)
18.	PCPGR-51 × PCPGR-112	0.00 (0.00)	2.96 (9.77)	8.89 (17.26)	15.56 (23.19)	27.41 (31.56)	31.11 (33.89)
19	PCPGR-51 × PCPGR-126	1.48 (5.71)	10.37 (18.76)	17.78 (24.91)	32.59 (34.81)	41.48 (40.09)	56.30 (48.62)
20	PCPGR-51 × PCPGR-138	6.67 (14.82)	9.63 (18.06)	18.52 (25.48)	27.41 (31.56)	34.07 (35.71)	45.93 (42.66)
21	PCPGR-51 × PCPGR-149	1.48 (5.71)	13.33 (21.37)	19.26 (26.03)	31.11 (33.89)	45.18 (42.240)	53.33 (46.91)
22	PCPGR-59 × PCPGR-83	3.70 (10.97)	7.41 (15.76)	15.56(23.19)	28.22 (32.07)	38.55 (38.37)	46.67 (43.09)
23	PCPGR-59 × PCPGR-112	0.00 (0.00)	2.22 (6.91)	3.70 (10.97)	6.67 (14.82)	15.56 (23.19)	30.37 (33.44)
24	PCPGR-59 × PCPGR-126	4.44 (11.90)	16.30 (23.80)	25.93 (30.60)	37.04 (37.49)	48.15 (43.93)	57.78 (49.48)
25	PCPGR-59 × PCPGR-138	6.67 (14.82)	11.85 (20.12)	20.00 (26.54)	31.85 (34.34)	37.78 (37.92)	49.63 (44.79)
26	PCPGR-59 × PCPGR-149	0.74 (2.86)	4.52 (12.04)	14.82 (22.62)	26.67 (31.08)	40.00 (39.22)	44.44 (41.81)
27	PCPGR-83 × PCPGR-112	0.00 (0.00)	1.48 (5.71)	3.70 (10.97)	7.04 (14.29)	22.22 (28.11)	31.11 (33.89)
28	PCPGR-83 × PCPGR-126	2.22 (6.91)	8.89 (17.26)	17.85 (24.97)	31.11 (33.89)	42.22 (40.52)	55.56 (48.19)
29	PCPGR-83 × PCPGR-138	3.70 (9.04)	17.04 (24.37)	23.70 (29.13)	30.37 (33.43)	43.70 (41.38)	51.11 (45.64)
30	PCPGR-83 × PCPGR-149	6.67 (14.83)	15.56 (23.19)	25.19 (30.10)	36.29 (37.04)	47.41 (43.51)	55.56 (48.19)
31	PCPGR-112 × PCPGR-126	0.00 (0.00)	2.96 (9.77)	4.52 (12.04)	11.85 (20.12)	20.00 (26.54)	31.85 (34.34)
32	PCPGR-112 × PCPGR-138	2.22 (6.91)	5.18 (13.10)	11.11 (19.41)	16.20 (23.72)	21.48 (27.61)	26.67 (31.08)
33	PCPGR-112 × PCPGR-149	0.00 (0.00)	2.22 (8.57)	11.85 (20.12)	17.04 (24.37)	28.15 (32.04)	35.56 (36.60)
34	PCPGR-126 × PCPGR-138	5.18 (13.09)	13.33 (21.37)	24.44 (29.61)	32.59 (34.81)	40.74 (39.66)	53.33 (46.91)
35	PCPGR-126 × PCPGR-149	1.48 (5.71)	11.85 (20.12)	21.48 (27.61)	33.33 (35.25)	44.44 (41.810)	54.82 (47.77)
36	PCPGR-138 × PCPGR-149	3.70 (10.97)	8.15 (16.56)	22.22 (28.11)	29.63 (32.95)	40.00 (39.23)	51.11 (45.64)
37	Poinsette	0.00 (0.00)	1.48 (5.71)	2.96 (9.77)	6.67 (14.83)	8.15 (16.56)	15.55 (23.19)
	Mean	2.78 (7.72)	8.83 (16.44)	16.84 (23.66)	26.10 (30.25)	36.18 (36.71)	46.03 (42.61)
	C.D.	2.77 (6.59)	2.66 (3.73)	3.46 (2.85)	3.639 (3.033)	3.17 (1.97)	3.34 (1.98)
	SE(m)	0.98 (2.33)	0.94 (1.32)	1.23 (1.01)	1.288 (1.073)	1.12 (0.70)	1.18 (0.70)

Table 4.25: Grading of F₁ hybrids and their parental population with check against Downy mildew (*Pseudoperonospora cubensis*)

S.N.	PDI	Reaction	Number of genotypes	Examples
1.	0-20	Resistant	1	Poinsette
2.	21-40	Moderately resistant	8	PCPGR-112 PCPGR-50 × PCPGR-112 PCPGR-51 × PCPGR-112 PCPGR-59 × PCPGR-112 PCPGR-83 × PCPGR-112 PCPGR-112 × PCPGR-126 PCPGR-112 × PCPGR-138 PCPGR-112 × PCPGR-149
3.	41-60	Susceptible	28	PCPGR-50,PCPGR-51, PCPGR-59 PCPGR-83,PCPGR-126, PCPGR-138 PCPGR-149 PCPG-50 × PCPGR-51 PCPGR-50 × PCPGR-59 PCPGR-50 × PCPGR-83 PCPGR-50 × PCPGR-126 PCPGR-50 × PCPGR-138 PCPGR-50 × PCPGR-149 PCPGR-51 × PCPGR-59 PCPGR-51 × PCPGR-83 PCPGR-51 × PCPGR-126 PCPGR-51 × PCPGR-138 PCPGR-51 × PCPGR-149 PCPGR-59 × PCPGR-83 PCPGR-59 × PCPGR-126 PCPGR-59 × PCPGR-138 PCPGR-59 × PCPGR-149 PCPGR-83 × PCPGR-126 PCPGR-83 × PCPGR-138 PCPGR-83 × PCPGR-149 PCPGR-126 × PCPGR-138 PCPGR-126 × PCPGR-149 PCPGR-138 × PCPGR-149
4.	>60.00	Highly susceptible	0	-

Moderately resistance reaction against downy mildew was observed in eight genotypes one of which was parent *viz.*, PCPGR-112 and seven hybrids *viz.*, PCPGR-50 × PCPGR-112, PCPGR-51 × PCPGR-112, PCPGR-59 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126, and PCPGR-112 × PCPGR-138. The remaining twenty-eight genotypes exhibited susceptible reactions to downy mildew disease, of which seven were parents namely PCPGR-50, PCPGR-51, PCPGR-59, PCPGR-83, PCPGR-126, and PCPGR-138 PCPGR-149 and rest twenty one were hybrids namely PCPGR-50 × PCPGR-51, PCPGR-50 × PCPGR-51, PCPGR-50 × PCPGR-59, PCPGR-50 × PCPGR-83, PCPGR-50 × PCPGR-126, PCPGR-50 × PCPGR-138, PCPGR-50 × PCPGR-149, PCPGR-51 × PCPGR -59, PCPGR-51 × PCPGR-83, PCPGR-51 × PCPGR-126, PCPGR-51 × PCPGR-138, PCPGR-51 × PCPGR-149, PCPGR-59 × PCPGR-83, PCPGR-59 × PCPGR-126, PCPGR-59 × PCPGR-138, PCPGR-59 × PCPGR-149, PCPGR-83 × PCPGR-126, PCPGR-83 × PCPGR-138, PCPGR-83 × PCPGR-149, PCPGR-126 × PCPGR-138, PCPGR-126 × PCPGR -149 and PCPGR-138 × PCPGR-149. However, none of the genotypes showed highly susceptible reaction against downy mildew.

On the basis of downy mildew severity many other researchers also categorized the cucumber genotypes against downy mildew. Bommesh *et al.* (2018) revealed that Genotype IIHR-438 and *Cucumis metuliferus* L. showed field resistance with an average PDI of 17.66 and 17.46; respectively compared to 73.12 PDI in highly susceptible genotype of IIHR-389. The disease reaction in selected genotypes of cucumber confirmed by artificial screening was in accordance with disease reaction under natural conditions. Resistant genotype IIHR-438 (14.3 PDI) and *Cucumis metuliferus* L. (12.8 PDI) had least average PDI as compared to susceptible check Swarna Agethi (58.00 PDI) under artificial condition. Screened of genotypes under field conditions, none of genotypes were found to be immune to downy mildew. Wherein the genotype, IIHR-438 and wild cucumber (*Cucumis metuliferus* L.) were found resistant to downy mildew disease.

Metwally *et al.* (2015) evaluated 133 such accessions for downy mildew resistance under natural field epidemics. Mean ratings for downy mildew leaf damage ranged from 1 to 9 on a 0 to 9 scale found most resistant PI accessions were PI 432870, PI 432873, PI 432878, PI 432884, and PI 432886 with a rating of 1. The most

susceptible PI accessions were Ames 7736, PI 211979, PI 288991, PI 288992 and PI 289698 with a rating of 9. The five most resistant and five most susceptible accessions were further evaluated in replicated experiments during the summer 2014. Results from the repeated test confirmed the results from the first screening. No PI accession was found immune to downy mildew. However, high levels of resistance were observed in several PI accessions.

Call *et al.* (2012) screened 1300 cultigens and found most resistant cultigens over all environments were PI 605996, PI 330628 and PI 197088. Cultigens have been found that significantly outperform checks in all resistance traits.

4.6 Analysis of molecular diversity in cucumber

Molecular marker technology provides information that can help to define the distinctiveness of germplasm and their ranking according to the number of close relatives and their polygenetic position. It is a complementary approach for genetic characterization. The present study was aimed to analyse diversity among thirty six cucumber lines using SSR molecular marker.

4.6.1 PCR optimization and primer screening

The polymerase chain reaction (PCR) amplification procedure was optimized by determining the most appropriate concentration of DNA template, Taq DNA polymerase and Mg⁺⁺ ion required to generate repeatable PCR amplification profiles. The random primers suitable for generation of polymorphic amplification profile among the genotypes of cucumber were identified by the screening of ten SSR primers. All thirty six genotypes were scored manually. Bands were recorded as present (1) or absent (0) across the lane. Very thin or faint bands were not considered for final scoring as these were inconsistent.

4.6.2 SSR amplification

SSR amplification of DNA extracted from thirty six genotypes was done with ten SSR primers for their molecular marker characterization and to establish distinctiveness among them. The PCR products run on agarose gel were scored manually. The amplification profile generated by each primer was compared and the relative molecular size of each band was examined by comparing with DNA size marker.

Ten SSR primers used for study and out of ten primers, six primers generated polymorphic bands. Total 17 bands amplified by 6 SSR primers in the thirty six cucumber genotypes of which polymorphic and monomorphic bands were 13 and 4, respectively. The range of amplified products was 150-400bp approximately (Table 4.26).

The number of SSR alleles scored, polymorphic information content observed for each primer in thirty six genotypes are presented in Table 4.26. The number of alleles per locus varied from two (SSR 13262, SSR 52, SSR 54, SSR 60, and SSR 61) to three (SSR 69). Average number of bands per primer was 2.16. Polymorphism was observed 100 per cent. Polymorphic information content (PIC) expresses the ability of a locus to discriminate between the parental lines at genome level. The PIC values of SSR markers ranged from 0.26 (SSR 52) to 0.55 (SSR 13262) with mean value of 0.37 (Table 4.26), in which marker, SSR 52 was least informative while marker, SSR 13262 was most informative due to highest PIC value among other markers, therefore this type of marker system could be efficiently applied to detect polymorphism in cucumber. The markers namely SSR 60 (0.38), SSR 61 (0.47) SSR 13262 (0.55), had PIC values more than average value, therefore, these markers could be classified as good marker for detecting molecular polymorphism among the cucumber genotypes. Similar PIC were also observed in Indian cucumber accessions (0.31 by Pandey *et al.* 2013), (0.33 by Dar *et al.*, 2017) and Chinese cucumber (0.39 by Hua *et al.*, 2010). Valcarcel *et al.* (2018) evaluated seven SSRs which showed a polymorphic information content (PIC) ranging from 0.31 to 0.44.

Kumar *et al.* (2020) observed a total of 171 alleles were amplified with a mean of 2.85 alleles per locus. The polymorphism information content (PIC) varied from 0.05 (UW084478) to 0.59 (UW084186) with a mean value of 0.36. Dar *et al.* (2017) also found polymorphism in cucumber genotypes with primers SSR 54, SSR 60, SSR 61 and SSR 69 they observed polymorphic information content ranged from 0.158 to 0.495 with the mean of 0.333.

A total of ten SSR primers were used in diversity analysis of thirty six genotypes of cucumber. The primer which showed polymorphism was used for characterization of germplasm. The amplification results in cucumber germplasm with individual primers are given below.

4.6.3 Amplification Profile of Markers

The primer wise analysis of SSRs markers has been described on ensuing page along with some amplification profiles.

SSR 13262

This primer paired revealed two amplified SSR loci. The size of SSR amplicons ranged from 190-200bp. This primer pair gave PIC value of 0.55 and per cent polymorphism was 100 per cent (Plate 4).

SSR 52

This primer paired gave two amplified SSR loci on agarose gel electrophoresis. The size of SSR amplicons ranged from 190-200bp. The primer pair gave PIC value of 0.26 and showed 100 per cent polymorphism (Plate 9).

SSR 54

Primer generated two amplified loci on agarose gel electrophoresis. The size of SSR amplicons ranged from 300-310bp. The primer pair revealed PIC value of 0.30 and 50 per cent polymorphism (Plate 7).

SSR 60

This primer revealed two amplified SSR loci and amplified products shown very less variations in size and very close to 200-210bp in size. Percent polymorphism shown by this primer was 100 percent. The PIC value was 0.38 (Plate 6).

SSR 61

Primer SSR65 amplified two amplified SSR loci on agarose gel electrophoresis. The size of SSR amplicons ranged from 250-360bp. This primer pair showed PIC value of 0.47 and revealed 100 per cent polymorphism (Plate 8).

SSR 69

This primer paired revealed three amplified SSR loci on agarose gel electrophoresis. The size of SSR amplicons ranged from 150-400bp. The primer pair gave PIC value of 0.30 and per cent polymorphism was 100 per cent (Plate 5).

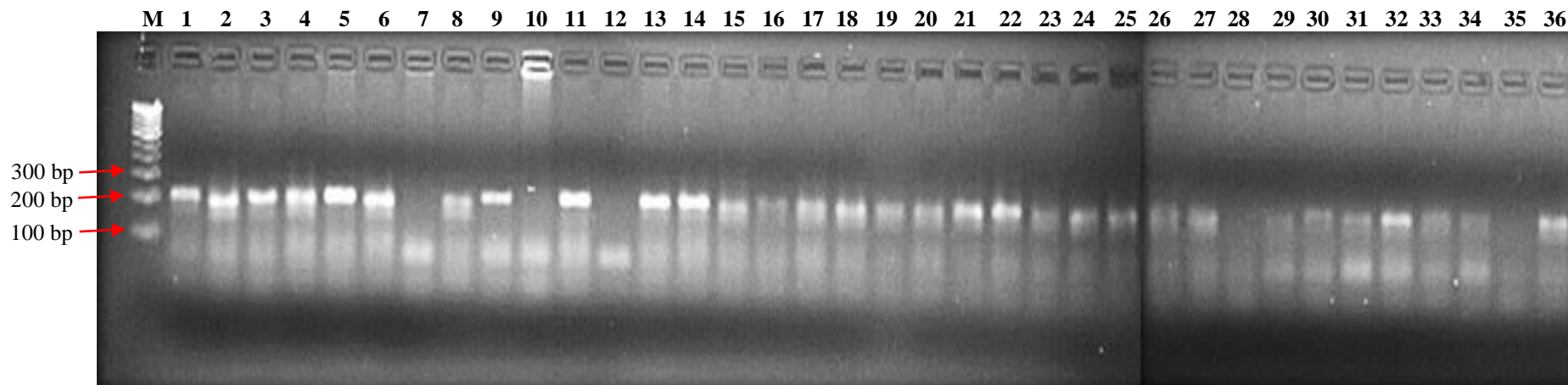


Plate 4: PCR amplification of 36 cucumber genotypes by SSR 13262

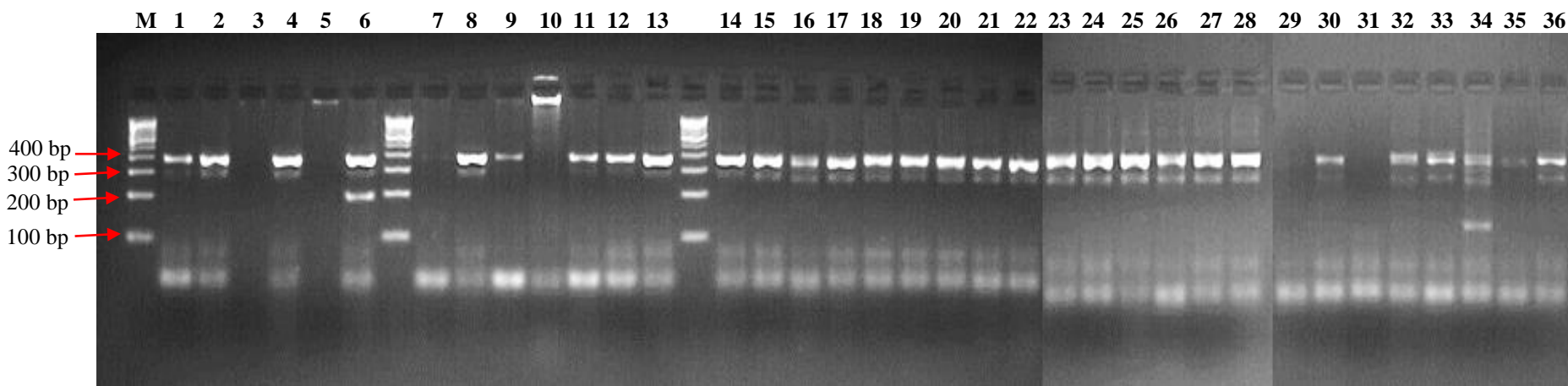


Plate 5: PCR amplification of 36 cucumber genotypes by SSR 69

1- PCPGR-50, 2- PCPGR-51, 3- PCPGR-59, 4- PCPGR-66, 5- PCPGR-112, 6- PCPGR-126, 7- PCPGR-138, 8- PCPGR-149, 9- PCPGR-4, 10- PCPGR-123, 11- PCPGR-25, 12- PCPGR-83, 13- PCPGR-106, 14- PCPGR-199, 15- PCPGR-73, 16- PCPGR-7657, 17- PCPGR-8, 18- PCPGR-478, 19- PCPGR-4273, 20- PCPGR-196, 21- PCPGR-210, 22- PCPGR-87, 23- PCPGR-211, 24- PCPGR-3888, 25- PCPGR-44, 26- PCPGR-264, 27- PCPGR-20, 28- EUC-1-07, 29- PCPGR-36, 30- PCPGR-37, 31- PCPGR-202, 32- PCPGR-55, 33- PCPGR-62, 34- PCPGR-135, 35- PCPGR-160, 36- PCPGR-7566

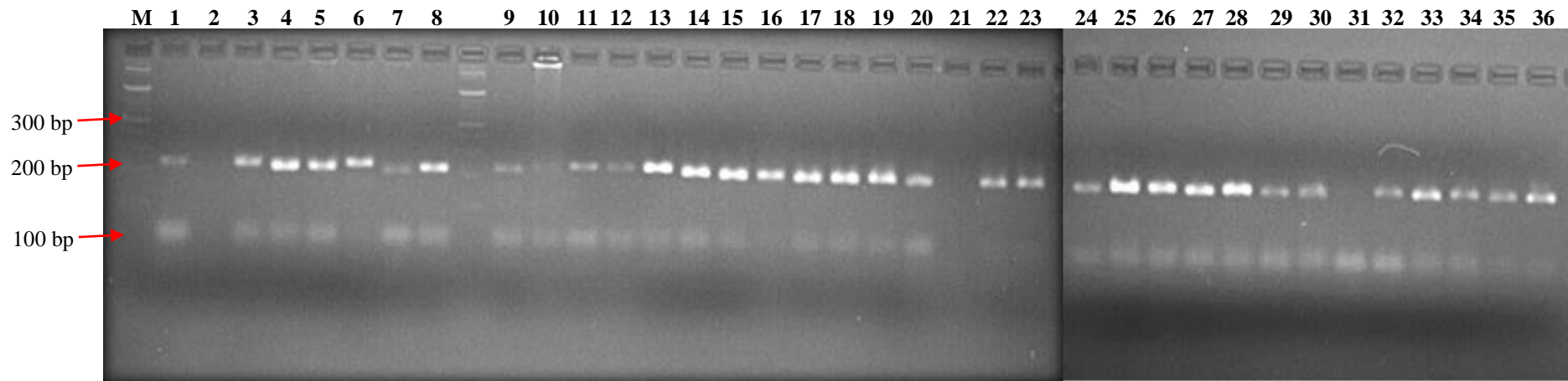


Plate 6: PCR amplification of 36 cucumber genotypes by SSR 60

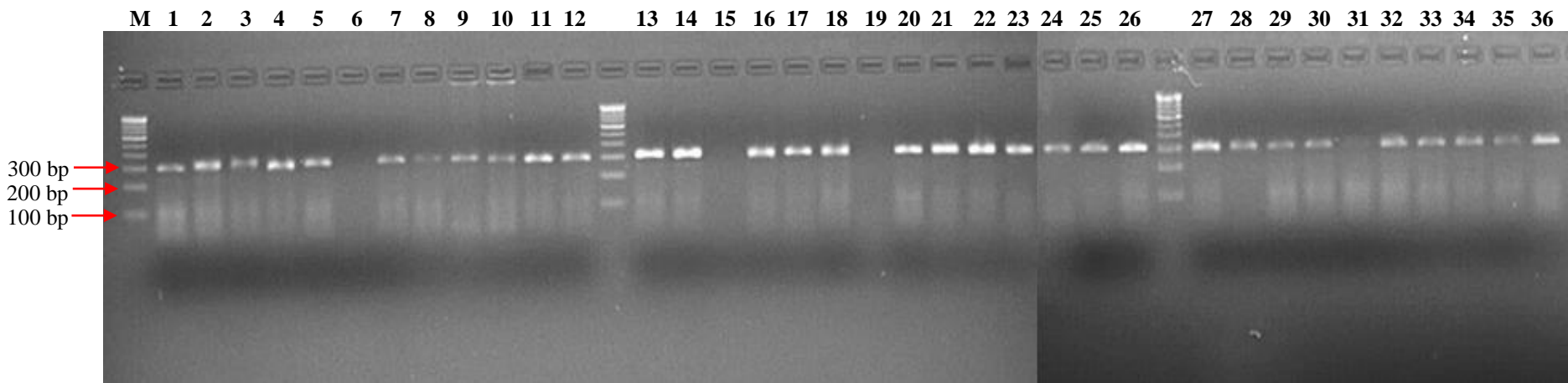


Plate 7: PCR amplification of 36 cucumber genotypes by SSR 54

1- PCPGR-50, 2- PCPGR-51, 3- PCPGR-59, 4- PCPGR-66, 5- PCPGR-112, 6- PCPGR-126, 7- PCPGR-138, 8- PCPGR-149, 9- PCPGR-4, 10- PCPGR-123, 11- PCPGR-25, 12- PCPGR-83, 13- PCPGR-106, 14- PCPGR-199, 15- PCPGR-73, 16- PCPGR-7657, 17- PCPGR-8, 18- PCPGR-478, 19- PCPGR-4273, 20- PCPGR-196, 21- PCPGR-210, 22- PCPGR-87, 23- PCPGR-211, 24- PCPGR-3888, 25- PCPGR-44, 26- PCPGR-264, 27- PCPGR-20, 28- EUC-1-07, 29- PCPGR-36, 30- PCPGR-37, 31- PCPGR-202, 32- PCPGR-55, 33- PCPGR-62, 34- PCPGR-135, 35- PCPGR-160, 36- PCPGR-7566

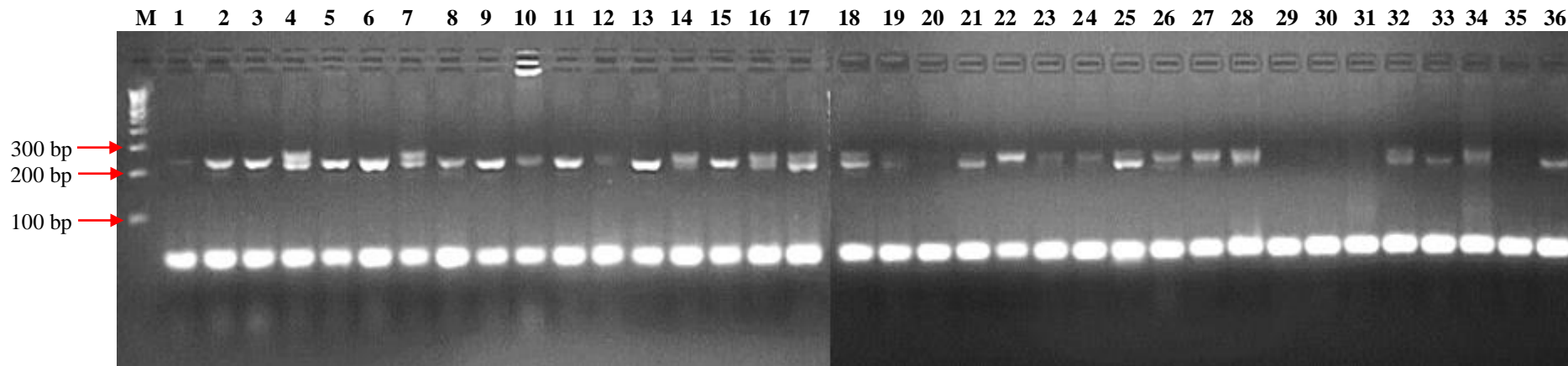


Plate 8: PCR amplification of 36 cucumber genotypes by SSR 61

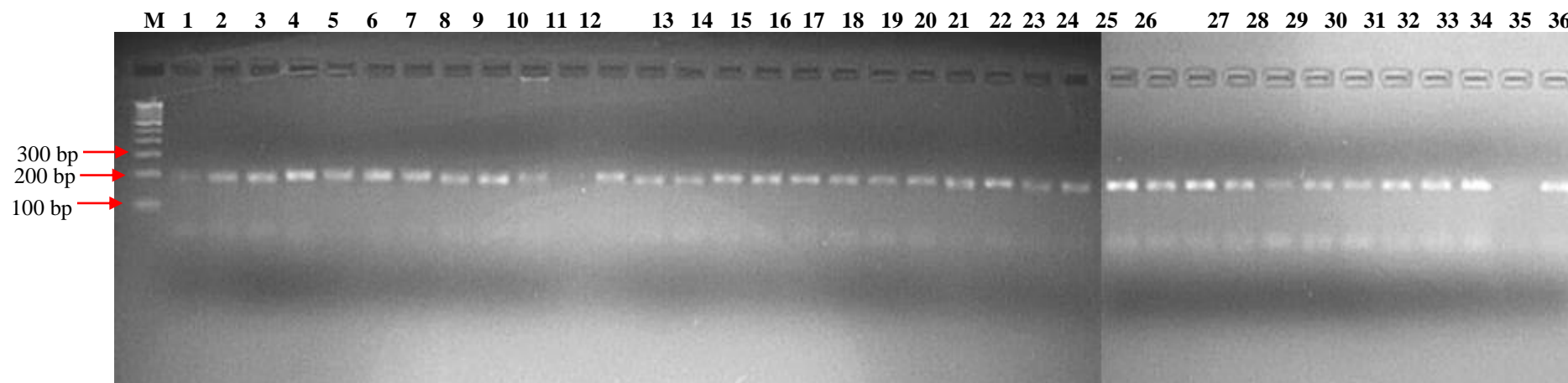


Plate 9: PCR amplification of 36 cucumber genotypes by SSR 52

1- PCPGR-50, 2- PCPGR-51, 3- PCPGR-59, 4- PCPGR-66, 5- PCPGR-112, 6- PCPGR-126, 7- PCPGR-138, 8- PCPGR-149, 9- PCPGR-4, 10- PCPGR-123, 11- PCPGR-25, 12- PCPGR-83, 13- PCPGR-106, 14- PCPGR-199, 15- PCPGR-73, 16- PCPGR-7657, 17- PCPGR-8, 18- PCPGR-478, 19- PCPGR-4273, 20- PCPGR-196, 21- PCPGR-210, 22- PCPGR-87, 23- PCPGR-211, 24- PCPGR-3888, 25- PCPGR-44, 26- PCPGR-264, 27- PCPGR-20, 28- EUC-1-07, 29- PCPGR-36, 30- PCPGR-37, 31- PCPGR-202, 32- PCPGR-55, 33- PCPGR-62, 34- PCPGR-135, 35- PCPGR-160, 36- PCPGR-7566

Table 4.26: Level of polymorphism revealed by ten SSR primers in thirty six genotypes of cucumber

S. N.	Primer code	Amplified product (bp)	Number of alleles amplified	Number polymorphic allele	Percent (%) polymorphism	PIC value
1	SSR13262	190-200	2	2	100.00	0.55
2	SSR52	190-200	2	2	100.00	0.26
3	SSR54	300-310	2	2	100.00	0.30
4	SSR60	200-210	2	2	100.00	0.38
5	SSR61	250-360	2	2	100.00	0.47
6	SSR69	150-400	3	3	100.00	0.30
Total			13	13		
Average			2.16	2.16	100.00	0.37

4.6.4 Genetic diversity analysis using SSR primers

Data scored on thirty six cucumber germplasm with ten microsatellite (SSR) primers were used to generate Jaccard's similarity coefficient presented in Table 4.27. In cucumber germplasm, Jaccard's similarity coefficient varied from 0.45 to 1.00. Minimum Jaccard's similarity coefficient was found in PCPGR-51 with PCPGR-66, PCPGR-196 and PCPGR-106 (0.45). Similar findings were also reported by many researchers in different cucumber genotypes, Pandey *et al.* (2013); Normohamadi *et al.* (2017); Dar *et al.* (2017); Pati *et al.* (2019); Kumar *et al.* (2020).

4.6.5 Cluster analysis based on SSR markers

The phylogenetic tree was constructed through NTSYSpc cluster analysis software using UPGMA (Un-weighted pair group method with arithmetic mean). All thirty six germplasm were demarcated into two major clusters I and II (Fig. 1) at 75 per cent Jaccard's similarity level.

The genotypes of cucumber were separated into major cluster I and II. Cluster I divided into two sub cluster (IA & IB), sub cluster IA comprised four genotypes namely PCPGR-149, PCPGR-112, PCPGR-138 and PCPGR-66 whereas, sub cluster IB contain only one genotype PCPGR-210 and rest of genotypes retained in cluster II. Cluster II was bifurcated into two sub clusters namely cluster IIA and IIB at 83 per cent similarity. Sub cluster IIB consisted of five genotypes namely PCPGR-4273, PCPGR-59, PCPGR-202, PCPGR-73 and PCPGR-51. Sub cluster IIA further divided in to sub cluster IIAa and IIAb at 92 per cent similarity. Sub cluster IIAb consist three genotypes namely PCPGR-160, PCPGR-199 and PCPGR-106 whereas, sub cluster IIAa further divided into subcluster IIAai and IIAaii. subcluster IIAaii contain only one genotypes namely PCPGR-135 whereas, IIAai again divided in to two groups a and b, groups b consist of five genotypes namely PCPGR-478, PCPGR-8, PCPGR-44, PCPGR-55 and PCPGR-7657 whereas, rest of genotypes contain in groups a.

Genetic diversity within a species gives us an important source of variation which could be exploited in crop improvement programme for desirable economically important characters. Under present investigation identified markers are highly informative and are extremely useful in distinguishing the polymorphism rate at a

specific locus in cucumber. Several researchers viz. Pandey *et al.* (2013); Normohamadi *et al.* (2017); Dar *et al.* (2017); Pati *et al.* (2019); Kumar *et al.* (2020) also constructed dendrogram to depict the genetic diversity in cucumber genotypes based on molecular markers.

Table 4.27: Pair wise similarity matrix based upon Jaccard's coefficient for 36 genotypes of cucumber

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36		
1	1.000																																					
2	0.500	1.000																																				
3	0.780	0.800	1.000																																			
4	0.700	0.550	0.580	1.000																																		
5	0.780	0.600	0.670	0.920	1.000																																	
6	1.000	0.750	1.000	0.700	0.780	1.000																																
7	0.570	0.630	0.500	1.000	0.900	0.570	1.000																															
8	0.800	0.640	0.670	0.920	1.000	0.800	0.900	1.000																														
9	1.000	0.780	0.800	0.730	0.800	1.000	0.700	0.820	1.000																													
10	1.000	0.600	0.800	0.900	1.000	1.000	0.880	1.000	1.000	1.000																												
11	1.000	0.710	0.750	0.670	0.750	1.000	0.630	0.780	1.000	1.000	1.000																											
12	1.000	0.600	0.820	0.750	0.820	1.000	0.670	0.830	1.000	1.000	1.000	1.000																										
13	1.000	0.450	0.670	0.620	0.670	0.800	0.500	0.690	0.820	0.800	1.000	0.830	1.000																									
14	1.000	0.450	0.670	0.620	0.670	0.800	0.500	0.690	0.820	0.800	1.000	0.830	1.000	1.000																								
15	1.000	1.000	1.000	0.670	0.750	1.000	0.630	0.780	1.000	1.000	1.000	1.000	0.780	0.780	1.000																							
16	0.900	0.550	0.750	0.850	0.750	0.900	0.800	0.770	0.910	0.900	0.890	0.920	0.770	0.770	0.890	1.000																						
17	0.900	0.550	0.750	0.850	0.750	0.900	0.800	0.770	0.910	0.900	0.890	0.920	0.770	0.770	0.890	1.000	1.000																					
18	0.900	0.550	0.750	0.850	0.750	0.900	0.800	0.770	0.910	0.900	0.890	0.920	0.770	0.770	0.890	1.000	1.000	1.000																				
19	1.000	0.750	1.000	0.700	0.780	1.000	0.570	0.800	1.000	1.000	1.000	1.000	0.800	0.800	1.000	0.900	0.900	0.900	1.000																			
20	1.000	0.600	0.820	0.750	0.820	1.000	0.670	0.830	1.000	1.000	1.000	1.000	0.830	0.830	1.000	0.920	0.920	0.920	1.000	1.000																		
21	0.880	0.450	0.600	0.910	0.800	0.750	0.880	0.820	0.780	0.800	0.710	0.900	0.640	0.640	0.710	0.910	0.910	0.910	0.880	0.900	1.000																	
22	1.000	0.640	0.830	0.770	0.830	1.000	0.700	0.850	1.000	1.000	1.000	1.000	0.850	0.850	1.000	0.920	0.920	0.920	1.000	1.000	0.820	1.000																
23	1.000	0.600	0.820	0.750	0.820	1.000	0.670	0.830	1.000	1.000	1.000	1.000	0.830	0.830	1.000	0.920	0.920	0.920	1.000	1.000	0.900	1.000	1.000															
24	1.000	0.600	0.820	0.750	0.820	1.000	0.670	0.830	1.000	1.000	1.000	1.000	0.830	0.830	1.000	0.920	0.920	0.920	1.000	1.000	0.900	1.000	1.000	1.000														
25	0.900	0.550	0.750	0.850	0.750	0.900	0.800	0.770	0.910	0.900	0.890	0.920	0.770	0.770	0.890	1.000	1.000	1.000	0.900	0.920	0.910	0.920	0.920	0.920	1.000													
26	1.000	0.640	0.830	0.770	0.830	1.000	0.700	0.850	1.000	1.000	1.000	1.000	0.850	0.850	1.000	0.920	0.920	0.920	1.000	1.000	0.820	1.000	1.000	1.000	0.920	1.000												
27	1.000	0.640	0.830	0.770	0.830	1.000	0.700	0.850	1.000	1.000	1.000	1.000	0.850	0.850	1.000	0.920	0.920	0.920	1.000	1.000	0.820	1.000	1.000	1.000	0.920	1.000	1.000											
28	1.000	0.780	0.800	0.730	0.800	1.000	0.700	0.820	1.000	1.000	1.000	1.000	0.820	0.820	1.000	0.910	0.910	0.910	1.000	1.000	0.780	1.000	1.000	1.000	0.910	1.000	1.000	1.000										
29	1.000	0.710	0.780	0.670	0.780	1.000	0.670	0.780	1.000	1.000	1.000	1.000	0.780	0.780	1.000	0.890	0.890	0.890	1.000	1.000	0.880	1.000	1.000	1.000	0.890	1.000	1.000	1.000	1.000									
30	1.000	0.750	0.780	0.700	0.780	1.000	0.670	0.800	1.000	1.000	1.000	1.000	0.800	0.800	1.000	0.900	0.900	0.900	1.000	1.000	0.880	1.000	1.000	1.000	0.900	1.000	1.000	1.000	1.000	1.000								
31	1.000	1.000	1.000	0.800	1.000	1.000	0.800	1.000	1.000	1.000	1.000	1.000	0.600	0.600	1.000	0.800	0.800	0.800	1.000	1.000	0.800	1.000	1.000	1.000	0.800	1.000	1.000	1.000	1.000	1.000	1.000							
32	0.900	0.550	0.750	0.850	0.750	0.900	0.800	0.770	0.910	0.900	0.890	0.920	0.770	0.770	0.890	1.000	1.000	1.000	0.900	0.920	0.910	0.920	0.920	1.000	0.920	0.920	0.910	0.890	0.900	0.800	1.000							
33	1.000	0.780	0.800	0.730	0.800	1.000	0.700	0.820	1.000	1.000	1.000	1.000	0.820	0.820	1.000	0.910	0.910	0.910	1.000	1.000	0.780	1.000	1.000	1.000	0.910	1.000	1.000	1.000	1.000	1.000	1.000	0.910	1.000					
34	0.880	0.670	0.700	0.640	0.700	0.880	0.600	0.730	0.910	0.880	0.890	0.900	0.730	0.730	0.890	0.820	0.820	0.820	0.880	0.900	0.670	0.910	0.900	0.900	0.820	0.910	0.910	0.910	0.890	0.900	0.800	0.820	0.910	1.000				
35	1.000	0.670	0.710	0.630	0.710	1.000	0.570	0.750	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.880	0.880	0.880	1.000	1.000	0.830	1.000	1.000	1.000	0.880	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.880	1.000	0.880	1.000		
36	1.000	0.640	0.830	0.770	0.830	0.100	0.700	0.850	1.000	1.000	1.000	1.000	0.850	0.850	1.000	0.920	0.920	0.920	1.000	1.000	0.820	1.000	1.000	1.000	0.920	1.000	1.000	1.000	1.000	1.000	1.000	0.920	1.000	0.910	1.000	1.000		

1- PCPGR-50, 2- PCPGR-51, 3- PCPGR-59, 4- PCPGR-66, 5- PCPGR-112, 6- PCPGR-126, 7- PCPGR-138, 8- PCPGR-149, 9- PCPGR-4, 10- PCPGR-123, 11- PCPGR-25, 12- PCPGR-83, 13- PCPGR-106, 14- PCPGR-199, 15- PCPGR-73, 16- PCPGR-7657, 17- PCPGR-8, 18- PCPGR-478, 19- PCPGR-4273, 20- PCPGR-196, 21- PCPGR-210, 22- PCPGR-211, 23- PCPGR-211, 24- PCPGR-3888, 25- PCPGR-44, 26- PCPGR-264, 27- PCPGR-20, 28- EUC-1-07, 29- PCPGR-36, 30- PCPGR-37, 31- PCPGR-202, 32- PCPGR-55, 33- PCPGR-62, 34- PCPGR-135, 35- PCPGR-160, 36- PCPGR-7566

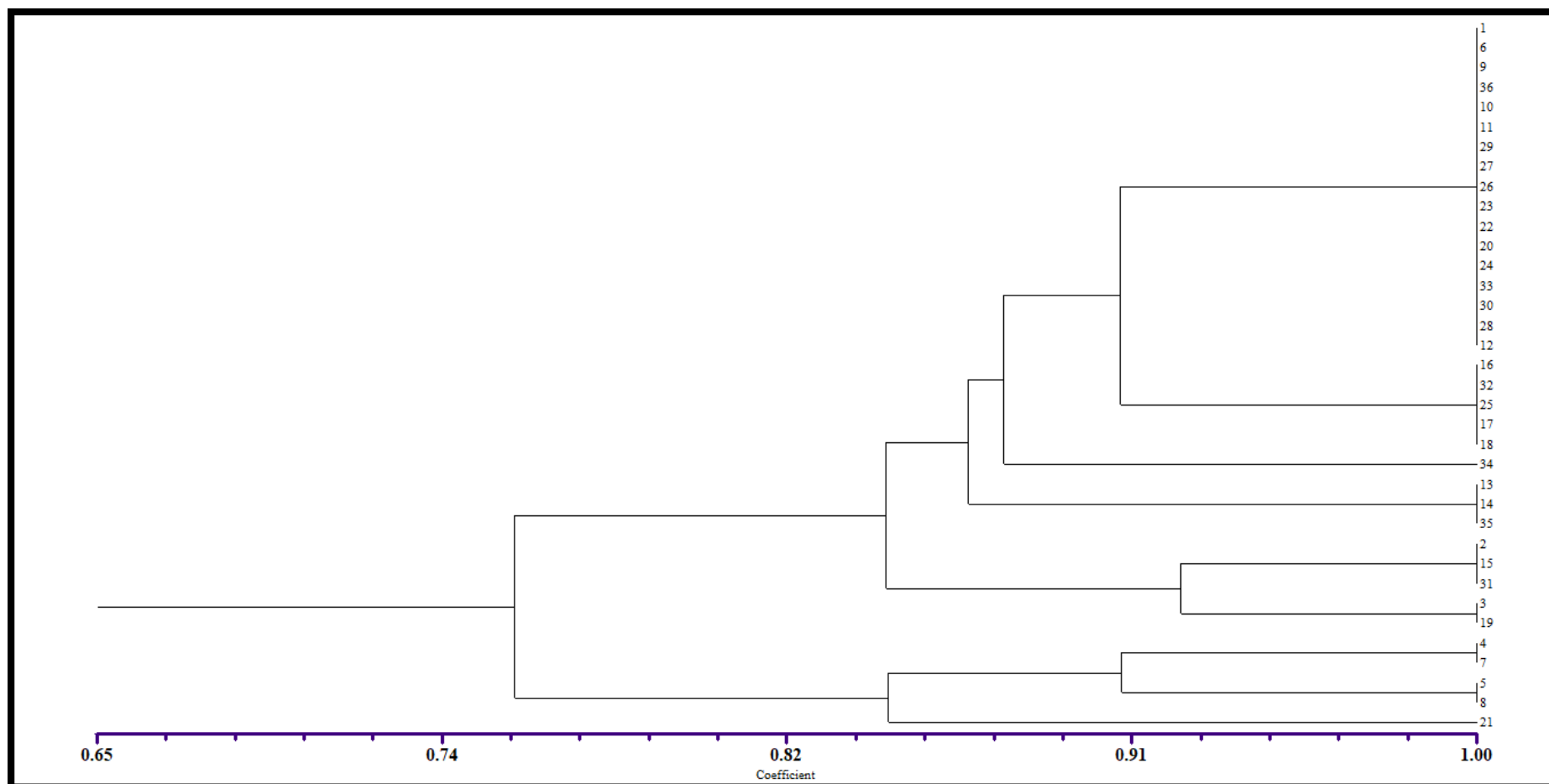


Fig. 1: Dendrogram of Cucumber lines based on the SSR marker data set using UPGMA based on Jaccard's similarity coefficient

1- PCPGR-50, 2- PCPGR-51, 3- PCPGR-59, 4- PCPGR-66, 5- PCPGR-112, 6- PCPGR-126, 7- PCPGR-138, 8- PCPGR-149, 9- PCPGR-4, 10- PCPGR-123, 11- PCPGR-25, 12- PCPGR-83, 13- PCPGR-106, 14- PCPGR-199, 15- PCPGR-73, 16- PCPGR-7657, 17- PCPGR-8, 18- PCPGR-478, 19- PCPGR-4273, 20- PCPGR-196, 21- PCPGR-210, 22- PCPGR-87, 23- PCPGR-211, 24- PCPGR-3888, 25- PCPGR-44, 26- PCPGR-264, 27- PCPGR-20, 28- EUC-1-07, 29- PCPGR-36, 30- PCPGR-37, 31- PCPGR-202, 32- PCPGR-55, 33- PCPGR-62, 34- PCPGR-135, 35- PCPGR-160, 36- PCPGR-7566



*Summary
and
Conclusions*



The present investigation entitled “**Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.)**” was carried out at the Vegetable Research Centre during 2018 - 2020 and molecular diversity work was carried out in the NAIP Laboratory, Department of Vegetable Science, G.B. Pant University of Agriculture and Technology, Pantnagar Uttarakhand, India. The major objectives of the study were to estimate the genetic variability parameters, and determination of heterosis, combining ability, screening for downy mildew disease and molecular diversity analysis in different line of cucumber.

The experimental material for the present study comprised of eight genotypes of cucumber (*Cucumis sativus* L.). All these genotypes were evaluated for yield related traits as well for screening against downy mildew. From the eight genotypes, 28 crosses were developed in a diallel mating design (excluding reciprocals). Thus, the experimental materials finally consisted of 36 treatments (28 F₁ and 8 parents) which were evaluated in a Randomized Block Design (RBD) for heterosis and combining ability studies. The genotypes were studied for fourteen yield related traits *viz.*, days to first male flower, node number to first male flower, days to first female flower, node number to first female flower, days to first harvest, days to last harvest, number of fruits per plant, inter nodal length (cm), plant height (m), fruit length (cm), average fruit diameter (cm), number of fruits per plant, fruit yield per plant (kg) and Fruit yield (q/ha). All parents with resistant check and their hybrids were screened against downy mildew. The data were subjected to appropriate statistical analysis. Further PCR based molecular diversity analysis of thirty six genotypes of cucumber was done using ten SSR markers. The salient finding of the investigation are summarized as follows:

- ✓ The analysis of variance revealed that highly significant genetic differences were present among the cucumber genotypes for all fourteen traits, which clearly indicated that there was enough variability for these traits among the genotypes utilized for the present investigation.

- ✓ Moderate to high mean values among the genotypes for different yield and its contributing traits were observed. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters, indicating the substantial influence of environmental variations on the performance of genotypes. Plant height, average fruit weight, fruit length, average fruit diameter, inter nodal length, days to first male flower, days to last harvest, days to first female flower and days to first harvest were less influenced by environmental factors.
- ✓ Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except days to first male flower, inter nodal length, days to last harvest, days to first female flower, and days to first harvest which indicate that these traits has ample scope for the improvement through selection.
- ✓ In the present study, the extent of heterosis was studied in twenty eight F₁ hybrids of cucumber. For the development of early fruiting genotypes, negative heterosis is desirable namely days to first male flower, days to first female, node number to first male flower, node number to first female flower, days to first harvest and intermodal length. Most of the crosses manifested highly significant heterosis over mid, better parent and standard parent for all the characters under study.
- ✓ For days to first male flower PCPGR-112 × PCPGR-138, for node number to first male flower PCPGR-51 × PCPGR-112, PCPGR-59 × PCPGR-138, PCPGR-50 × PCPGR-138, PCPGR-51 × PCPGR-59 and PCPGR-112 × PCPGR-126, for days to first female flower PCPGR-50 × PCPGR-59 and for node number to first female flower PCPGR-50 × PCPGR-112, PCPGR-50 × PCPGR-149, PCPGR-83 × PCPGR-112 showed desirable significant positive relative heterosis, heterobeltiosis and standard heterosis.
- ✓ For inter nodal length PCPGR-83 × PCPGR-149 exhibited desirable significant negative heterosis over mid parent, better parent and standard check variety. In case of days to first harvest, days to last harvest and plant height none of the hybrid showed desirable significant heterosis over standard check.
- ✓ In case of average fruit diameter PCPGR-50 × PCPGR-138 and PCPGR-51 × PCPGR-138, for number of fruits per plant PCPGR-50 × PCPGR-112, PCPGR-51

× PCPGR-59, PCPGR - 51 × PCPGR-138, PCPGR-59 × PCPGR-138, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-149 and PCPGR-138 × PCPGR-149, average fruit weight PCPGR-50 × PCPGR-59, PCPGR-50 × PCPGR-126, PCPGR-50 × PCPGR-138, PCPGR-51 × PCPGR-112, PCPGR-51 × PCPGR-138, PCPGR-59 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126, PCPGR-112 × PCPGR-138, PCPGR-112 × PCPGR-149 and PCPGR-126 × PCPGR-149 exhibited desirable significant positive relative heterosis heterobeltiosis and standard check variety.

- ✓ Desirable significant positive heterosis over mid parent, better parent and over check variety for fruit yield per plant and fruit yield per hectare was observed in F₁ hybrid crosses namely PCPGR-50 × PCPGR-59, PCPGR-50 × PCPGR-112, PCPGR-50 × PCPGR-138, PCPGR-51 × PCPGR-59, PCPGR-51 × PCPGR-112, PCPGR-51 × PCPGR-138, PCPGR-59 × PCPGR-112, PCPGR - 59 × PCPGR-138, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-138, PCPGR-112 × PCPGR-149, and PCPGR-138 × PCPGR-149.
- ✓ PCPGR-112 was found as a best general combiner for maximum number of traits viz., days to first male flower, node number to first male flower, days to first female flower, node to first female flower, days to first harvest, average fruit diameter, number of fruits per plant, average fruit weight, fruit yield per plant and fruit yield per hectare followed by PCPGR-59 (node number to first male flower, node number to first female flower, plant height, average fruit weight, fruit yield per plant, and fruit yield per hectare. PCPGR-138 (For days to first male flower, number of fruits per plant, fruit yield per plant, and fruit yield per hectare), PCPGR-51 (for days to last harvest, internodal length, plant height and number of fruits per plant) and PCPGR-50 (for average fruit weight and fruit yield per hectare).
- ✓ Best specific combiner were PCPGR-50 × PCPGR-59 (for days to first male flower, days to first female flower, days to first harvest, average fruit weight, fruit yield per plant and fruit yield per hectare), PCPGR-51 × PCPGR-59 (for days to first male flower, node number to first male flower, node number to first female flower and fruit length), PCPGR-138 × PCPGR-149 (for days to first male flower,

number of fruits per plant, fruit yield per plant, and fruit yield per hectare), PCPGR-50 × PCPGR-138 (node number to first male flower, fruit length and average fruit diameter), PCPGR-51 × PCPGR-138 (average fruit weight, fruit yield per plant and fruit yield per hectare), PCPGR-59 × PCPGR-138 (node number to first male flower, fruit length and number of fruits per plant), PCPGR-50 × PCPGR-149 (node number to first female flower, plant height and days to last harvest), PCPGR-83 × PCPGR-112 (number of fruits per plant, fruit yield per plant and fruit yield per hectare), PCPGR-112 × PCPGR-149 (fruit length and average fruit diameter), PCPGR-83 × PCPGR-126 (node number to first female flower and plant height), PCPGR-112 × PCPGR-126 (days to first male flower and node number to first male flower).

- ✓ For downy mildew disease resistant reaction out of all parents and F₁ hybrids only check variety Poinsette exhibited resistant reaction against downy mildew while none of the parents and hybrids showed resistant reaction to downy mildew. Moderately resistance reaction against downy mildew was observed in eight genotypes one of which was parent *viz.*, PCPGR-112 and seven hybrids *viz.*, PCPGR-50 × PCPGR-112, PCPGR-51 × PCPGR-112, PCPGR-59 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126, and PCPGR-112 × PCPGR-138.
- ✓ Ten SSR primers used for molecular diversity study and out of ten primers, six primers generated polymorphic bands. Total 17 bands amplified by 10 SSR primers in the thirty six cucumber genotypes of which polymorphic and monomorphic bands were 13 and 4, respectively. The range of amplified products was 150-400bp approximately.
- ✓ A range of polymorphism was observed 100 per cent. The PIC values of SSR markers ranged from 0.26 (SSR 52) to 0.55 (SSR 13262) with mean value of 0.37. Primer SSR 52 was least informative while marker, SSR 13262 was most informative due to highest PIC value among other markers, therefore this type of marker system could be efficiently applied to detect polymorphism in cucumber. The markers namely SSR 60 (0.38), SSR 61 (0.47) SSR 13262 (0.55), had PIC values more than average value, therefore, these markers could be classified as

good marker for detecting molecular polymorphism among the cucumber genotypes.

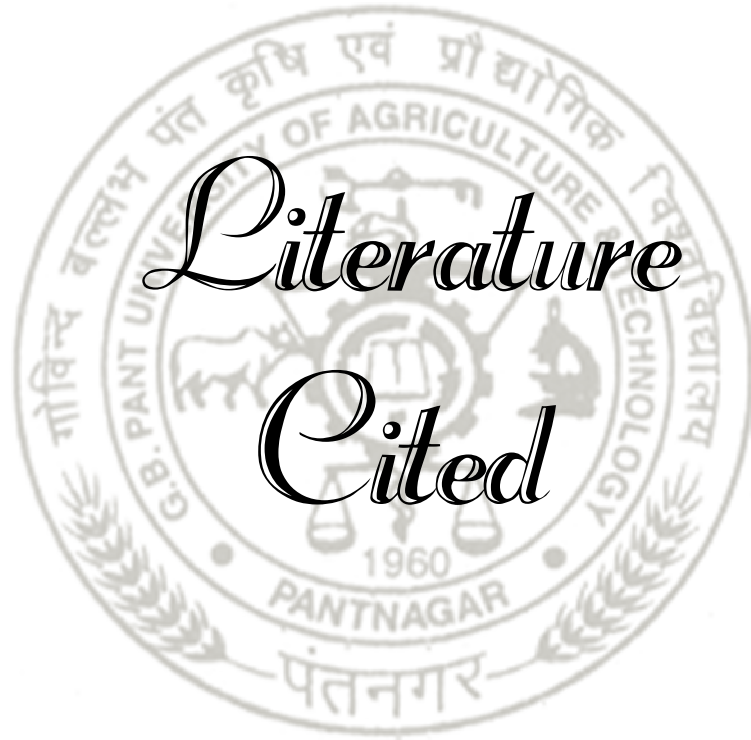
- ✓ Jaccard's similarity coefficient varied from 0.45 to 1.00. Minimum Jaccard's similarity coefficient was found in PCPGR-51 with PCPGR-83, PCPGR-106 and PCPGR-196 (0.45).

CONCLUSION:

According to findings of present investigation, it can be concluded that sufficient quantum of genetic variability was generated involving diverse genotypes of cucumber, which indicates the existence of considerable scope for the improvement of these genotypes through selection and hybridization. Furthermore, moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except characters related to earliness which indicated that these characters were less influenced by environmental factors thus these traits has ample scope for the improvement of concerned traits through selection.

PCPGR-112 was identified as a best general combiner for maximum number traits followed by PCPGR-59 and PCPGR-138. Thus, these parents could be used for the development of superior varieties suitable for most of the yield related traits. The best specific combiner were PCPGR-50 × PCPGR-59 followed by PCPGR-51 × PCPGR-59 and PCPGR-138 × PCPGR-149 for most of the yield and its contributing traits. Hence, these crosses can be utilized in heterosis breeding for improvement in yield related traits.

It is concluded that three cross combinations namely PCPGR-50 × PCPGR-59, PCPGR-51 × PCPGR-138 and PCPGR-138 × PCPGR-149 (Plate 5) have significant positive heterosis for maximum numbers of traits including yield over standard check and showed their value in combining ability studies. Therefore, these cross combinations can be commercially exploited for hybrid development after multi location testing.



*Literature
Cited*



LITERATURE CITED

- Adato, A., Sharon, D., Lavi, U., Hillel, J. and Gazit, S. 1995.** Application of DNA fingerprints for identification and genetic analyses of mango (*Mangifera indica*) genotypes. *J. Am. Soc. Hortic. Sci.*, 120(2): 259-264.
- Afangideh, U. and Uyoh, E. A. 2007.** Genetic variability and correlation studies in some varieties of cucumber (*Cucumis sativus* L.). *Jordan J. Agric. Sci.*, 3(4): 376-384.
- Airina, C. K., Pradeepkumar, T. and Krishnan, S. 2017.** Combining ability studies exploiting gynoecy in cucumber (*Cucumis sativus* L.). *Electron. J. Plant Breed.*, 8(2): 724-731.
- Airina, C. K., Pradeepkumar, T., George, T. E., Sathankumar, P. G. and Krishnan, S. 2013.** Heterosis breeding exploiting gynoecy in cucumber (*Cucumis sativus* L.). *J. Trop. Agric.*, 51(1-2): 144-148.
- Al-Araby, A. A., Ahmed, M. E., Omran, S. A. and Aboshanady, A. M. 2019.** Heterosis and combining ability in cucumber (*Cucumis sativus* L.) Using line × tester analysis. *Egypt. J. Plant Breed.*, 23(6): 1169-1194.
- Alcazar, E. J. T. and Gulick, P. J. 1983.** Genetic resources of Cucurbitaceae-A Global report, Rome, International Board for Plant Genetic Resources, Rome. 101p.
- Allard, R. W. 1960.** Principles of Plant breeding. Welley and Sons Inc. New York., 254p.
- Anantham, M. and Pappiah, C. M. 1997.** Combining ability and correlation studies in cucumber (*Cucumis sativus* L.). *South Indian Hortic.*, 45(1-2):57-58.
- Bains, S. S. and Jhooty, J. S. 1976.** Overwintering of *Pseudoperonospora cubensis* causing downy mildew of muskmelon. *Indian Phytopathol.*, 29: 213-214.
- Bairagi, S. K., Ram, H. H. and Singh, D. K. 2013.** Analysis of combining ability in cucumber (*Cucumis sativus* L.) through half diallel mating system. *Ann. Hortic.*, 6: 308-314.

- Bairagi, S. K., Ram, H. H., Singh, D. K. and Maurya, S. K. 2005.** Exploitation of hybrid vigour for yield and attributing traits in cucumber. *Indian J. Hortic.*, 62(1): 41-45.
- Bairagi, S. K., Singh, D. K. and Ram, H. H. 2001.** Diallel analysis of combining ability in cucumber (*Cucumis sativus* L.). *Progress. Hortic.*, 33(2): 178-183.
- Bairagi, S. K., Singh, D. K. and Ram, H. H. 2002.** Studies on heterosis for yield attributes in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 29: 75-77.
- Balliu, A., Hallidri, M., Katzir, N. and Paris, H. S. 2000.** Combining ability test between some lines of *Cucumis sativus* L. Cucurbitaceae. Proceeding of the 7th EUCARPIA meeting on cucurbit Hamisha. Israel. *Acta Hortic.*, 510: 263-268.
- Baranwal, S. 1995.** Studies on combining ability and heterosis in cucumber (*Cucumis sativus* L.) M.Sc.Ag. thesis submitted to G.B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand (India).
- Barnes, W. C. and Epps, W. M. 1954.** An unreported type of resistance to cucumber downy mildew. *Plant Dis. Rep.*, 38: 620.
- Basavarajeshwari, Mulge R., Nagaraja, K. S., Srikant, L. G., Mahamad, T. H. N., Raveendra, Y. C. and Gowda, H. V. 2014.** Genetic variability, heritability and genetic advance for yield and yield parameters and fruit and seed quality parameters in cucumber (*Cucumis sativus* L.). *Trends Biosci.*, 7: 1965-1967.
- Berkeley, M. S., and Curtis, A. 1868.** *Peronospora cubensis*. *Bot. J. Linn. Soc.*, 10: 363p.
- Bhat, N. A., Masoodi, S. D., Ahmad, M. and Zargar, M. Y. 2007.** Occurrence and severity of angular leaf spot of cucumber in Kashmir. *Ann. Plant Prot. Sci.*, 15(2): 410-413.
- Bhatnagar, M. 1998.** Heterosis and combining ability in cucumber (*Cucumis sativus* L.) M.Sc.Ag. Thesis submitted to G.B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand (India).
- Bhutia, T. L., Munshi, A. D., Behera, T. K., Sureja, A. K., Lal, S. K. and Seyie, A. 2018.** Estimates of heterosis for yield and its contributing traits in cucumber. *Indian J. Hortic.*, 75(2): 332-336.

- Bommesh, J. C., Pitchaimuthu, M., Sadashiva, A. T., Sriram, S., Varalakshmi, B. and Ravishankar, K. V. 2018.** Identification and confirmation of downy mildew (*Pseudoperonospora cubensis* Berk. & Curt.) resistance sources in cucumber (*Cucumis sativus* L.). *Indian Phytopathol.*, 71(3): 337-348.
- 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.
- Burton, G. W. and Devane, E. M. 1953.** Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, 45: 478-481.
- Call, A. D., Criswell, A. D., Wehner, T. C., Ando, K. and Grumet, R. 2012.** Resistance of cucumber cultivars to a new strain of cucurbit downy mildew. *Hortic. Sci.*, 47(2): 171-178.
- Call, A. D., Criswell, A. D., Wehner, T. C., Klosinska and Kozik, E. U. 2012.** Screening of cucumber for resistance to Downy Mildew caused by *Pseudoperonospora cubensis* (Berk. and Curt.) Rostov. *Crop Sci.*, 52: 577-592.
- Cavagnaro, P. F., Senalik, D. A., Yang, L., Simon, P. W., Harkins, T. T., Kodira, C. D. and Weng, Y. 2010.** Genome-wide characterization of simple sequence repeats in cucumber (*Cucumis sativus* L.). *BMC genomics*, 11(1): 1-18.
- Chikezie, O. E., Peter, E. O., Christian, U. A. and Uche, P. 2016.** Evaluation of sixteen cucumber (*Cucumis sativus* L.) genotypes derived in savannah environment using path coefficient analysis. *Not. Sci. Biol.*, 8(1): 85-92.
- Chirani, J. O., Peyvast, G., Lahiji, H. S., Rabiei, B. and Khodaparast, S. A. 2011.** General yield and specific combining ability and heterosis of some cucumber lines in partial diallel design. *Iranian J. Hortic. Sci.*, 42(1): 53-64.
- Choudhary, H. and Singh, D. K. 2010.** Breeding potential of Indian germplasm of *Cucumis sativus* var. *hardwickii* for cucumber improvement. *Acta Hort.*, 871: 409-416.
- Choudhary, M. L., Joshi, S. and Singh, A. 1985.** Genetic studies in cucumber (*Cucumis sativus* L.). *Progress. Hortic.*, 17(3): 236-240.

- Cizove, S. L. 1945.** Yield of hybrid cucumbers in glass house. *Proc. Sci. Conf. Timirja Zeo. Agric. Acad.* 1: 42-43.
- Cohen, Y. 1977.** The combined effects of temperature, leaf wetness and inoculum concentration on infection of cucumbers with *Pseudoperonospora cubensis*. *Canad. J. Bot.*, 55: 1478-1487.
- Danin-Poleg, Y., Reis, N., Tzuri, G. and Katzir, N. 2000.** Development and characterization of microsatellite markers in *Cucumis*. *Theor. Appl. Genet.*, 96: 950-956.
- Dar, A. A., Mahajan, R., Lay, P. and Sharma, S. 2017.** Genetic diversity and population structure of *Cucumis sativus* L. by using SSR markers. *Biotech.*, 7(5): 1-12.
- Das, S., Choudhary, D. N. and Maurya, K. R. 2005.** Genotype × environment interaction studies in cucumber. *Harya. J. Hortic. Sci.*, 34(1-2): 122-124.
- De Candolle, A. 1882.** Origin of cultivated plants. Hafnar Publishing Co, New York, pp. 264-267.
- Dogra, B. S. and Kanwar, M. S. 2011.** Exploitation of combining ability in cucumber (*Cucumis sativus* L.). *Res. J. Agric. Sci.*, 2(1): 55-59.
- Dogra, B. S. and Kanwar, M. S. 2011.** Exploiting for yield and horticultural traits in cucumber (*Cucumis sativus* L.). *Indian J. Plant Gen. Res.*, 24: 332-339.
- Dogra, B. S., Rastogi, K. B., Kahli, V. K. and Sharma, H. R. 1997.** Studies on combining ability in cucumber (*Cucumis sativus* L.). *Ann. Agric. Res.*, 18(4): 559-560.
- Doyle, J. J. and Doyle, J. L. 1990.** Isolation of plant DNA from fresh tissue. *Focus*, 12: 13-15.
- Ene, C. O., Ogonna, P. E., Agbo, C. U and Chukwudi, U. P. 2019.** Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *Inf. Process. Agric.*, 6(1): 150-157.
- Falconer, D. S., Gauld, I. K., Roberts, R. C. and Williams, D. A. 1981.** The control of body size in mouse chimaeras. *Genet. Res.*, 38: 25-46.

- Fang, G. X., Ping, Z. S. and Qing, X. C. 2004.** Analysis of combining ability of early-yield and total-yield character of cucumber cultivated in open field in spring. *China Veg.*, 6: 13-15.
- FAOSTAT. 2018.** FAO statistical database. Food and Agriculture Organization, Rome. Assessed online on 27-01-2021. <http://www.fao.org>
- Fazio, G., Staub, J. E. and Chung, S. M. 2002.** Development and characterization of PCR marker in cucumber. *J. Am. Soc. Hortic. Sci.*, 127: 545-557.
- Fonesca, A. and Patterson, F. L. 1968.** Hybrid vigour in a seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Sci.*, 8: 85-88.
- Franco, L., Crossa, J., Rhauf, J. M., Betran, J., Warhurton, M. J. and Khairallah, M. 2001.** A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. *Theor. Appl. Genet.*, 103: 944-952.
- Gaikwad, A. G., Musmade, A. M., Dlrupal, S. S. and Sonawane, H. G. 2011.** Variability studies in cucumber (*Cucumis sativus* L.). *Ecol. Environ. Conserv.*, 17: 799-802.
- Galton, F. 1889.** Co-relations and their measurement, chiefly from anthropometric data. *Proc. Roy. Soc. London*, 45: 135-145.
- Gilbert, N. 1967.** Additive combining abilities fitted to plant breeding data. *Biometrics*. 23: 45-50.
- Godoy, A. R., Higuti, A. R. O. and Cardoso, A. I. I. 2008.** Yield and heterosis in cucumber inbred lines crosses. *Bragantia*, 67(4): 839-844.
- Golabadi, M., Golkar, P. and Eghtedarv, A. R. 2012.** Assessment of genetic variation in cucumber (*Cucumis sativus* L.) genotypes. *Eur. J. Exp. Biol.*, 2(3): 826-831.
- Golabadi, M., Golkar, P. and Eghtedary, A. R. 2015.** Combining ability analysis of fruit yield and morphological traits in greenhouse cucumber (*Cucumis sativus* L.). *Canad. J. Plant Sci.*, 95(2): 377-385.
- Griffing, B. 1956.** Concept of general and specific combining ability in relation to diallel crossings systems. *Aust. J. Biol. Sci.*, 10: 463-493.

- Gulam-ud-Din., Ahmed, N., Narayan, R., Nazir, G. and Hussain, K. 2006.** Variability studies in cucumber. *Haryan. J. Hortic. Sci.*, 35(3-4): 297-298.
- Hanchinamani, C. N. and Patil, M. G. 2009.** Combining ability through line × tester analysis in cucumber (*Cucumis sativus* L.). *Asian J. Hortic.*, 4(1): 70-73.
- Hanchinamani, C. N. and Patil, M. G. 2009.** Heterosis in cucumber (*Cucumis sativus* L.). *Asian J. Hortic.*, 4(1): 21-24.
- Hanchinamani, C. N., Patil, M. G., Dharmatti, P. R. and Mokashi, A. N. 2008.** Studies on variability in cucumber (*Cucumis sativus* L.). *Crop Res.*, 36(1&3): 273-276.
- Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956.** Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.*, 48(6): 268-272.
- Hayes, H. D. and Footer, C. A. 1976.** Heterosis in self-pollinated crops with particular reference to barley, pp. 239-256.
- Hayes, H. K., Immer, I. R. and Smith, D. C. 1956.** Methods of plant breeding. New York, McGraw Hill Company Inc. 535p.
- Hays, H. K. and Jones, D. F. 1916.** First generation crosses in cucumber. *Ann. Rep. Connect. Agric. Exp. Sta.*, pp. 319-322.
- Hector, V., Randall, T. H. and Fukuda, S. 1993.** Vegetable Gardening guide. *J. Uni. Hawaii Coop. Exten. Ser.*, 16: 23-48.
- Horinuzdi, S. G. and More, T. A. 1989.** Studies on heterosis combining ability in cucumber. *Indian J. Genet. Plant Breed.*, 49: 161-165.
- Hossain, M. F., Rabbani, M. G., Hakim, M. A., Amanullah, A. S. M. and Ahsanullah, A. S. M. 2010.** Study on variability character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh Res. Pub. J.*, 4(3): 297-311.
- Huang, S., Li Zhang, Z., Li, L., Gu, X., Fan, W., Lucas, W.J., Wang, X., Xie, B., Ni, P. and Ren, Y. 2009.** The genome of the cucumber, *Cucumis sativus* L. *Nat. Genet.*, 41: 1275-1281.

- Innark, P., Ratanachan, T., Khanobdee, C., Samipak, S. and Jantasuriyarat, C. 2014.** Downy mildew resistant/susceptible cucumber germplasm (*Cucumis sativus* L.) genetic diversity assessment using ISSR markers. *Crop Prot.*, 60: 56-61.
- Jat, G. S., Munshi, A. D., Behera, T. K., Choudhary, H. and Dev, B. 2015.** Exploitation of heterosis in cucumber for earliness, yield and yield components utilizing gynococious lines. *Indian J. Hortic.*, 72: 494-499.
- Jeffrey, C. 1980.** Systematics of the Cucurbitaceae: an overview. *In: Biology and utilization of the Cucurbitaceae.* Cornell University Press, Ithaca, New York, pp. 3-9.
- Jenkins, S. F. and Wehner, T. C. 1983.** A system for the measurement of foliar diseases in cucumbers. *Rep. Cucurbit. Genet. Coop.*, 6: 10-12
- Johnson, H. W., Robinson, H. F. and Comstock, R. S. 1955.** Estimation of genetic and environmental variability in Soyabean. *Agron. J.*, 41: 314-318.
- Joshi, S., Joshi, M. C., Singh, B. and Vishnoi, A. K. 1980.** Genotypic and phenotypic variability in cucumber. *Veg. Sci.*, 8(2): 114-119.
- Kandasamy, R. 2017.** Variability studies in cucumber (*Cucumis sativus* L.) *The Asian J. Hortic.*, 12(1): 84-87.
- Kanobdee, J., Lavapaurya, T., Subhadrabandhu, S. and Srinives, P. 1990.** Combining ability of yield and yield components in pickling cucumber. *Agric. Nat. Resour.*, 24(1): 102-107.
- Karthick, K., Arumugam, T., Rajasree, V., Ganesan, K. N. and Karthikeyan, M. 2019.** Evaluation and assessment of genetic variability of cucumber (*Cucumis sativus* L.) genotypes. *Pharm. Innov. J.*, 8(11): 156-160.
- Karuppaiah, R., Kavitha, and kumar, S. 2002.** Studies on variability, heritability and genetic advance in ridge gourd. *Indian J. Hortic.*, 59(3): 307-312.
- Kaur, K., Dhall, R. K. and Chawala, N. 2016.** Heterosis and combining ability for quality attributing traits in cucumber (*Cucumis sativus* L.). *Agric. Res. J.*, 53: 475-47.

- Kempthorne, O. 1969.** An introduction to genetic statistics. Iowa State University Press, Ames. pp. 89-97.
- Knerr, L. D., Staub, J. E., Holder, D. J., May, B. P. 1989.** Genetic diversity in *Cucumis sativus* L. assessed by at 18 allozyme coding loci. *Theor. Appl. Genet.*, 78: 119-128.
- Krishna Reddy, A. N., Munshi, A. D., Behera, T. K., Sureja, A. K. and Sharma, R. K. 2014.** Studies on combining ability in cucumber. *Indian J Hortic.*, 71: 349-353.
- Kumar, A. 2006.** Studies on heterosis and inheritance of resistance to fruit fly in cucumber (*Cucumis sativus* L.). Ph.D. Thesis, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan (HP). 109p.
- Kumar, A., Kumar, S. and Pal, A. K. 2008.** Genetic variability and characters association for fruit yield and yield traits in cucumber. *Indian J Hortic.*, 65(4): 423-428.
- Kumar, J., Munshi, A. D., Kumar, R. and Sureja, A. K. 2009.** Combining Ability Studies in Cucumber (*Cucumis sativus* L.) under Salinity Condition. *Indian J. Plant Genet. Res.*, 22(3): 221-224.
- Kumar, J., Munshi, A. D., Kumar, R. and Sureja, A. K. 2010.** Studies on heterosis in slicing cucumber. *Indian J Hortic.*, 67(2): 197-201.
- Kumar, J., Munshi, A. D., Kumar, R., Sureja, A. K. and Sharma, R. K. 2013.** Combining ability and its relationship with gene action in slicing cucumber. *Indian J Hortic.*, 70(1): 135-138.
- Kumar, R. and Kumar, S. 2017.** Usefulness of combining ability and gene action studies for parthenocarpic gynoecious hybrid development in cucumber. *J. Hill Agric.*, 8: 158-165.
- Kumar, R. Kumar, S., Kumar D. and Kansal, S. 2018.** Heterosis, combining ability and gene action studies for insect-pest and disease resistance in cucumber. *Electron. J. Plant Breed.*, 9(3): 815-828.

- Kumar, R., Munshi, A., Behera, T., Jat, G., Choudhary, H., Singh, M. and Talukdar, A. 2020.** Genetic diversity of cucumber (*Cucumis sativus*) accessions differing in quantitative traits and microsatellite markers. *Indian J. Agric. Sci.*, 90(11): 2161-2167.
- Kumar, S., Kumar D., Kumar, R., Thakur, K. S. and Singh, D. B. 2013.** Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis Sativus* L.) in North-Western Himalayas. *Univers. J. Plant Sci.*, 1(2): 27-36.
- Kumar, S., Kumar, R., Kumar, D., Gautam, N., Dogra, R. K., Mehta, D. K., Sharma, H. D. and Kansal, H. 2016.** Parthenocarpic gynoecious parental lines of cucumber introduced from Netherlands for developing high-yielding, quality hybrids. *J. Crop Improv.*, 30: 352-369.
- Kumar, S., Kumar, R., Kumar, D., Gautam, N., Singh, N., Prakash, 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.). *N. Z. J. Crop Hortic. Sci.*, 45: 175-190.
- Kumbhar, H. C., Dumbre, A. D. and Patil, H. C. 2005.** Heterosis and combining ability studies in cucumber (*Cucumis sativus* L.). *J. Maharashtra Agric. Univ.*, 30(3): 272-275.
- Kushwaha, M. L., Yadav, L. B. and Maurya R. P. 2011.** Heterobeltiosis and combining ability in cucumber (*Cucumis sativus* L.) under mid hilly areas of Uttarakhand. *Progress. agric.*, 11(1): 103-107.
- Lang, N. T., Xa, T. T. T., Yen, H. P. and Tlii, T. K. 2007.** Genetic divergence analysis on *Cucumis* spp. by RAPD marker. *OmonRice*, 15: 46-53.
- Lebeda, A. 1992.** Susceptibility of accessions of *Cucumis sativus* to *Pseudoperonospora cubensis*. Tests of agrochemicals and cultivars. *Ann. Appl. Biol.*, 120: 102-103.
- Lebeda, A. and Widrlechner, M. P. 2003.** A set of Cucurbitaceae taxa for differentiation of *Pseudoperonospora cubensis* pathotypes. *J. Plant Dis. Prot.*, 110: 337-349.

- Levi, A. and Rowland, L. J. 1997.** Identifying blueberry cultivars and evaluating their genetic relationships using randomly amplified polymorphic DNA (RAPD) and simple sequence repeat-(SSR-) anchored primers. *J. Am. Soc. Hortic. Sci.*, 122(1): 74-78.
- Li, L. L., Xu, Q. and Chen, X. 2005.** Analysis of combining ability on quality characters of pickling cucumber. *China Veg.*, 1: 13-15.
- Lonnquist, J. H. and Gardner, C. O. 1961.** Heterosis in inter-varietal crosses in maize and its implication in breeding procedure. *Crop Sci.*, 1: 179-183.
- Lopez-Sese, A. I. and Staub, J. 2002.** Combining ability analysis of yield components in cucumber. *J. Am. Soc. Hortic. Sci.*, 127(6): 931-937.
- Lower, R.L., Nienhuis, J. and Miller, C. H. 1982.** Gene action and heterosis for yield and vegetative characteristics in a cross between a gynoeocious pickling cucumber inbred and a *Cucumis sativus* var. *harduickii* line. *J. Amer. Soc. Hort. Sci.* 107: 75-82.
- Manish, T., Kumar, R. and Kansal, S. 2019.** Heterosis, combining ability and gene action studies in cucumber for different biotic stresses to developed resistant hybrids. *Genetika*, 51(1): 199-212.
- Manohar, S. H., Murthy, H. N. and Ravishankar, K. V. 2013.** Genetic diversity in a collection of *Cucumis sativus* L. assessed by RAPD and ISSR markers. *J. Plant Biochem. Biotechnol.*, 22: 241-244.
- Mayo, O. 1980.** The theory of plant breeding. Clarendon Press, Oxford, U.K.
- Meglie, V. and Staub, J. E. 1996.** Genetic diversity in cucumber (*Cucumis sativus* L.). II. An evaluation of selected cultivars related between 1846 and 1978. *Genet. Resour. Crop Evol.*, 43: 533-546.
- Mehdi, M. and Khan, F. A. S. 2009.** Variability and character association analysis in cucumber germplasm. *J. Agric. Biol. Res.*, 25(2): 87-91.
- Metwally, E. I. and Rakha, M. T. 2015.** Evaluation of selected *Cucumis sativus* accessions for resistance to *Pseudoperonospora cubensis* in Egypt. *Czech. J. Genet. Plant Breed.*, 51: 68-74.

- Mhameed, S., Sharon, D., Hillel, J., Lahav, E., Kaufman, D. and Lavi, U. 1996.** Level of heterozygosity and mode of inheritance of variable number of tandem repeat loci in avocado. *J. Am. Soc. Hortic. Sci.*, 121(5): 768-772.
- Mule, P. N., Khandelwal, V., Lodam, V. A., Shinde, D. A., Patil, P. P. and Patil, A. B. 2012.** Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *Madras Agric. J.*, 99: 420-423.
- Munshi, A. D., Kumar, R. and Panda, B. 2005.** Heterosis for yield and its component in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 32(2): 133-135.
- Munshi, A. D., Kumar, R. and Panda, B. 2006.** Combining ability in cucumber (*Cucumis sativus* L.). *Indian J. Agric. Sci.*, 76(12): 750-752.
- Munshi, A. D., Panda, B., Behera, T. K., Kumar, R., Bisht, I. S. and Behera, T. K. 2007.** Genetic variability in *Cucumis sativus* var. *hardwickii* R. germplasm. *Cucurbit Genet. Coop.*, 30: 5-10.
- Musmade, A. M. and Kale, P. N. 1986.** Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *Veg. Sci.* 13(1): 60-68.
- Nehe, A. S., Bangar, N. D., Chavan, B. H. and Wattamwar, M. J. 2007.** Heterosis studies in cucumber. *J. Maharashtra Agric. Univ.*, 32(2): 244-246.
- NHB. 2018.** NHB statistical database, National Horticulture Board, Gurugram (India). assessed online on 27-01-2021 <http://www.nhb.gov.in>
- Normohamadi, S., Solouki, M. and Heidari, F. 2017.** Diversity in cucumber genotypes based on morphological traits and SSR molecular-markers. *Biosci. Biotechnol. Res. Asia*, 14: 775-782.
- Olfati, J. A., Peyvast, G., Samizadeh, L. H., Rabie, B. and Khodaparast, S. A. 2013.** General and specific combining ability and heterosis estimation of some cucumber lines for qualitative traits in partial diallel design. *J. Hortic. Sci.*, 26(4): 43-46.
- Olfati, J. A., Samizadeh, H. and Rabiei, B. 2012.** Griffing's methods comparison for general and specific combining ability in cucumber. *Sci. World J.*, 2(4):1-4.

- Om, Y. H., Choi, K. S., Lee, C. H. and Choi, C. I. 1978.** Diallel analysis of several characters in cucumber (*Cucumis sativus* L.). *Korean J. Breed. Sci.*, 10: 44-50.
- Palti, J. 1975.** *Pseudoperonospora cubensis*. Descriptions of pathogenic fungi and bacteria, no. 457. *Commonwealth Mycological Institute*, Kew, England.
- Palti, J. and Cohen, Y. 1980.** Downy mildew of cucurbits (*Pseudoperonospora cubensis*). The fungus and its hosts, distribution, epidemiology and control. *Phytoparasitica*, 8: 109-147. doi:10.1007/BF02994506.
- Pandey, S., Ansaii, W. A., Mishra, V. K., Singh, A. K. and Singh, M. 2013.** Genetic diversity in Indian cucumber based on microsatellite and morphological markers. *Biochem. Syst. Ecol.*, 51: 19-27.
- Pandey, S., Singh, B., Singh, M. and Rai, M. 2005.** Heterosis in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 32: 143-45.
- Panse, V. G. and Sukhatme, P. V. 1967.** Statistical method for Agricultural workers. 4th Edn., ICAR, New Delhi.
- Papadopoulos, A. P. 1994.** Growing greenhouse cucumber in soil and soil-less media. Documentary from Agriculture and Agri-Food Ottawa, Canada, pp. 5-126.
- Parvathaneni, R. K., Natesan, S., Devaraj, A. A., Muthuraja, R., Venkatachalam, R., Subranrani, A. P. and Laxntanan, P. 2011.** Fingerprinting in cucumber and melon (*Cucumis* spp.) genotypes using morphological and ISSR markers. *J. Crop Sci. Biotechnol.*, 14: 39-43.
- Pati, K., Munshi, A. D., Behera, T. K. and Sureja, A. K. 2015.** Gynoecious inbred improves yield and earliness in cucumber. *Indian J. Agric. Sci.*, 85(12): 1609-1613.
- Pati, K., Munshi, A. D., Behera, T. K., Kumar, R. and Karmakar, P. 2015.** Estimating combining ability for yield and yield contributing traits in cucumber. *Indian J. Agric. Sci.*, 72(1): 49-53.
- Pati, K., Munshi, A. D., Verma, M., Behera, T. K. and Arya, L. 2019.** Genetic diversity of cucumber genotypes revealed by SSR markers and agronomic traits. *Genetika*, 51(2): 405-416.

- Phillips, R. L. 1999.** Research needs in heterosis. *In: Coors, J. G. and Pandey, S. (eds.) Genetics and Exploitation of heterosis in crops.* pp. 501-507.
- Prasad, V. S. R. K., Singh, D. P., Rai, M. and Pan, R. S. 2002.** Development of new slicing cucumber cv. Swarna Ageti through genetic architecture. *International Conference on Vegetables*, Bangalore, 113p.
- Quiang, X., Sheng, C. B., Hao, C. X., Xu, Q., Cao, B. S. and Chen, X. H. 1998.** Combining ability and genetic analysis of parthenocarpic yield of cucumbers. *Adv. Horti.* 2: 439-442.
- Rajaguru, K., Arumugam, T., Sassikumar, D. and Jeeva, S. 2020.** Combining ability study for yield and quality traits in cucumber (*Cucumis sativus* L.). *Electron. J. Plant Breed.*, 11(2): 650-655.
- Ranjan, P., Gangopadhyay, K. K., Bag, M. K., Roy, A., Srivastava, R., Bhardwaj, R. and Dutta, M. 2015.** Evaluation of cucumber (*Cucumis sativus* L.) germplasm for agronomic traits and disease resistance and estimation of genetic variability. *Indian J. Agric. Sci.*, 85(2): 234-239.
- Rastogi, K. B. and Arya, D. 1990.** Variability studies in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 17(2): 224-226.
- Reddy, A. N., Munshi, A. D., Behera, T. K., Sureja, A. K. and Sharma, R. K. 2014.** Studies on combining ability in cucumber. *Indian J. Hortic.*, 71(3): 349-353.
- Reddy, N. S. 2002.** Biochemical mechanism of downy mildew resistance in musk melon (*Cucumis melo* L.) caused by *Pseudoperonospora cubensis* (Berk and Curt) Rostow. *M.Sc. thesis, University of Agricultural Sciences*, Bangalore, 21p.
- Reuveni, R. 1983.** Resistance of *Cucumis melo* to *Pseudoperonospora cubensis*. *Ann. Appl. Biol.*, 102: 533-537.
- Robinson, R. W. and Decker-Walters, D. S. 1999.** *Cucurbits*. CAB International, Wallingford, Oxford, UK, 226p.
- Robou, A. M. A. and Hamed, A. A. 2011.** Heterosis and combining ability in cucumber. *Egypt. J. Plant Breed.*, 15: 181-191.

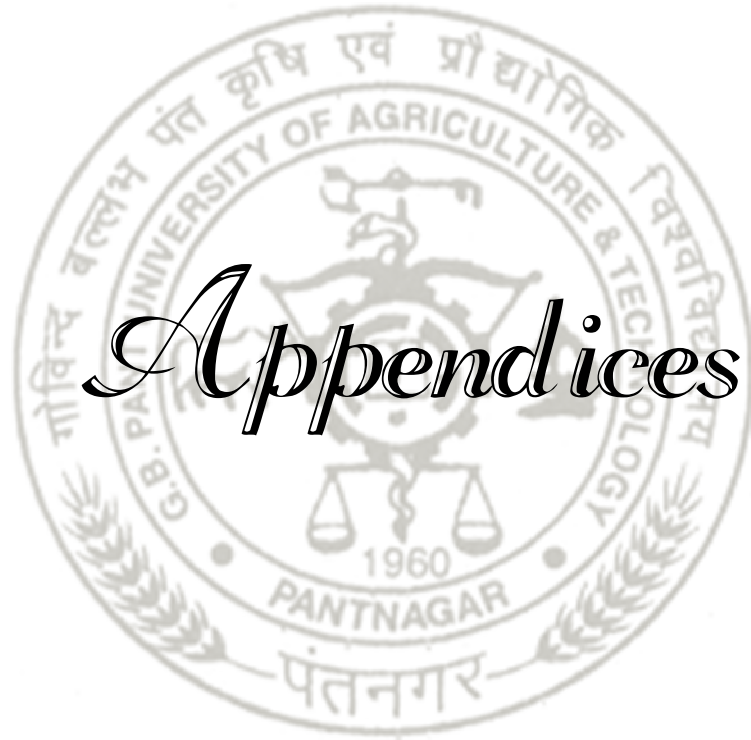
- Roldan-Ruiz, I., Dendauw, J., Van Bockstaele, E., Depicker, A. and De Loose, M. A. F. L. P. 2000.** AFLP markers reveal high polymorphic rates in ryegrasses (*Lolium* spp.). *Mol. Breed.*, 6(2): 125-134.
- Saiki, R. K., Gelfand, D. H., Stoffel, S., Scharf, S. J., Higuchi, R., Horn, G. T and Erlich, H. A. 1988.** Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. *Science*, 239(4839): 487-491.
- Saikia, J., Shadeque, A. and Bora, G. C. 1995.** Genetic studies in cucumber: correlation and path coefficient analysis. *Haryan. J. Hortic. Sci.*, 24(2): 126-130.
- Saikia, J., Shadeque, A. and Bora, G. C. 1995.** Genetic studies in cucumber. *Haryan. J. Hortic. Sci.*, 24(1): 73-76.
- Samant, A. 2014.** Studies on heterosis, combining ability and seed quality parameters in cucumber (*Cucumis sativus* L.). *Ph.D.* dissertation. G. B Pant University of Agriculture and Technology, Pantnagar, Uttarakhand.
- Sarkar, M. and Sirohi, P. S. 2010.** Combining ability analysis for yield and its contributing characters in cucumber. *Indian J. Hortic.*, 64(4): 325-328.
- Sarkar, M. and Sirohi, P. S. 2011.** Exploitation of heterosis in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 38(2): 237-238.
- Savory, E., Gramke, L., Quesada-Ocampo, L., Varbanova, M., Hausbeck, M. and Day, B. 2010.** The Cucurbit Downy Mildew Pathogen *Pseudoperonospora cubensis*. *Mol. Plant Pathol.*, 12: 217-226.
- Sebastian, P., Schaefer, H., Telford, I. R. H. and Renner, S. S. 2010.** Cucumber (*Cucumis sativus*) and melon (*Cucumis melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings of the National Academy of Sciences, USA*, 107: 14269-14273.
- Seshadri, V. S. and Parthasarathy, V. A. 2002.** Cucurbits. *In: Vegetable Crops in India*. TK Bose, J Kabir, TK Maity, VA Parthasarathy and MG Som (eds.). Naya Prakash, Calcutta. 668p.

- Shailaja, P., Singh, D. K., Makanur, B., Singh, N. K. and Pandey, D. T. 2017.** Heterosis studies for yield and yield contributing traits in cucumber (*Cucumis sativus* L.). *Plant Arch.*, 17: 21-27.
- Sharma, A. K., Vidyasagar and Pathania, N. K. 2001.** Studies on combining ability for earliness and marketable fruit yield in cucumber (*Cucumis sativus* L.). *Him. J. Agric. Res.*, 26(1-2): 54-61.
- Shull, G. H. 1948.** What is heterosis. *Genetics*, 33: 439-446.
- Shushir, K. V., Dirnbre, A. D., Patil, H. E., Kanidi, S. R. and Saitwal, V. M. 2005.** Combining ability studies in cucumber. *J. Soil. Crop.*, 15: 72-75.
- Simi, F., Ivy, N. A., Saif, H. B., Akter, S. and Anik, M. F. A. 2017.** Heterosis in cucumber (*Cucumis sativus* L.). *Bangladesh J. Agr. Res.*, 42(4): 731-747.
- Singh, D. K., Tewari, R., Singh, N. K. and Singh, S. S. 2016.** Genetic diversity cucumber using inter simple sequence repeats (ISSR). *Transcriptomics*, 4: 129.
- Singh, G., Brar, P. S. and Dhall, R. K. 2016.** Exploiting yield potential in cucumber (*Cucumis sativus* L.) through heterosis breeding. *Plant Gene Trait*, 7: 1-5.
- Singh, H. K., Pandev, S., Tiwari, A. and Singh, M. C. 2010.** Heterosis and combining ability for yield and contributing traits in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 37: 64-66.
- Singh, R., Singh, A. K., Kumar, S. and Singh, B. K. 2012.** Heterosis and inbreeding depression for fruit characters in cucumber. *Indian J. Hortic.*, 69(2): 200-204.
- Singh, R., Singh, A. K., Kumar, S., Singh, B. K. and Singh, S. P. 2011.** Combining ability studies in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 38: 49-52.
- 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: 47-51.
- Singh, S. K., Singh, S. V. and Srivastava, J. P. 2015.** Studies on heterosis and inbreeding depression in cucumber (*Cucumis sativus* L.). *Agriways*, 3: 107-111.
- Singh, Y. and Sharma, S. 2006.** Combining ability through line x tester analysis in cucumber (*Cucumis sativus* L.). *Crop Res., Hissar*, 31(1): 110-115.

- Solanki, S. S. and Seth, J. N. 1980.** Studies on genetic variability in cucumber. *J. South Indian Hortic.*, 28: 43-49.
- Sprague, G. F. and Tatum, L. A. 1942.** General vs. specific combining ability in single crosses of corn. *Agron. J.*, 34: 923-932.
- Sudhakar, P., Singh, B., Major, S. and Rai, M. 2005.** Heterosis in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 32(2): 143-145.
- Tatlioglu, T. 1993.** Cucumber (*Cucumis sativus* L.). In: Genetic improvement of vegetable crops. G Kalloo and BO Beorgh (eds.). Pergamon Press, Oxford. pp. 197-233.
- Tautz, D. 1989.** Hypervariability of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Res.*, 17(16): 6463-6471.
- Thakur, M., Kumar, R. and Kansal, S. 2019.** Heterosis, combining ability and gene action studies in cucumber for different biotic stresses to developed resistant hybrids. *Genetika*, 51(1): 199-212.
- Tiwari, J. K., Munshi, A. D., Kumari, R., Sharma, R. K. and Sureja, A. K. 2009.** Combining ability for yield and related traits in cucumber (*Cucumis sativus* L.). *Veg. Sci.*, 36(2): 159-162.
- Turner, J. M. 1953.** A study of heterosis in upland cotton II Combining ability and inbreeding effects. *Agron. J.*, 43: 487-490.
- Uddin, G., Ahmed, N., Narayan, R., Nazir, G. and Hussain, K. 2006.** Variability studies in cucumber. *Haryana J. Hortic. Sci.*, 35(3&4): 297-298.
- Uddin, M. N., Hossain, M. M., Rahman, M. M., Ahmad, S. and Quamruzzaman, A. K. M. 2009.** Combining ability and gene action in Cucumber. *SAARC J. Agri.*, 7(1): 64-72.
- Ullah, M. Z., Hasan, M. J., Chowdhuiy, A. Z. M. K. A., Saki, A. I. and Rahman A. H. M. A. 2012.** Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. *Bangladesh J. Plant Breed. Genet.*, 25(1): 17-23.

- Ullah, M. Z., Hasan, M. J., Chowdhury, A. Z. M. K. A., Saki, A. I. and Rahman, A. H. M. A. 2012.** Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. *Bangladesh J. Plant Breed. Genet.*, 25(1): 17-23.
- Uzodike, E. B. and Onuoha, I. N. 2009.** The effect of cucumber (*Cucumis sativus* L.) extract on acid induced corneal burn in Guinea Pigs. *African J.*, 15: 3-7.
- Valcarcel Germes, J. V., Pérez De Castro, A. M., Díez Niclós, M. and Peiró Barber, R. M. 2018.** Molecular characterization of the cucumber (*Cucumis sativus* L.) accessions held at the COMAVs genebank. *Span. J. Agric. Res.*, 16(1): 1-11.
- Vavilov, N. I. 1951.** The origin, variation, immunity and breeding of cultivated plants. *Cronica botanica*, 13(1/6): 36-37.
- Veena, R., Sidhu, A. S., Pitchaimuthu, M. and Souravl, K. 2012.** Genetic evaluation of cucumber (*Cucumis sativus* L.) genotypes for some yield and related traits. *Electron. J. Plant Breed.*, 3: 945-948.
- Verma, T. S., Singh, R. V. and Sharma, S. C. 2000.** Line \times Tester analysis for combining ability in cucumber. *Indian J. Hortic.*, 57(2): 144-147.
- Vidhya, C. and Kumar, S. 2014.** Studies on combining ability in cucumber (*Cucumis sativus* L.). *BioSci. Trend.*, 7: 1891-1892.
- Vijayakumari, P., More, T. A. and Sheshadri, V. S. 1991.** Evaluation of gynoecious F₁ hybrids for horticultural characters in cucumber. *Veg. Sci.*, 81: 167-176.
- Waterhouse, G. and Brothers, M. 1981.** The taxonomy of *Pseudoperonospora cubensis*. *Mycol. Res.*, 148: 1-28.
- Weber, C. R. and Moorthy, H. R. 1952.** Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F₂ generation of soyabean crosses. *Agron. J.*, 44: 202-209.
- Whitehouse, R. N. H., Thompson, J. B. and Ribiero, M. A. M. 1958.** Studies on the breeding of self-pollinated cereals. *Euphytica*, 7: 147-169.

- Yadav, J. R., Singh, S. P., Parihar, N. S., Yadav, J. K., Mishra, G., Kumar S. and Yadav, A. 2007.** Combining ability for yield and its contributing characters in cucumber (*Cucumis sativus* L.). *Progress. Agri.*, 7(1-2): 116-118.
- Yadav, J. R., Singh, S. P., Singh, N. and Singh, P. B. 2008.** Heterosis in cucumber (*Cucumis sativus* L.). *Progress. Res.*, 3(1): 87-88.
- Yadav, Y. C., Kumar, S., Biseu, B. and Dixit, S. K. 2009.** Genetic variability, heritability and genetic advance for some traits in cucumber. *Indian J. Hortic.*, 66(4): 488-491.
- Yeboah, M. A., Xuehao, C., Feng, C. R., Liang, G. and Gu, M. 2007.** A genetic linkage map of cucumber (*Cucumis sativus* L.) combining SRAP and ISSR markers. *Afr. J. Biotechnol.*, 6: 2784-2791.
- Yoshioka, Y., Sugiyama, M. and Sakata, Y. 2010.** Combining ability analysis of fruit texture traits in cucumber by mechanical measurement. *Breed. Sci.*, 60(1): 65-70.
- Yudhvir, S. and Shurma, S. 2006.** Combining ability through line × tester analysis in cucumber. *Crop Res.*, 31(1): 110-115.



Appendices



APPENDICES

APPENDIX - I

Weekly weather data 2018

STATION NAME : PANTNAGAR LONGITUDE : 79 deg. 30' E
 LATITUDE : 29 deg. N ALTITUDE : 243.84 m. AMSL

Month	Date	Metro Week No.	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	No. of Rainy Days	Sun-Shine Hrs.	Wind Velocity (km/hr.)	Evap. (mm)
			Max.	Min.	0712 am	1412 pm					
Jan-Feb	29-04	5	20.6	6.9	94	60	000.0	0	05.8	3.9	1.2
Feb	05-11	6	23.2	5.6	95	50	000.0	0	06.4	5.4	1.8
Feb	12-18	7	23.0	9.2	93	61	004.0	2	06.1	5.3	1.9
Feb	19-25	8	26.9	11.5	89	51	000.0	0	07.7	3.0	2.3
Feb-Mar	26-04	9	28.7	11.5	91	44	000.0	0	07.5	5.6	3.1
Mar	05-11	10	29.5	10.7	92	39	000.0	0	08.8	5.5	4.0
Mar	12-18	11	31.1	11.8	81	44	000.0	0	08.5	4.9	4.3
Mar	19-25	12	31.9	12.7	83	40	000.0	0	09.0	4.6	4.3
Mar-Apr	26-01	13	33.6	14.5	78	47	000.0	0	08.2	5.3	5.8
Apr	02-08	14	33.4	18.7	78	52	029.2	1	08.0	5.2	6.0
Apr	09-15	15	31.3	16.2	81	49	013.0	2	06.4	4.6	4.8
Apr	16-22	16	37.2	17.2	73	19	000.0	0	09.4	6.1	7.4
Apr	23-29	17	36.2	19.5	65	36	000.0	0	09.2	7.1	7.7
Apr-May	30-06	18	35.1	22.0	70	41	002.8	1	09.2	9.6	7.2
May	07-13	19	37.0	21.1	67	32	000.0	0	08.4	7.5	8.3
May	14-20	20	35.6	23.1	76	52	005.8	1	08.4	7.6	7.9
May	21-27	21	39.7	22.5	65	34	000.0	0	09.3	7.8	9.4
May-Jun	28-03	22	35.5	23.0	70	55	038.4	4	07.1	9.6	8.3
Jun	04-10	23	35.1	26.0	82	64	087.6	2	07.7	7.5	8.0
Jun	11-17	24	34.6	26.2	85	63	042.8	2	05.2	5.0	5.7
Jun	18-24	25	37.2	26.1	76	45	000.0	0	07.9	6.0	6.8
Jun-Jul	25-01	26	35.9	26.6	81	68	018.2	1	06.4	7.5	7.3
Jul	02-08	27	32.6	25.4	90	70	180.8	3	06.0	3.5	5.6
Jul	09-15	28	32.5	26.0	88	78	173.2	3	03.1	6.1	4.2
Jul	16-22	29	33.3	26.9	82	73	079.6	2	06.7	3.7	6.6
Jul	23-29	30	31.2	25.7	91	80	169.0	5	02.2	5.6	4.6
Jul-Aug	30-05	31	29.7	24.1	94	84	218.1	7	01.0	2.2	3.5

APPENDIX-II

Reagents for Genomic DNA isolation and PCR amplification

I. Reagents for Genomic DNA isolation

Requirements:

Tris base, EDTA- Na_2 , NaCl, Potassium Acetate, Glacial acetic acid, isopropanol, chloroform, isoamyl alcohol, and Absolute alcohol.

Preparation of solutions:

STOCKS SOLUTIONS:

1. 1M Tris-Cl buffer (pH 8.0), 100 ml

12.114 g Tris-base was dissolved in 80 ml ddw. The pH was adjusted to 8.0 by 6 N HCl. The volume was made upto 100 ml with ddw. Autoclaved and stored at 4°C.

2. 0.5 M EDTA (pH 8.0), 50 ml

9.3 g EDTA- Na_2 was dissolved in 30 ml of ddw (10N NaOH was added to make the pH 8.0). The final vol. was made upto to 50 ml, Autoclaved and stored at 4°C.

3. 10N NaOH, 50 ml

20 g of NaOH was dissolved in 30 ml of autoclaved ddw. The volume was made upto 50 ml. Stored in a plastic bottle at RT.

4. 5 M NaCl, 50 ml

14.6 g NaCl was dissolved in 30 ml of ddw. The final vol. was made upto 50 ml. Autoclaved and stored at RT.

WORKING SOLUTIONS

1. DNA extraction buffer 25 ml

2% (w/v) CTAB	:	0.5 g
100 mM Tris-Cl	:	2.5 ml (1M stock)
1.4 M NaCl	:	2.0475 g
20 mM EDTA	:	1 ml (0.5 M stock)
0.2 % beta mercaptoethanol	:	50 μ l

The final vol. was made upto to 25 ml with ddw.

2. 5 M potassium Acetate (pH 5.4) 50 ml

24.8 g potassium acetate was dissolved in 30 ml of ddw. The pH was adjusted to 5.4 with glacial acetic acid. The final volume was made upto 50 ml with ddw. Autoclaved and stored at RT.

3. Isopropanol : Kept at 0°C.

4. Chloroform: isoamyl alcohol : 24:1, 25 ml

5. 70% ethanol : 10 ml

6. TE Buffer (pH 8.0) 25 ml

10 mM Tris-Cl : 250 µl (1M stock)

1mM EDTA : 50 µl (0.5 M stock)

Volume was made up by adding ddw to 25 ml. Autoclaved and stored at RT.

II. PCR Ingredients

(i) Design and Synthesis of the primers

The most essential requirement of PCR is the availability of short oligonucleotides called primers having sequence complementary to either ends of the target DNA segment called template DNA to be synthesized. The primers used in the study are synthesized from Eurofins, Bangalore

(ii) *Taq* DNA polymerase

Taq DNA polymerase is a thermostable enzyme that replicates DNA at 72-74°C and remains functional even after incubation at 95°C. The enzyme has 5'-3' polymerase and 3'-5' exonuclease activity. The concentration of the enzyme was 3units per µl (3U/µl).

(iii) dNTPs

The dNTPs used in this reaction were obtained from Genei Pvt. Ltd. Bangalore as 10mM each (dATP, dGTP, dCTP, dTTP).

(iv) Assay Buffer (10X)

Assay buffer (10X) contained 10 mM Tris-Cl (pH 9.0), 15 mM MgCl₂, 50 mM KCl and 0.01% gelatin.

III. Running buffer, Dye and Reagents

Running Buffer

0.5 X TBE buffer

Dye

98% formamide, 10mM EDTA, 0.023mg Bromophenol Blue, 0.023mg Xylene Cynol

Reagents used and preparation

1. Electrophoresis buffer (5X)	100ml
Tris base (0.045M)	54 g
Boric acid	27.5g
EDTA (0.001M)	10ml (1M stock)

Components were dissolved in 80ml of de-ionized water. pH was adjusted to 8.0 with 6N. Final volume was made up to 10 ml, autoclaved and stored at 40°C. 0.5X was the working solution of TBE buffer.

2. DNA loading dye (Double Dye)	10ml
Bromophenol Blue (0.25% w/v)	0.025g
Xylenecynol FF (0.25% w/v)	0.025g
Sucrose (40% w/v)	

The components were dissolved in 8.0ml of sterile de-ionized water. pH was adjusted to 8.0 and finally volume was made 10ml. Aliquots were made and stored at -20°C.

3. DNA staining solution and Ethidium Bromide (10000X)

Ethidium Bromide	10ml
Sterile de-ionized water	1ml

Note:

- Working solution for staining gel was made by dissolving 60µl ethidium bromide
- Stock (10mg/ml) in 3000ml of de-ionized water.
- Stock was stored at 4°C
- Ethidium bromide being highly carcinogenic was handled wearing gloves

CURRICULUM VITAE

Name : Sandeep Yadav

Phone Number : 8317015135

Mailing Address:

Village and post - Chehari,
District- Maharajganj
Uttar Pradesh
273303
rtsandy89@gmail.com

Permanent Address:

Village and post - Chehari,
District- Maharajganj
Uttar Pradesh
273303

Career Objective: To work for the improvement in vegetable crops


Educational Qualification:

S. No.	Examination Passed	Institution	Year	Percentage/ CGPA
1.	Ph.D. Vegetable Science	GB Pant University of Agriculture and Technology, Pantnagar, UK, 263145	2021	75.94
2.	M.Sc. Ag. (Horticulture) Vegetable Science	ANDUAT Kumarganj Ayodhya	2017	83.79
3.	B.Sc. Agriculture	DDUGU Gorakhpur UP	2015	72.03
4.	Intermediate	SAJIC Anandnagar Maharajganj UP	2011	69.20
5.	High School	PTDDIC Maharajganj UP	2009	68.16

- **Specialization :** Major: **Vegetable Science** Minor: Genetics and Plant Breeding
- **Thesis Title :** “Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.”
- **Publications:**
- **Papers published from thesis :** “Assessment of genetic variability in cucumber”
- **Papers published other than thesis: 10**
- **Conferences/Seminars/Workshops/Trainings Attended: 8**
- **List of papers presented in conference/seminar during degree programme: 2**
- **Software skills:** MS word, Excel
- **Professional Affiliations:**
 1. Life member of the Indian Society of Vegetable Science
- **Awards/Honours/Achievements:**
 1. **University Gold Medal** for securing first rank in M.Sc., ANDUAT Kumarganj Ayodhya
 2. **DST Inspire fellowship (government of India)**
 3. **Qualified ASRB NET 2018**

Place : Pantnagar

Date : February, 2021


(Sandeep Yadav)

Name : Sandeep Yadav **Id. No.** : 52603
Sem. & Year of Admission : 1st Sem., 2017-18 **Degree** : Ph.D.
Major : Horticulture (Vegetable Science) **Department** : Vegetable Science
Minor : Genetics and Plant Breeding
Thesis Title : “Studies on Genetic and Molecular Diversity in Cucumber (*Cucumis sativus* L.)”
Advisor : Dr. Dinesh Kumar Singh

ABSTRACT


The present investigation was carried out at Vegetable Research Center of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar with the objectives to assess the genetic variability, heterosis, combining ability, screening for downy mildew disease and molecular diversity in Cucumber (*Cucumis sativus* L.).

The analysis of variance for RBD and combining ability revealed the significant genetic differences among 37 cucumber genotypes for the fourteen yield contributing traits under study. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except days to first male flower, inter nodal length, days to last harvest, days to first female flower and days to first harvest. Three cross combinations namely PCPGR-50 × PCPGR-59, PCPGR-51 × PCPGR-138 and PCPGR-138 × PCPGR-149 have significant positive heterosis for maximum numbers of traits including yield over standard check and showed their value in combining ability studies. Therefore, these cross combinations can be commercially exploited for hybrid development after multi location testing. PCPGR-112 was identified as a best general combiner for maximum number traits followed by PCPGR-59 and PCPGR-138. Thus, these parents could be used for the development of superior varieties suitable for most of the yield related traits. The best specific combiner were PCPGR-50 × PCPGR-59 followed by PCPGR-51 × PCPGR-59 and PCPGR-138 × PCPGR-149 for most of the yield and its contributing traits. Hence, these crosses can be utilized in heterosis breeding for improvement in yield related traits.

For downy mildew disease resistant reaction, out of all parents and F₁ hybrids only check variety ‘Poinsette’ exhibited resistant reaction while none of the parents and hybrids showed resistant reaction to downy mildew. Moderately resistance reaction against downy mildew was observed in eight genotypes one of which was parent *viz.*, PCPGR-112 and seven hybrids *viz.*, PCPGR-50 × PCPGR-112, PCPGR-51 × PCPGR-112, PCPGR-59 × PCPGR-112, PCPGR-83 × PCPGR-112, PCPGR-112 × PCPGR-126, and PCPGR-112 × PCPGR-138.

Ten SSR primers were used for the molecular diversity analysis. Out of ten primers, six primers generated polymorphic bands. Total 17 bands were amplified by 10 SSR primers in the thirty six cucumber genotypes of which polymorphic and monomorphic bands were 13 and 4, respectively. The range of amplified products was 150-400bp approximately. The range of polymorphism was observed 100 per cent. The PIC values of SSR markers ranged from 0.26 (SSR52) to 0.55 (SSR13262) with mean value of 0.37. Primer SSR52 was least informative while marker, SSR13262 was most informative due to highest PIC value among other markers, therefore this type of marker system could be efficiently applied to detect polymorphism in cucumber. The markers namely SSR60 (0.38), SSR 61 (0.47) and SSR13262 (0.55) had PIC values more than average value, therefore, these markers could be classified as good marker for detecting molecular polymorphism among the cucumber genotypes. Jaccard’s similarity coefficient varied from 0.45 to 1.00. Minimum Jaccard’s similarity coefficient was found in PCPGR-51 with PCPGR-83, PCPGR-106 and PCPGR-196 (0.45).

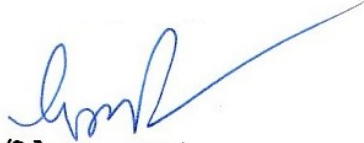

(Dinesh Kumar Singh)
Advisor

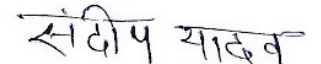

(Sandeep Yadav)
Author

नाम	: संदीप यादव	परिचयांक	: 52603
सत्र एवं प्रवेश वर्ष	: प्रथम, 2017-18	उपाधि	: पीएच. डी.
मुख्य विषय	: उद्यानिकी (सब्जी विज्ञान)	विभाग	: सब्जी विज्ञान
गौण विषय	: आनुवंशिकी एवं पादप प्रजनन		
शोध ग्रन्थ शीर्षक	: “खीरे (<i>कुकुमिस स्टाइवस</i> एल.) में आनुवंशिक और आण्विक विविधता पर अध्ययन”		
सलाहकार	: डॉ. दिनेश कुमार सिंह		

सारांश

वर्तमान शोध कार्य गोविन्द बल्लभ पंत कृषि एवं प्रौद्योगिकी विश्वविद्यालय पंतनगर के सब्जी अनुसन्धान केंद्र में आनुवंशिक भिन्नता, संकर ओज, संयोजन क्षमता, मृदुल आसिता बीमारी के लिए जाँच एवं आण्विक विविधता के अध्ययन के उद्देश्य के साथ संपन्न किया गया। यादच्छिकी खण्ड अभिकल्पना (आर. बी. डी.) एवं संयोजन क्षमता की भिन्नता विश्लेषण के आधार पर 37 खीरा जननद्रव्यों में सभी चौदह उपज और उनको प्रभावित करने वाले कारको में भिन्नता पाई गयी। पी. सी. वी. की अनुमानित मात्रा सभी गुणों के लिए जी. सी. वी. के अनुमानित मात्रा से अधिक पायी गयी। मध्यम उच्च जी. सी. वी. के साथ मध्यम से उच्च आनुवंशिकी एवं आनुवंशिकी विकास का औसत खीरे के अधिकांश गुणों के लिए पाया गया, जिसमें प्रथम नर पुष्प का आगमन दिन, अंतरगाँठ की लम्बाई, अंतिम फल तुड़ाई का दिन, प्रथम मादा पुष्प का आगमन दिन और प्रथम फल तुड़ाई का दिन सम्मिलित नई है। फल उपज के लिए तीन क्रॉस संयोजन जैसे पी सी पी जी आर -50 × पी सी पी जी आर -59, पी सी पी जी आर -51 × पी सी पी जी आर -138, और पी सी पी जी आर -138 × पी सी पी जी आर -149 शंकर उत्कृष्ट आशाजनक पाए गए। अतः इन संकरों को उच्च उपज के लिए बहु स्थान परीक्षण के बाद संकर विकास के लिए व्यावसायिक उपयोग किया जा सकता है। अधिकतम उपज सम्बन्धित लक्षणों के लिए पी सी पी जी आर -112, पी सी पी जी आर -59 और पी जी आर -138 को सर्वश्रेष्ठ सामान्य संयोजक के रूप में पहचाना गया अध्ययन किये गए फल उपज के अधिकांश लक्षणों के लिए क्रमशः पी सी पी जी आर -50 × पी सी पी जी आर -59, पी सी पी जी आर -51 × पी सी पी जी आर -59 और पी सी पी जी आर -138 × पी सी पी जी आर -149 उत्कृष्ट विशिष्ट संयोजक पाए गए। अतः इन संयोजनों का उपयोग उपज सम्बन्धित गुणों में सुधार हेतु संकर ओज प्रजनन में किया जा सकता है। सभी जननद्रव्यों में से केवल Poinsette किस्म में मृदरोमिल आसिता रोग हेतु प्रतिरोधी क्षमता पायी गयी जबकि 8 जननद्रव्यों ने मध्यम प्रतिरोध प्रक्रिया दिखाई। कुल 10 SSR मार्कर का परीक्षण किया गया जिसमें 6 बहुरूपी थे एवं 4 मार्कर एग्रोस जैल पर एकरूपी दिखे। इस प्रकार खीरे के 36 जननद्रव्यों में 10 प्राइमर द्वारा 17 बैंडों की कुल संख्या प्रदर्शित की गयी एवम 13 बहुरूपी और 4 एकरूपी थे। प्रवर्धित उत्पादों की सीमा लगभग 150-400 बी. पी. थी एवं प्रति स्थान पर ऐलील की संख्या दो से तीन थी। प्रति प्राइमर बैंड की औसत संख्या 2.16 थी। बहुरूपता संकेतन मात्रा 0.26 से 0.55 देखा गया जिसकी औसत मात्रा 0.37 थी। जैकार्ड समानता गुणांक 0.45 से 1.00 पाया गया। न्यूनतम जैकार्ड समानता गुणांक पी सी पी जी आर -51 के साथ पी सी पी जी आर -83, पी सी पी जी आर -106 और पी सी पी जी आर -196 (0.45) में पाया गया। SSR 13262 अन्य मार्करों में उच्चतम पी. आई. सी. मान के कारण सबसे ज्यादा सूचना पूर्ण था जबकि SSR 52 सबसे कम सूचनात्मक था। SSR 13262, SSR 61 और SSR 60 मार्कर में PIC मान औसत से अधिक था इसलिए यह मार्कर खीरे की जननद्रव्यों के बीच आण्विक विविधता का पता लगाने के लिए उपयोगी है।


(दिनेश कुमार सिंह)
सलाहकार


(संदीप यादव)
लेखक