

Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)

THESIS

By

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(A-2018-40-020)**

Submitted to



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CERTIFICATE – I

This is to certify that the thesis entitled “**Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)**” submitted in partial fulfilment of the requirements for the award of the degree of **Doctor of Philosophy (Agriculture)** in the discipline of **Horticulture (Vegetable Science)** of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Ms. Manpreet Kaur (Admission No. A-2018-40-020)** daughter of Sardarni Baljinder Kaur and Sardar Gurcharan Singh, under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

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

Place: Palampur
Dated: 21st May, 2022

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CERTIFICATE- II

This is to certify that the thesis entitled “**Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)**” submitted by **Ms. Manpreet Kaur (Admission No. A-2018-40-020)** daughter of Sardani Baljinder Kaur and Sardar Gucharan Singh to the CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of **Doctor of Philosophy (Agriculture)** in the discipline of **Vegetable Science**, has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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(Manpreet Kaur)

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LIST OF ABBREVIATIONS USED

Sr. No.	Abbreviation	Meaning
1	<i>et al.</i>	et alii (and others)
2	<i>i.e.</i> ,	id est (that is)
3	<i>viz.</i>	vi delicet (namely)
4	p.	page
5	pp.	particular Page
6	°C	degree Celsius
7	RH	Relative humidity
8	g	gram
9	m	meter
10	F ₁	first filial
11	/	per
12	%	per cent
13	Fig.	figure
14	mm	Millimeter
15	cm.	centimeter
16	ml	milliliter
17	mg	milligram
18	Kg	Kilogram
19	Kg/m ²	Kilogram per square metre
20	ha	hectare
21	nm	nanometer
22	N	normal
23	rpm	revolutions per minute
24	OD	optical density
25	M	molar
26	df	degrees of freedom
27	vs	against
28	@	at the rate
29	active ingredient	a.i.
30	Vol.	volume

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ABSTRACT

The present investigation entitled “Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)” was carried out at the Experimental Farm, Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur to gather information on combining ability, gene action and magnitude of heterosis in parthenocarpic cucumber. Eight parental lines were used to develop F₁ hybrids through half diallel mating design (excluding reciprocals). All parental lines and hybrids were evaluated along with standard check Kian in RBD with three replications under modified naturally ventilated polyhouses during spring-summer seasons of 2020 and 2021. Genetic diversity of eight parental lines was assessed using SSR markers to identify the diverse parents. PCA revealed 54.04 per cent variation as justified by first three principal components and maximum genetic variation (21.10%) was contributed by PC1. Eight cucumber genotypes were grouped into two clusters and both the clusters were divided into 2 sub clusters (NTSYS software) and DARwin software exhibited three clusters out of which cluster II was further divided into two sub clusters and was also confirmed by population structure. The analysis of variance indicated significant differences among genotypes (G) for fruit yield and other component traits in all the environments. Significant differences for environment (E) and G × E interaction for most of the traits indicated the role of environment on the performance of genotypes/crosses. Combined analysis of variance also indicated that mean squares due to parents, hybrids and parents vs. hybrids were significant for most of the traits. Variances due to GCA, SCA and their interaction with environment were significant for most of the traits, indicating the importance of testing parents as well as hybrids across environments. The top cross combinations identified on the basis per se performance were DDPCG1 × DDPCG2, DDPCG1 × DDPCG5, DDPCG1 × PPC-2 and DDPCG1 × PPC-3 for fruit yield and its component traits under protected environment. Parents DDPCG1, DDPCG4, PPC-2 and DDPCG5 were observed to be good general combiners for earliness, fruit yield and its component traits. Cross combinations viz., DDPCG4 × DDPCG5, DDPCG1 × PPC-2, DDPCG1 × DDPCG5, PK-1 × PPC-3 and DDPCG1 × DDPCW1 were the most promising crosses on the basis of SCA effects for yield and its related traits. For most of the traits, there was preponderance of non-additive gene action which reaffirms the importance of hybrids in cucumber. A wide variation in magnitude and direction of heterosis was noticed for majority of the traits with maximum manifestation for number of fruits per plant and marketable yield per plant. Hybrids DDPCG1 × DDPCG2, DDPCG1 × DDPCG5, DDPCG1 × PPC-2, DDPCG1 × PK-1 and DDPCG1 × DDPCW1 were the most promising crosses with significant economic heterosis for yield and yield related traits. Based on *per se* performance, SCA effects and heterosis, DDPCG1 × DDPCG2, DDPCG1 × DDPCG5, DDPCG1 × PPC-2, DDPCG1 × PK-1 and DDPCG1 × DDPCW1 were the most promising hybrid combinations for protected environment.

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1. INTRODUCTION

Cucumber is a member of the diverse and distinct Cucurbitaceae family which is widely grown for both fresh and processing purpose around the world. Primary centre of origin was India where both wild and cultivated species exist while; China and Near East were secondary centres of origin (De Candolle 1882). Both cultivated and wild species viz., *Cucumis sativus* var. *hardwickii* render enormous variation for various traits like growth habit, sex expression, fruit size, spines and flesh bitterness. About 70% of the cucumber world production is contributed by Asia, followed by China, Turkey, Iran and Russia. Cucumber is the fourth most important vegetable crop grown in the world after tomato, cabbage and onion (Tatlioglu 1993).

Cucumber crop covers a huge area in India ranging from North Western Himalayan region to Southern peninsular region as well as floating gardens of Dal Lake and riverbeds. In India, in open field conditions area under cucumber is 1,04,000 hectares with a total production of 16,03,000 MT (Anonymous 2020). In Himachal Pradesh, cucurbits occupy an area of 2,927.41 hectares with annual production of 73,361 MT (Anonymous 2021). The important cucumber growing states of India are Andhra Pradesh, Jammu & Kashmir, Assam, Punjab, Bihar and Tamil Nadu. Cucumber has low calorific value, higher water content and its immature fruits are consumed as salad. It is also a rich source of vitamin B, C, protein, fibre, fat, carbohydrates, folic acid and minerals like iron, calcium, phosphorus (Keopraparl 1997). Cucumber fruits provide cooling effect and relief from sun burns. It is useful to cure jaundice, constipation, arthritis and also used in ayurvedic preparations. Oil extracted from cucumber seeds keeps the body smooth and helps in brain development. Apart from this, fruits are high in demand in manufacturing of cosmetics and soaps.

Cucumber is a thermophilic crop which is mainly grown in tropical and subtropical regions. The best temperature for growth and development of crop ranges from 18-24°C and is very sensitive to frost conditions. It can be successfully grown on light sandy to heavy clay with well drained and fertile soils. There is a need to protect

the vegetable crops from unfavorable climatic conditions by maintaining the micro environment with the initiation of protected cultivation. Poly house cultivation is a simplest and largely used way of protected vegetable cultivation where natural environment is altered by different means of sound engineering principles for optimum plant growth and yield. In Himachal Pradesh, protected vegetable cultivation has been gaining importance since last fifteen years due to congenial growing condition inside these structures. Among all the vegetables, cucumber is one of the major vegetable crop grown under protected conditions.

Parthenocarpy is an important yield related trait in cucumber under protected conditions which sets fruit without pollination (Sun et al. 2006). Fruits of parthenocarpic varieties are more firm and fleshier which seldom give higher yield due to association of gynoecy in comparison to conventional seeded varieties. Parthenocarpic gynoecious varieties do not require pollination for fruit development and bears only female flowers that increases the fruit yield with other traits like earliness, uniformity and early yield under protected conditions which is the main objective of a breeding programme. Moreover, seedless fruits fetch higher economic returns as compared to conventional seeded fruits.

In spite of huge variability, it has narrow genetic base with only 12% polymorphism which limits the new cultivar development by cross breeding (Pandey et al. 2018). Due to higher consumption of cucumber, there is a scope for improvement of productivity with the use of improved varieties or hybrids of cucumber (Pandey et al. 2016). Selection of suitable parents for breeding programme depends on the existence of variability in the germplasm and is most imperative for hybridization. Recent progress in plant genomics offers an opportunity for assessing genetic diversity through use of molecular markers (Yang et al. 2015). Cucumber is an ideal model crop for genetic studies due to smaller genome size of approximately 367Mb with shorter life cycle (Ren et al. 2009). Breeding in cucumber for enhancing yield, quality and biotic and abiotic stress tolerance is a major challenge for the breeders, globally (Yuan et al. 2008). Different types of molecular markers like random amplified polymorphic DNA (RAPD), sequence characterized amplified

regions (SCAR), amplified fragment length polymorphisms (AFLP) and simple sequence repeats (SSR) are available (Dar et al. 2017). Among all, SSR markers are widely used in plant genomics like gene mapping, quantitative trait loci (QTL), marker assisted selection (MAS), evolutionary studies and genetic diversity analysis (Mahajan et al. 2016). SSR markers are more or less used in cucumber for assessment of genetic diversity (Yang et al. 2015). Genetic diversity and population structure is very important for the maintenance, conservation and improvement in productivity in agriculture. Plant genetic diversity can be preserved and stored in the form of plant genetic resources in gene banks and DNA libraries for long term conservation. These plant genetic resources could be utilized in future for the crop improvement against various biotic and abiotic stresses to meet global food security (Garzon-Martinez et al. 2015). Due to narrow genetic base and use of limited number of SSR markers for genetic diversity analysis, there is a dire need for studying genetic diversity using molecular markers for bridging the gap for the crop improvement by hybridization. The selection of cucumber genotypes with a high genetic diversity of the genes could be used in cross breeding, QTL mapping, gene tagging and other imperative genomic studies.

Heterosis breeding in cucumber is of commercial significance due to higher yield as well as better quality exhibited by hybrids. The term heterosis was first coined in 1914 by Shull and is referred as the superiority of F_1 hybrid in one or more traits over its parents. In 1916, Hayes and Jones first reported heterosis in cucumber and observed increase in yield by 24-30 per cent over the high yielding parents. Commercial F_1 hybrid Pusa Sanyog bred by IARI, Katrain by crossing gynoeocious line (Japanese variety i.e, Kaga Aomaga Fushinavi) and Green Long of Naples (an Italian variety) at national level enhanced 128.78 per cent yield over recommended variety (Gill et al. 1973). Heterosis can be measured over mid parent, heterobeltiosis over better parent or economic heterosis over standard check. The selection of suitable parent is of much importance for exploitation of heterosis. Combining ability concept was first given by Sprague and Tatum in 1942 namely general combining ability (GCA) and specific combining ability (SCA). Estimation of combining ability studies is very important in heterosis which helps to assess the ability of an inbred line

to combine with other inbred lines to develop a hybrid. General combining ability (GCA) is the average performance of an inbred line in a series of hybrid combinations while, specific combining ability is the performance of a hybrid combination of a particular genotype in a specific cross. The combining ability of genotypes relies on the nature of the genetic system operating in the parent, which predicts the efficiency of selection.

The selection of the breeding method depends upon the type of gene action controlling the inheritance of a character for crop improvement. Therefore, the knowledge of genetic variances is also essential for selection of breeding method for genetic gain in yield and its component traits. In 1942, Sprague and Tatum suggested the use of combining ability as a measure of gene action in maize. Since yield is controlled by polygenes, information about the gene action and inheritance pattern of various quantitative characters helps to exploit appropriate breeding method. The selection of highly heterotic combination including parents with non-additive gene action is required for commercial use as a hybrid.

Diallel analysis suggested by (Jinks and Hayman 1953; Hayman 1954) helps to provide valuable knowledge about combinations of different parental lines by determining the overall genetic structure of the parental lines. Traits studied on the basis of diallel analysis (Griffing 1956a) suggested a method for the estimation of combining ability which helped in categorizing the parental lines on the basis of performance of hybrids to select the parents for hybrid development which when crossed may give rise to more desirable segregants. This information is of great importance and is a backbone of any breeding programme.

The drawback related to cross breeding programme in cucumber is a limited knowledge about heterosis and combining ability in parthenocarpic lines and availability of only few hybrids under public sector for growers. Therefore, considering these drawbacks and significance of this crop, there is a need to develop new parthenocarpic cucumber hybrids suitable to grow under protected conditions for higher yield and yield attributing traits. Keeping this in view, the present study

entitled “Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)” under naturally ventilated polyhouse was executed with the following objectives:

- i. To assess genetic diversity of parthenocarpic lines using molecular markers.
- ii. To estimate the extent of heterosis for fruit and related traits,
- iii. to assess the combining ability effects and gene action for fruit yield and component traits

2. REVIEW OF LITERATURE

Hybrid development has been proved an important step for improvement of yield to fulfill the demands of vegetables in India. Cucumber is an important vegetable having huge germplasm with wide variation. Selection of suitable parents for hybridization and breeding procedure adopted in the genetic material are the main factors on which the success of breeding primarily depends. Knowledge of the genetical information like nature of combining ability, type of gene action, inheritance of characters and heterosis are the chief requirement for parent selection and designing the proper breeding programme. Combining ability of genotypes offers valuable genetic information for the selection of suitable parents. Several methods have been developed to determine the general combining ability. Diallel mating design is a useful method for analyzing general combining ability (GCA) and specific combining ability (SCA) partitioning into additive and dominance gene action, respectively (Griffing 1956a; Falconer and Mackay 1996).

Extensive work has been carried out on heterosis and combining ability in monoecious cucumber in open field conditions but little information is available in gynoecious parthenocarpic inbreds and hybrids under protected conditions. In this chapter, a brief review of literature pertaining to the present study in cucumber is presented under the following headings:

2.1 Genetic diversity studies through molecular markers

2.2 Combining ability

2.3 Gene action

2.4 Heterosis

2.1 Genetic diversity studies through molecular markers

Analysis of genetic diversity in crop species is a main component for crop improvement. Morphological characters have limited use due to environmental influence and developmental stages of a plant. Molecular markers are more advantageous than morphological due to more stability under variable environmental

conditions (Ammar et al. 2015). Different types of molecular markers like random amplified polymorphic DNA (RAPD), sequence characterized amplified regions (SCAR), amplified fragment length polymorphisms (AFLP) and simple sequence repeats (SSR) are used to assess the genetic diversity (Dar et al. 2017). Among all, SSR markers are widely used in plant genomics like gene mapping, quantitative trait loci (QTL), marker assisted selection (MAS), evolutionary studies and genetic diversity analysis (Mahajan et al. 2016).

Hu et al. (2010) assessed the molecular diversity in cucurbit accessions using SSR primers. A total of 392 SSR were designed as representative samples including 35 primer pairs and usable markers comprising 28 primer pairs. Out of 28 usable primers, 26 showed high polymorphism with 2-7 alleles with an average value of 3.77 and polymorphism information content (PIC) ranged from 0.091-0.748 with an average of 0.388. The polymorphism was observed mainly from the null alleles which appear at multiple homoeoloci identified by the primers.

Hu et al. (2011) estimated genetic diversity in 29 cucumber accessions using 13 SSR and 16 expressed sequence tag (EST) SSR (eSSR) markers. gSSR markers and eSSR markers detected a mean of 4.46 alleles and 3.38 alleles, respectively. A mean value of polymorphic information content (PIC) was observed 0.664 and 0.397 with gSSR and eSSR markers, respectively. A clear consistency was observed between gSSR and eSSR with respect to positioning of most cucumber accessions. gSSR markers help to divide the whole cucumber accessions into different type but in eSSR tree the grouping was not based on their geographical origins. eSSR markers identified an independent sub-group comprising five accessions resistant to downy mildew, revealing the relationship between eSSR markers and disease-resistance character.

Lv et al. (2012) studied the genetic diversity using 23 Simple sequence repeat (SSR) markers in 3,342 accessions collected from the Chinese, Dutch and U.S. A total of 316 alleles were produced from 23 SSR markers. Out of 316 alleles, 64 showed more than 5% frequency which were designated as 'common' alleles while, frequency between 1-5% were displayed by 64 alleles were regarded as 'less common' alleles. Out of 188 remaining alleles, 121 alleles showed frequency between 0.1-15 were

regarded as 'rare alleles' and 67 alleles displayed less than 0.1% frequency which were denoted as 'very rare' alleles. Using STRUCTURE analysis, mega-collections were divided into population 1, 2 and 3 comprising 1399, 1129 and 404 accessions, respectively and 410 accessions were regarded as admixtures. Principal component analysis (PCA) separated accessions into three populations and P3 was further divided into two subgroups including mainly Indian and Xishuangbanna accessions. Based on the AMOVA analysis, population was categorized into three groups indicating 68.1% and 31.9% variation due to differences within populations and among populations, respectively.

Pandey et al. (2013) analyzed the genetic diversity of 44 cucumber accessions using 70 simple sequence repeat primer pairs. Among all, 53 SSR markers showed high polymorphism with a total of 163 amplification products. An average value of 3.05 was observed for number of alleles per locus and amplicon size varied from 126 bp (SSR02123) to 498 bp (SSR13189). Maximum PIC value were reported in SSR05737, SSR12810 and SSR15477 with mean value of 0.31 while recorded minimum PIC in SSR06670. Based on similarity coefficient index, maximum similarity was found between BAM-HR-107 and BAM-HR-126 accessions and minimum between BAM-HR-128 and BAM-HR-115. The dendrogram based on Jaccard's similarity coefficient index, 44 accessions were divided into five major clusters. Close similarity was observed among BAM-HR-126 and BAM-HR-107 and BAM-HR-102 and BAM-HR-111 based on dendrogram. PCA revealed 28, 22 and 15% of total variation in PC1, PC2 and PC3, respectively. Two dimensional plot analysis grouped the accessions into 5 clusters indicating the high genetic diversity among genotypes.

Yang et al. (2015) analyzed genetic diversity in 42 cucumber genotypes using 51 pairs of simple sequence repeat (SSR) markers. A total of 129 polymorphic loci were identified using SSR markers indicating 95.6% polymorphic. An average value of alleles was 0.36 with mean Shannon's information index of 0.21. Cluster analysis divided the 42 genotypes into three clusters comprising 27, 7 and 8 cultivars. The similarity coefficient ranged from 0.25 to 0.88 with an average value of 0.56. Principal component analysis (PCA) also divided population into three groups displaying 65.6, 79.2 and 85.6% of the variation.

Singh et al. (2016a) assessed the genetic diversity using 8 Inter simple sequence repeats (ISSR) in 11 cucumber genotypes comprising monoecious and parthenocarpic genotypes. Out of 8 primers, 6 were found polymorphic and produced a total of 49 polymorphic alleles. A total of 40-100% polymorphism was recorded among all the genotypes. Total number of alleles varied from 5-14 per loci with the mean value of 9.5 per locus. Dendrogram constructed using ISSR data grouped the genotypes into two major clusters and five sub-clusters. Pair wise similarity index showed maximum differentiation between Pant Parthenocarpic Cucumber-2 and Kian while; Pant Parthenocarpic Cucumber-2 and Pant Parthenocarpic Cucumber-3 were closely related.

Someh et al. (2016) evaluated 20 varieties of cucumber using 15 RAPD for genetic diversity analysis. The PIC value ranged from 0.12-0.44 was observed for PIC value for 15 primers with the mean value of 0.21. Primer OPA-11 and OPH-16 gave maximum and minimum PIC values, respectively. Jaccard's similarity matrix varied from 0.56 to 0.88 indicating the similarity among genotypes. Varieties PLA and ASG showed maximum similarity index whereas, minimum similarity of MAX with CLO and LOCG with HUP. Genotypes were grouped into 3 main clusters based on UPGMA cluster analysis. Cluster A was the largest which was further divided into two sub clusters A₁ and A₂ comprising 6 and 5 genotypes, respectively. Group B consists of 5 genotypes with 0.84 similarity index while, group C consists of 4 genotypes with 0.76 genetic similarities.

Dar et al. (2017) studied the genetic diversity, marker attributes and population structure in 104 cucumber genotypes using 23 SSR markers. Total 67 alleles were identified with an average of 2.91 per locus. Allele frequency ranged from 0.215 to 0.561 with an average value of 0.403 while, polymorphic information content (PIC) and marker index (MI) varied from 0.158 to 0.495 and 0.316 to 1.54, respectively. SSR65 gave maximum allele frequency whereas; maximum PIC and resolving power was reported with SSR61. Primer SSR60 gave maximum marker index. Jaccard's similarity coefficient varied from 0.07 to 0.897. Among genotypes, G40 and G41 showed maximum similarity while, G16 with G20 and G16 with G100 showed minimum similarity. Based on PCA grouping and clustering, genotypes were categorized into two clusters with maximum number of genotypes in cluster B. In population structure analysis, 47 and 39 genotypes were grouped in population 1 and 2 respectively, while 18 genotypes were identified as admixtures.

Normohamadi et al. (2017) assessed the genetic diversity using 9 SSR markers in 20 genotypes of local cucumber. The total number of alleles were 41 with an average of 4.55 alleles per marker. SSR19430 identified maximum number of alleles while, SSR06660 and SSR15477 produced lowest number of alleles. The size of amplicon ranged from 144-220 bp. SSR13251 and SSR15477 showed maximum and minimum PIC, respectively with an average value of 0.69 indicating higher level of diversity. Among genotypes, Jaccard similarity coefficient index varied from 0.51 to 0.92. TN-141-94 and TN-154-94 genotypes displayed maximum similarity with 0.94 genetic similarity coefficients while TN-186-94 and TN-218-94 exhibited minimum similarity with 0.51 genetic similarity coefficients.

Punetha et al. (2017a) studied the genetic diversity using eight ISSR primers in 13 cucumber genotypes. Six ISSR primers gave 52 alleles showing 92.30% polymorphism. Primer UBC-855 and UBC-890 detected maximum of 11 loci while, primers UBC-808, UBC-840 and UBC-855 gave unique bands. The similarity index varied from 22-80% with the mean value of 46%. Pgyn-1 genotype was found most diverse with 33% similarity than other genotypes. All the genotypes were grouped into two major clusters. Group A comprises Pgyn-1 which is most unique genotype while, group B includes maximum number of genotypes which was further divided into two sub clusters B₁ consisting seven genotypes and B₂ containing PCUC-35 and Punjab Naveen.

Pandey et al. (2018) assessed the genetic diversity using 21 EST-SSR markers in 40 cucumber genotypes. Among all the primers, EC50, EC52 and EC19 produced highest number of alleles and PIC values ranged from 0.002-0.989 with an average value of 0.308. Expected heterozygosity varied from 0.074-0.428 with the mean value of 0.255 while, unbiased expected heterozygosity ranged from 0.074-0.434 with an average value of 0.258. Based on Jaccard's similarity coefficients, genotype IIHR-81 and IIHR-407 were clearly differentiated while; close similarity was found between VRC-26 and Pilibhet Local. All genotypes were grouped into three main clusters comprising 4, 2 and 34 genotypes in major cluster I, II and III, respectively. Cluster III was grouped into 4 sub cluster comprising 1, 2, 2 and 29 genotypes in sub cluster IIIA, IIIB, IIIC and sub cluster IIID, respectively.

Valcarcel et al. (2018) studied molecular genetic diversity of 131 Spanish accessions with 23 simple sequence repeat (SSRs). Out of 23 markers, 18 were found highly polymorphic. The total number of alleles varied from 2-6 with an average value of 3.2. The total number of 58 alleles were found in all accessions out of which, 34 were 'common', 15 were 'less common', 8 were 'rare' alleles and 1 was categorized as 'very rare' allele. An average value of 3.2, 0.065 and 0.229 were observed for number of alleles, observed heterozygosity and polymorphic information content, respectively. A range of 0.31-0.44 was observed for PIC by seven SSR markers. The similarity index of cucumber accessions were ranged from 0.01 to 0.44 with an average of 0.14. Dendrogram constructed using Nei coefficient grouped the accessions into three clusters comprising 1, 131 and 2 accessions, respectively.

Karakurt et al. (2020) evaluated 18 cucumber lines for their genetic diversity using eight AFLP markers. Total of 1975 AFLP fragments were generated showing 75.34% polymorphism. Based on the dendrogram, genetic distance varied from 0.92 to 0.96. Cluster analysis divided all the cucumber lines into three major clusters. The similarity index ranged from 0.888-0.982 indicating lower level of genetic variation.

Park et al. (2021) studied the genetic diversity using a core set of single nucleotide polymorphisms (SNPs) in 280 cucumber accessions. The heterozygosity of the SNP varied from 4.76-82.76% per loci with the mean value of 32.1. All the accessions were clustered into four sub-populations based on geographical location by the population structure analysis. Maximum similarity was observed between Korean F₁ hybrids and Asian accessions and minimum between Asian and European accessions. American and European accessions showed maximum differentiation. Among all the accessions, mean value of 0.414 Nei's genetic distance was reported. For cultivar identification, heterozygosity varied from 12.20 to 69.14% of the SNP per loci with the mean value of 34.2%. Based on the grouping of component analysis, Baekdadagi and Gasi types showed maximum similarity while minimum similarity between Nakhap and Baekdadagi type.

2.2 Combining ability

The concept of combining ability plays an important role to identify the best combiners for hybrid development and crop improvement for exploitation of heterosis

and combining desirable genes. Parents with good combining ability helps to develop superior hybrids. Sprague and Tatum (1942) was the first who gave the concept of combining ability and coined the two terms general combining ability (GCA) and specific combining ability (SCA). General combining ability (GCA) is the average performance of a line in hybrid combinations while, specific combining ability (SCA) is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved in a cross (Sprague and Tatum 1942). The estimates of GCA helps in the selection of appropriate parents for hybridization while, SCA helps in the identification of superior cross combinations.

Sushir et al. (2005) observed maximum GCA effects for yield per vine for parents Sheetal, Shubhangi and Talegaon Local. Cross combinations viz., Improved Long Green \times Himangi and Poona Khira \times Junnar Local exhibited maximum SCA effects for yield per vine.

Yadav et al. (2007) conducted an experiment to study combining ability effects in 45 F₁ hybrids developed by crossing 15 lines and 3 testers. Among the parents, 2020 exhibited maximum combining ability for days to first female flower, number of nodes per vine and number of fruits per plant while, parent 2014 for days to first female flower, fruit length, fruit diameter and fruit yield/plant. Among hybrids, 2015 \times 2014, 2229 \times 2226, 2237 \times 2238, 2016 \times 2238, 2237 \times 2226 and 2028 \times 2238 displayed higher specific combining ability effects for fruit yield per plant and its attributing traits which can be exploited through hybridization programme for crop improvement.

Sharma (2006) studied combining ability in gynoeocious cucumber using five lines and eleven testers. Among parents, G-1 exhibited maximum general combining ability effects for marketable yield per vine and Plp-Gy-1 was the good general combiner for total soluble solids. The best specific combinations for days to first female flower were Plp \times K-75, PCUCP-4 \times KL-3, G-3 \times Poinsette, EC-5082 \times Poinsette and PCUCP-4 \times JLG; Plp \times DPC-1, PCUCP-4 \times JLG, Plp \times Poinsette, EC5082 \times KL-3 and Plp \times K-Pap for fruit weight; PCUCP-4 \times JLG, Plp \times Poinsette, G-1 \times K-75, Plp \times DPC-1 and Plp \times K-Pap for marketable yield per vine.

Sarkar and Sirohi (2010) estimated combining ability effects for different traits in a 10×10 diallel cross excluding reciprocals. Among parents, DC-1 was good general combiner for fruit weight, fruit length and total yield per plant whereas, DC-2 exhibited higher general combining ability effects for node number of first female flower and number of fruits per plant. Among hybrids, maximum SCA effects were showed by DC-1 \times CHC-1 for days to first fruit harvest, DC-2 \times VRC-11-1 for fruit weight, CH-20 \times Poona Khira for fruit diameter, PCUC-28 \times VRC-11-1 for fruit length and DC-2 \times CH-20 for number of fruits per plant. Hybrid combinations PCUC-28 \times VRC-11-1, DC-1 \times PCUC-28 and CH-20 \times Himangi were found most promising for total yield per plant over top parent.

Singh et al. (2010) reported that parent Peelibheet Local and PCUC-28 exhibited maximum general combining ability for yield and its attributing traits among 10 diverse parental lines. Hybrid combination PCUC-28 \times Peelibheet Local showed high specific combining ability effects for vine length, yield, fruit length, fruit diameter and average fruit weight. Out of 45 F_1 hybrids, 19 hybrids showed positive SCA effects for yield per plant.

Yoshioka et al. (2010) estimated combining ability effects for fruit texture traits in 28 F_1 hybrids derived by crossing eight diverse cucumber genotypes in a half-diallel mating design. The results indicated that the GCA effects were more significant than SCA effects. Genotypes AO, N8 and K4 exhibited positive GCA effects for placenta firmness; TO, N8, SH and K4 for flesh firmness; FD, AO, N8 and EN for crispness index and also showed their contribution in hybrids. These traits can be improved by selection of superior GCA parental genotype.

Mule et al. (2012) studied the performance of 27 cross combinations developed from 3 lines and 9 testers. Parent CCP-9, Gujarat Local and SPP-44 were found as best general combiner for traits related to fruit yield. However, hybrid Pilibhit Local \times K-90 was best specific combiner for number of fruits per vine; Pilibhit Local \times K-90, Sheetal \times SPP-44 and Sheetal \times CC-9 for fruit yield per vine.

Singh et al. (2012) studied combining ability in cucumber and their results showed that parent C-99-12 was the best general combiner for yield per vine, days to first male flower, fruit length, fruit weight and vine length. Hybrids EC-43342 \times C-

99-10, EC-43342 × C-98-6 and PCUC-15-1 × C-98-6 were identified as good general combiners for yield per vine.

Bairagi et al. (2013) estimated combining ability effects in 28 F₁ hybrids developed using eight parental lines for horticultural traits. Among parents, PCUC-25, PCUC-15 and PCUC-83 were found best general combiner for number of fruits, fruit weight and fruit yield per plant. The best specific combining ability effects were observed for number of fruits and fruit yield per plant in hybrids PCUC-83 × PCUC-25, PCUC-83 × PCUC-15, PCUC-25 × PCUC-15 and PCUC-8 × PCUC-15.

Kumar et al. (2013) assessed combining ability studies for yield and its attributing traits in hybrids and parents. The best general combiner among parents were CRC-8, CHC-2, Pusa Uday and DC-1 for most of the characters including yield per plant. Hybrid combinations CRC-8 × Pusa Uday, CHC-2 × Pusa Uday and CHC-2 × DC-1 were found best specific combiners for days to first female flower, node number of first female flower, days to first fruit harvest, average fruit weight, number of fruits per plant, fruit length, fruit diameter and yield per plant.

Reddy et al. (2014) estimated combining ability effects in 36 F₁ hybrids developed by crossing nine diverse genotypes in half diallel mating system. For days to first fruit harvest, CHC-1 was the best general combiner while, Pusa Uday was found best general combiner for average fruit weight, fruit diameter, yield per plant and number of fruits per plant. Hybrid Poona Khira × Sel. 97-7 displayed heterosis for days to first female flower anthesis, node number of first female flower and days to first fruit harvest whereas, DC-1 × Himangi hybrid exhibited higher level of specific combining ability effects. Vidhya and Kumar (2014) reported that genotypes CS-37 and CS-39 showed higher GCA effects for all the traits while, higher SCA effects were exhibited by CS-39 × CS-19, CS-37 × CS-17, CS-37 × CS-39 and CS-17 × CS-39.

Kaur et al. (2016) assessed combining ability studies in cucumber and parent 'Gy-14' was identified as a best combiner for flesh to seed cavity ratio and β-carotene whereas, for ascorbic acid and dry matter content Swarna Sheetal was observed as a best combiner. Parents viz., Japanese Long Green, NCH-1, Summer Kheera and EC-27075 were found best general combiner for total soluble solids. For total soluble

solids, cross EC-27075 × Summer Kheera had maximum specific combining ability effects while cross combination Pant Kheera-1 × Japanese Long Green had maximum SCA for ascorbic acid. For mineral content, crosses Pant Kheera-1 × Summer Kheera and Swarna Sheetal × EC-27075 had maximum specific combining ability effects. Hybrid combinations viz., Gy14 × Punjab Naveen and EC-27075 × NCH-1 showed higher level of specific combining ability effects for flesh to seed cavity ratio.

Kumar et al. (2016) while studying 16 parent and 48 F₁ hybrids for combining ability analysis identified that 5 parents including LC-1-1, CGN-20953, CGN-19533, Gyne-5 and K-75 displayed positive GCA effects for marketable yield per plant. Among 48 cross combinations, 5 hybrids namely, CGN-19533 × K-75, LC-25-7 × Japanese Long Green, LC-1-1 × K-75, CGN-20953 × Poinsette and Gyne-5 × K-75 showed high SCA for marketable yield per plant.

Moradipour et al. (2016) analyzed combining ability for fruit yield and its contributing traits by crossing seven diverse parents in a half-diallel design to obtain 21 F₁ hybrids. Parents namely, B10 and B12 while, hybrid combinations B12 × A0 and B10 × A4 exhibited maximum general combining ability and specific combining ability (SCA) for early yield, respectively while, parents B10, A4, B12 and hybrid combinations B12 × A0, B10 × A11 and B10 × A4 displayed maximum general combining ability and specific combining ability on marketable yield, respectively. Parents B10, B12, A11 and cross B10 × A4 showed maximum general combining ability and specific combining ability for simple weight index in cucumber. Therefore, parents B10 and A4 were selected as most promising for hybrid development.

Singh et al. (2016b) crossed eight cucumber parental lines to develop 28 F₁ hybrids in a half-diallel for combining ability studies. Among parents, ACC-8 showed high GCA effects for fruit diameter and fruit yield, ACC-2 for days to first fruit harvest and number of fruits per vine and ACC-4 for average fruit weight were found to be the best general combiner. Hybrid ACC-2 × ACC-6 was the excellent specific combiner for days taken to first fruit harvest while, ACC-4 × ACC-7 for number of fruits per vine and ACC-3 × ACC-4 for fruit diameter and ACC-1 × ACC-4 for average fruit yield.

Tiwari and Singh (2016) studied combining ability effects in 11 cucumber parents and their 24 F₁ hybrids. Higher SCA for earliness and yield characters were reported in PCUCP-3 × PCUC-15 and Nun-3139 × PCUC-8 while, Nun-3139 × PCUC-8 showed higher SCA for yield attributing traits. Hybrid combination Nun-3139 × PCUC-8 displayed higher specific combining ability for node number to first female flower, number of fruits per plant and fruit yield. Parent Isatis and Kian exhibited significant general combining ability for earliness and yield, respectively.

Kaur and Dhall (2017) conducted a study on 8 × 8 diallel set of cucumber genotypes excluding reciprocals to estimate the combining ability for yield and yield attributing traits. The results revealed that hybrid JLG × EC27075 and Gy-14 × Punjab Naveen showed higher SCA effects for node number of first female flower and marketable yield per plant, respectively. Hybrid combination EC-27075 × NCH-1 displayed maximum SCA effects for fruit weight.

Thapliyal (2017) conducted combining ability analysis using parthenocarpic gynoecious hybrids and inbred lines in cucumber. Among parental lines, PBRK-10 was found best general combiner for fruit length, fruit weight, vine length, total soluble solids and flesh to seed cavity ratio while, PBRK-4 showed higher general combining effects for number of fruits per plant, days to first fruit harvest and yield per plant. Hybrid PBRK-4 × PBRK-12 was found best specific combiner for number of fruits per plant and yield per plant; PBRK-12 × PBRK-7 for fruit weight and fruit diameter and PBRK-10 × PBRK-1 for fruit length. Among hybrids, PBRK-4 × PBRK-12, PBRK-4 × PBRK-9 and PBRK-9 × PBRK-1 showed higher SCA effects for yield per plant.

Malav et al. (2018) conducted an experiment to study combining ability effects on fruit yield and yield attributing traits in cucumber and observed Poinsette as a best general combiner for traits like fruit length, fruit diameter, fruit weight, number of branches per plant and vine length while, for yield per plant, parents Hilton and Isatis were identified as good general combiner. For fruit yield and yield attributing traits, crosses Poinsette × JWRC-1, Hilton × Swarna Sheetal and Isatis × Swarna Ageti exhibited highest specific combining ability effects in cucumber.

Thakur and Kumar (2020) conducted a half-diallel analysis to assess combining

ability studies. Parent PI 618860 was observed to be best general combiners for earliness viz., appearance of days to first female flower, node number bearing first female flower and days to marketable maturity while, UHF CUC-1, UHF CUC-2 and PI 618860 for marketable yield per hectare. Parent Khira-75 showed higher level of GCA for fruit length, fruit breadth and harvest duration. Cross combinations Khira-75 \times PI 618860, UHF CUC-3 \times PI 618860, UHF CUC-3 \times Poinsette and UHF CUC-3 \times PI 618860 exhibited higher specific combining ability effects for marketable yield per hectare.

Kumar et al. (2021) developed 36 F_1 hybrids by crossing 12 lines and 3 testers in line \times tester to study combining ability effects. Significant variances were reported for general and specific combining ability effects for all the traits. Parents Pahari Barsati and Poinsett exhibited high level of GCA for yield/plant while, Pahari Barsati, Swarn Ageti and Swarna Poona were also identified as best general combiners for days to first fruit picking. Hybrid combination No 40 \times PCUC-8, Punjab Naveen \times Boro Patana and Pusa Uday \times Boro Patana showed higher SCA effects based on per se performance.

Manggoel et al. (2021) evaluated 15 F_1 hybrids and 5 parents for combining ability studies and observed that parent Odukpani recorded positive GCA for vegetative characters, fruit diameter, girth and average fruit weight. Hybrid combinations Odukpani \times Griffaton, Odukpani \times Ashley, Odukpani \times Marketmore, Odukpani \times Monarch, Griffaton \times Poinsett, Griffaton \times Ashley, Griffaton \times Monarch and Ashley \times Monarch showed high SCA effects for average fruit weight while, nine hybrids including Odukpani \times Marketmore, Griffaton \times Poinsett, Griffaton \times Ashley, Griffaton \times Marketmore, Griffaton \times Monarch, Poinsett \times Ashley, Poinsett \times Marketmore, Ashley \times Marketmore and Ashley \times Monarch exhibited higher specific combining ability effects for number of fruits per plant.

2.3 Gene action

A successful genetic analysis of the polygenic characters commenced with the work of Fisher (1918). The genetic variances were partitioned into three genetic components viz., additive portion arising from the average effects of genes, dominance portion resulting from intra-allelic interactions and epistatic portion

related with inter-allelic interactions. The selection of breeding method depends upon the type of gene action involved in controlling the inheritance of several characters in crop improvement programme. Therefore, it is essential to estimate the genetic components of variances to devise suitable breeding method for higher genetic gain in yield and its attributing traits.

Lopez-Sese and Staub (2002) reported higher GCA effects for days to anthesis, number of female flowers per node, number of fruits, fruit length to diameter ratio and number of lateral branches indicating the role of additive genetic components and selection is an effective for improvement of these traits in cucumber. Munshi et al. (2006) suggested the role of non-additive gene action for the inheritance of days to first fruit harvest, number of fruits per plant and yield per plant revealing the significance of heterosis for improvement of above traits. The predominance of additive gene action was observed for fruit length.

Sarkar and Sirohi (2006) observed preponderance of dominance gene action for vine length and days to first fruit harvest while, days to first female flower opening, node number at which first female flower appear, fruit weight and total fruit yield per plant showed over-dominance component of genetic variation. Sharma (2006) reported the preponderance of non-additive gene action in inheritance of days to first female flower, nodal position of first female flower, days taken to first fruit harvest, fruit length, fruit diameter, fruit weight, marketable fruits/vine, marketable yield/vine, harvest duration, number of primary branches, vine length and total soluble solids.

Tiwari et al. (2009) observed higher SCA effect for days to first female flower, node number of first female flower, days to first fruit harvest, number of fruits per plant and total yield per plant indicating the predominance of non-additive gene action whereas, higher GCA effect was observed for fruit weight, fruit length and fruit diameter revealing the role of additive gene action for improvement of these traits. Kumar et al. (2010) reported over-dominance gene action for days to first female flower, node number of first female flower, days to first fruit harvest, number of fruits per plant and yield per plant whereas, partial dominance for fruit length, fruit diameter and fruit weight. Dominance gene action was observed for vine length.

Singh et al. (2010) reported that GCA and SCA variances were significant for various traits indicating the role of both additive and non-additive genetic components. The GCA variances were higher for vine length, fruit length, fruit diameter, average fruit weight and yield per plant than the SCA variances while, predominance of non-additive gene action for number of branches per plant due to lower GCA variances. Singh et al. (2012) observed that GCA variances were lower than SCA variances indicating the predominance of non-additive genetic components for all the traits.

Bairagi et al. (2013) reported higher GCA mean squares for days to anthesis of first female flower, nodal position of first female flower, number of primary branches per plant, fruit length, vine length, number of fruits per plant, fruit yield per plant revealing the role of additive gene action whereas, non-additive gene action for fruit diameter. Kumar et al. (2013) reported that mean squares due to general and specific combining ability was highly significant for all the traits demonstrating the role of both additive and non-additive gene action. Predominance of non-additive gene action was observed for days to first female flower, node number of first female flower, days to first fruit harvest, number of fruits per plant and total yield per plant whereas, fruit weight, fruit length and fruit diameter indicated the role of additive gene action.

Pati et al. (2015) observed the role of non-additive genetic components for the inheritance of various traits, *viz.*, node at first female flower, days to first female flower, days to fruit set, days to first fruit harvest, number of fruits per plant and yield per plant indicating the exploitation of heterosis breeding for improvement of these traits. However, predominance of additive gene action was reported for fruit length, average fruit weight and vine length and selection will be more effective for the improvement of these traits.

Kaur et al. (2016) demonstrated the predominance of non additive gene effects for flesh to seed cavity ratio, total soluble solids (°brix), β -carotene ($\mu\text{g}/100\text{g}$), ascorbic acid ($\text{mg}/100\text{g}$ flesh weight), dry matter content (%) and mineral content (%). Therefore, the improvement for these characters can be achieved through hybrid development. Tiwari and Singh (2016) reported the major role of non-additive genetic components due to higher specific combining ability effect (SCA) which may be exploited in heterosis breeding.

Kaur and Dhall (2017) studied the gene action for yield and yield attributing traits in 28 F_1 cross combinations involving 8 parental lines. The predominance of non-additive gene effects was reported to be involved in the inheritance of most of the traits viz., node at which first female flower appears, fruit length, fruit diameter, marketable yield per plant, fruit weight except vine length. Thapliyal (2017) demonstrated that dominant variances were higher for most of the traits including total soluble solids, fruit diameter, vine length, flesh to seed cavity ratio, days to first fruit harvest, days to last fruit harvest and yield per plant indicating the predominance of non-additive gene action. The additive genetic components were higher for fruit weight, fruit length and number of fruits per plant representing the role of additive gene action. Malav et al. (2018) reported that estimates of SCA variances were higher for days to fruit maturity and fruit weight indicating the role of non-additive genetic components.

Rai et al. (2018) carried out gene action studies for fruit yield and its attributing traits in cucumber. Results revealed the role of additive gene action in number of fruits per vine, average fruit weight, fruit length and fruit width. The predominance of additive gene effect was observed for fruit yield per vine and fruit yield per hectare in ACS12-31 \times B19 and ACS12-51 \times Poinsett hybrid combinations while, dominant gene effect was reported in ACS12-29 \times Belgaum Local and ACS12-51 \times Poinsett for sex ratio, number of fruits per plant, fruit yield per hectare, fruit yield per vine and pericarp thickness. Additive \times dominance genetic components were observed for average fruit weight in hybrid combinations ACS12-29 \times Belgaum Local and ACS12-51 \times Poinsett and for number of fruits per vine in ACS12-31 \times B19 hybrid.

Thakur and Kumar (2020) suggested the predominance of non-additive gene action for days to first female flower, node number bearing first female flower, days taken to first fruit harvest, fruit diameter, average fruit weight and marketable yield per hectare. Additive gene action is important for improvement of fruit length, number of marketable fruits per plant and harvest duration.

Manggoel et al. (2021) reported that additive gene action played a major role in controlling number of branch per plant, days to first fruit set and days to 50%

fruiting, fruit girth while, dominant effects were exhibited for number of leaves per plant, vine length, number of staminate flowers per plant, and number of pistillate flowers per plant.

2.4 Heterosis

The term heterosis was coined by Shull (1914) refers to the superiority of F_1 hybrid over its parents in one or more characters. The superiority of F_1 over the mid parent is relative heterosis whereas; heterobeltiosis is the superiority over the better parent. Standard or commercial or economic heterosis is the superiority of F_1 over the standard check variety. Hayes and Jones (1916) first reported heterosis in cucumber and observed 24-30% higher yield over the parents. The available literature on heterosis in cucumber on various traits has been summarized below.

Bairagi et al. (2005) evaluated 28 hybrids developed by crossing eight cucumber genotypes and reported significant heterobeltiosis in nine hybrids for number of fruits per plant. Hybrid PCUC-83 \times PCUC-25, PCUC-25 \times DC-1, PCUC28 \times DC-1 and PCUC-83 \times DC-1 were top heterotic crosses for days to anthesis of first female flower over better parent. Significant heterobeltiosis was expressed by PCUC-25 \times DC-1, PCUC-83 \times PCUC-25 and PCUC-83 \times DC-1 hybrids for nodal position of first female flower. Hybrid PCUC-25 \times PCUC28 exhibited maximum heterobeltiosis for vine length and number of primary branches per plant. Cross combinations viz., PCUC-83 \times PCUC-15, PCUC-83 \times PCUC-25 and PCUC-25 \times PCUC-15 showed maximum heterosis for fruit yield per plant over better parent and standard check.

Kumbhar et al. (2005) reported that 28 non-reciprocal hybrids exhibited significant heterosis for all the traits studied over better parent, top parents and standard parents. The extent of heterosis ranged from 0.53 to 44.82% and 2.85 to 44.81% for total yield per plant over better parent and standard parent (Pusa Uday), respectively. Hybrid combination, CRC-5 \times Pusa uday exhibited maximum heterosis for number of fruits per plant over standard and over top parent. For fruit yield per plant, crosses CRC-8 \times Pusa Uday, CRC-8 \times DC-1, CHC-2 \times Pusa Uday and CHC-2 \times DC-1 displayed maximum heterosis over the standard check parent. CRC-8 \times Pusa Uday was earliest and high yielding hybrid exhibiting 44.81% heterosis over Pusa

Uday for yield and may be recommended for commercial hybrid breeding in future for crop improvement.

Pandey et al. (2005) reported significant heterosis over better parent and mid parent for all the traits studied. Hybrid DC-1 × B-159 and VRC-11-2 × Bihar-10 exhibited positive heterosis for number of fruits, fruit length and total fruit yield over better parent and mid parent. Cross combination DC-1 × B-159 expressed positive heterosis for fruit weight and fruit diameter over mid parent and better parent. Increase in yield was attributed due to higher number of fruits per plant. A positive heterosis was observed for fruit length, fruit diameter, average fruit weight and number of fruit. Godoy et al. (2008) evaluated parents and hybrids to estimate the heterosis and reported that hybrid H35 × H43 exhibited positive heterosis for yield per plant.

Hanchinamani and Patil (2009) revealed significant heterosis for most of traits over better parent and mid parent. Heterosis for days to first female flower ranged from -0.52 to -16.49 over mid parent and -1.0 to -19.0 over better parent. Cross combination, BGD L × White long and BGD L × Hot season showed highest negative heterosis over mid parent and better parent, respectively. Heterosis for average fruit weight varied from -29.12 to 15.33 over mid parent and -25.39 to 9.38 over better parent while a range of -43.43 to 60.47 and -50.51 to 31.73 for total fruit yield per vine was observed over mid parent and better parent, respectively. Hybrid combination BGD L × Hot Season displayed an increase of 94.03 and 31.73% heterosis over mid parent and better parent for yield, respectively.

Kumar et al. (2010) recorded significant heterosis for yield and its related characters in 15 F₁ hybrids developed by crossing six genotypes in half-diallel design. Mean values for days to first pistillate flower opening varied from 52.10 to 57.33 days and 47.10 to 55.87 among parents and crosses, respectively. Out of 15 hybrid combinations, 7 and 15 crosses exhibited negative heterosis over better parent and standard check, respectively for days to first pistillate flower opening. Mean values for fruit weight varied from 116.30-159.80 g for parents and 123.03-187.07 g for hybrids and 5 hybrids exhibited positive heterosis for fruit weight over standard check. Heterosis for number of fruits ranged from 0.84 to 25.21% over better parent,

7.70 to 55.13% and 0.85 to 25.20% over standard parent and over top parent, respectively. Cross combination CRC-8 × Pusa Uday exhibited positive heterosis for number of fruits over standard parent and top parent. Heterosis varied from 0.53 to 44.82% over better parent, 2.85 to 44.81% over standard and top parent. Cross combination CRC-8 × Pusa Uday showed maximum heterosis for yield per plant over better parent, standard and top parent.

Singh et al. (2010) reported a considerable heterosis for yield per plant, vine length, average fruit weight, number of branches per plant, fruit length and fruit diameter over better parent. Cross combinations viz., VRC-18-2 × Patna-3, Baramasi × BSC-2 and PCUC-28 × Peelibheet local exhibited maximum heterosis for yield per plant over better parent while, PCUC-28 × Peelibheet local, PCUC-28 × VRC-18-2 and VRC-11-2 × BSC-2 for average fruit weight over better parent.

Dogra and Kanwar (2011) assessed the heterosis in 28 F₁ hybrids developed using eight parents in a half diallel design. Hybrid combination EC173934 × LC-40 and G₂ × Gyn1 exhibited maximum heterobeltiosis and standard heterosis for earliness, respectively. Maximum heterobeltiosis and standard heterosis was reported for yield and number of fruits in hybrid K-90 × G₂.

Kushwaha et al. (2011) developed 21F₁ hybrids by crossing seven genotypes in half diallel mating design. Hybrid BC-11 × BC-12 exhibited maximum heterosis for nodal position of first female flower, BC-16 × Poinsette for fruit length, BC-14 × BC-16 for fruit diameter, BC-15 × BC-16 for fruit weight and BC-11 × BC-16 for number of fruits per plant and fruit yield per vine.

Robou and Hamed (2011) while evaluating ten F₁ hybrids reported positive heterosis over the better parent for total yield/plant ranging from 18.24 to 138.39%. Hybrid *Cus* 2-11-519 × *Cus* 2-23-576, *Cus* 2-11-519 × *Cus* 1-12-26 and *Cus* 3-2-14 × *Cus* 1-12-26 exhibited maximum heterosis for total yield/plant.

Mule et al. (2012) revealed considerable heterosis for yield and its contributing traits. Among all hybrid combinations, 7 crosses were found heterotic for node number on which first female flower appear, 3 crosses for number of lateral branches per vine, 5 crosses for fruit length, 6 crosses for fruit diameter, 7 crosses for average fruit weight, 5 crosses for vine length, 8 crosses for number of fruit per vine

and 7 crosses for fruit yield per vine showed significant heterosis over better parent. Hybrid combinations viz., Sheetal \times SPP-44, Sheetal \times CC-9 and Pilibhit Local \times K-90 exhibited maximum heterosis over better parent for number of fruits per vine; Pilibhit Local \times K-90, Gujarat Local \times SPP-44, Sheetal \times CC-9 for average fruit weight and Pilibhit Local \times K-90, Sheetal \times SPP-44, Sheetal \times CC-9 for fruit yield per plant.

Twelve F_1 hybrids were developed by Airina et al. (2013) by crossing twelve monoecious and single gynoeious parent. Considerable extent of heterosis and heterobeltiosis was observed for days to first harvest, number of fruits per plant, fruit length, fruit diameter and yield per plant. Hybrid combination EC 709119 \times IC 538155 exhibited maximum heterobeltiosis for number of harvest, number of fruits per plant and yield per plant.

Jat et al. (2015) determined heterosis for yield and yield related traits in twenty one F_1 hybrids developed using seven parental lines in a half diallel mating. Hybrid combination GPC-1 \times PPC-2, PPC-2 \times Pusa Uday and GPC-1 \times Pusa Uday exhibited maximum heterosis over top parent for number of fruits per plant; DC-1 \times Pusa Uday, Punjab Naveen \times Pusa Uday and Swarna Poorna \times Pusa Uday for average fruit weight. Three heterotic hybrids namely PPC-2 \times Pusa Uday, GPC-1 \times Pusa Uday and PPC-2 \times Punjab Naveen were identified best for yield per plant exhibiting 64.51, 55.61 and 54.57% heterosis respectively, over standard check Pusa Uday.

Arya and Singh (2016) estimated heterosis for fruit yield and its attributing traits by crossing 6 parental lines in a half-diallel design to obtain 15 F_1 hybrids. Significant heterosis was observed for all the traits over better parent and check parent. Hybrid combination PCUCP-1 \times PCUCP-3, PCUCP-3 \times PCUCP-4 and PCUCP-2 \times PCUCP-3 exhibited maximum heterosis for fruit yield.

Kaur et al. (2016) evaluated twenty-eight hybrids developed by crossing eight diverse cucumber varieties to study the heterosis in cucumber. Hybrid combination JLG \times NCH-1 revealed maximum heterosis for flesh to seed cavity ratio over better parent and standard check while, maximum heterosis for total soluble solids was observed in JLG \times Summer Kheera over better parent and standard check. Gy-14 \times EC27075 hybrid showed maximum heterosis over mid parent for ascorbic acid followed by Pant Kheera-1 \times JLG and Pant Kheera-1 \times NCH-1.

Kumar et al. (2016) reported considerable heterosis for fruit size and fruit weight in ten cross combinations. For earliness, hybrid combination CGN-19533 × K75, CGN-20953 × Poinsette, LC-1-1 × K-75, LC-2-2 × K-75, LC-2-2 × Poinsette, LC-21-6 × K-75, LC-28-8 × K-75 and Gyne-5 × K-75 exhibited negative heterosis over mid parent and better parent. The results showed that hybrid combination Gyne-5 × K-75, LC-1-1 × K-75 and CGN-19533 × K-75 exhibited maximum heterosis for fruit length whereas, LC-1-1 × K-75, CGN-20953 × K-75 and CGN-20515 × Japanese Long Green for fruit breadth; CGN-19533 × K-75, Gyne-5 × K-75 and LC-1-1 × K-75 for average fruit weight.

Sharma et al. (2016) evaluated 55 F₁ hybrids developed by crossing 5 lines and 11 testers to estimate the heterosis for yield and its attributing traits. Among crosses, 50 crosses exhibited positive heterosis over better parent, 42 and 41 crosses over Pusa Sanyog and Solan Khira Hybrid-1 (Standard checks), respectively for marketable yield per vine. For average fruit weight, 31 crosses had significant positive heterosis over their respective better parent, 34 and 27 crosses over Pusa Sanyog and Solan Khira Hybrid-1, respectively. Hybrid combinations namely, Plp × K-pap, G-3 × Sel-75-2-10 and G-1 × K-pap showed maximum standard heterosis for marketable yield/vine. For TSS, 29 hybrids showed positive heterosis over better parent, 40 crosses over Pusa Sanyog and 24 crosses exhibited positive heterosis over Solan Khira Hybrid-1.

Singh et al. (2016b) evaluated eight genetically diverse cucumber parental lines and their 28 F₁ hybrids to estimate heterosis for yield and its attributing traits. The extent of heterosis for days taken to first fruit harvest varied from -14.31 to 18.27 and -21.26 to 2.24 over better parent and standard check, respectively. For number of fruits per vine, an extent of heterosis varied from -28.15 to 32.15 and -17.80 to 35.17 over better parent and standard check, respectively. Among 28 cross combinations, 7 and 17 hybrids exhibited significant positive heterosis for number of fruits per vine over better parent and standard check, respectively. Six crosses over better parent and 11 crosses over standard check expressed significant positive heterosis for average fruit weight while, hybrid combinations viz., ACC-3 × ACC-8 and ACC-4 × ACC-6 showed maximum heterosis over better parent and standard check, respectively. For number of fruits, 12 hybrids over better parent and 10 hybrids over standard check

expressed significant positive heterosis. Cross combinations viz., ACC-1 \times ACC-4 and ACC-2 \times ACC-6 exhibited maximum heterosis i.e. 39.25% and 32.23% for average fruit yield over standard check, respectively.

Tiwari and Singh (2016) investigated the extent of heterosis for earliness and yield characters using line \times tester mating design with 11 parents (8 lines and 3 testers) and 24 F₁ hybrids in cucumber. Appreciable heterosis was identified over better parent in cross combination PCUCP-3 \times PCUC-15 (days to first female flower), Nun-3139 \times PCUC-8 (node number to first female flower), Isatis \times PCUC-8 (plant height), while, maximum heterobeltiosis for number of fruits per plant and fruit yield was found in Kian \times PCUC-15.

Kaur and Dhall (2017) developed twenty-eight F₁ hybrids using eight diverse cucumber genotypes in half diallel mating design, excluding reciprocals to study the heterosis for yield and yield attributing traits. Based on heterosis, JLG \times Summer Kheera and JLG \times NCH-1 hybrid combinations were found best for marketable yield and fruit weight whereas, for fruit length and diameter, hybrids viz., Swarna sheetal \times EC-27075 and Pant Kheera-1 \times EC-27075 were identified best in cucumber.

Thirty F₁ hybrids were developed by Punetha et al. (2017b) by crossing 3 gynoecious lines and 10 testers (monoecious) to estimate heterosis. The extent of heterosis for days to first female flower ranged from 19.44 to 44.57% over better parent. Maximum heterosis for days to first female flower and days to first harvest was observed in hybrid Pgyn-1 \times PCUC-35 over better parent while, Pgyn-5 \times US-832 over standard parent. The cross combination Pgyn-1 \times PCUC-35 displayed maximum heterosis over better parent while, Pgyn-5 \times US-832 over standard parent for days to first female flower and days to first harvest. Pgyn-5 \times PCUC-28 (31.79%) exhibited highest heterobeltiosis for average fruit weight and fruit yield while, Pgyn-4 \times US-832 for number of fruit per vine.

Twenty eight F₁ hybrids of parthenocarpic gynoecious cucumber involving eight parthenocarpic gynoecious inbred lines were studied by Thapliyal (2017) in diallel fashion excluding reciprocals to estimate the extent of heterosis for yield and its attributing traits. Hybrid combinations namely, PBRK-4 \times PBRK-12, PBRK-4 \times PBRK-9 and PBRK-4 \times PBRK-8 exhibited maximum heterosis for yield per plant

over commercial check (Multistar). For number of fruits per plant, hybrid combinations viz., PBRK-4 × PBRK-12, PBRK-4 × PBRK-9, PBRK-4 × PBRK-8, PBRK-9 × PBRK-1, PBRK-4 × PBRK-1, PBRK-8 × PBRK-9, PBRK-7 × PBRK-8, PBRK-7 × PBRK-9, PBRK-8 × PBRK-1 and PBRK-4 × PBRK-2 exhibited maximum heterosis over commercial check. The extent of heterosis ranged from -33.85 to 28.29 and -2.18 to 53.27 over better parent and check, respectively. 12 and 17 crosses showed significant heterosis for fruit weight over better parent and check, respectively. Hybrid combinations viz., PBRK-9 × PBRK-2 and PBRK-12 × PBRK-10 exhibited significant positive heterosis for total soluble solids over better parent and check, respectively. For flesh to seed cavity ratio, hybrid combination PBRK-4 × PBRK-9 over better parent and PBRK-4 × PBRK-7 over check expressed significant positive heterosis.

Kumari et al. (2018) observed maximum average heterosis for the yield per hectare followed by the seed vigour index II, number of marketable fruits per plant, severity of downy mildew, fruit weight, harvest duration, severity of powdery mildew, node number bearing first female flower, fruit length, fruit breadth, seed vigour index I, total soluble solids, seed germination, days to marketable maturity and days to first female flower appearance. Five hybrids namely LC-1-1 × K-75, LC-1-1 × Poinsette, LC-2-2 × K-75, LC-2-2 × Poinsette and CGN-20515 × Poinsette exhibited maximum heterosis for most of the traits. Among 18 F₁ hybrids, 10, 6 and 11 hybrids expressed positive heterosis for fruit length, fruit breadth and average fruit weight, respectively. Hybrid LC-1-1 × K-75 showed maximum heterosis for fruit length and average fruit weight whereas, CGN-20515 × JLG for fruit breadth. An extent of heterosis ranged from -31.18 to 138.70% over mid parent for yield per hectare. Hybrid LC-1-1 × K-75 showed maximum heterosis over average or mid parent and 12 crosses exhibited heterosis for yield per hectare over mid parent.

Malav et al. (2018) observed considerable amount of heterosis for yield and its attributing characters in cucumber. The heterosis for hybrid Hilton × Swarna Sheetal for yield per plant ranged from -36.10% to 25.78% over mid parent, -41.26% to 17.87% over better parent and -39.74% to 15.99% over standard check.

Singh and Tiwari (2018) developed 45 F₁ hybrids by crossing 10 cucumber parental lines in half diallel mating system, excluding reciprocals. A significant

amount of heterosis was observed for different traits. The extent of heterosis for yield per plant varied from 8.07 to 80.95% and 14.51 to 102.11% over better parent and mid parent, respectively. Hybrids Swarna Ageti \times Patna-3, PCUC-28 \times Peelibheet Local and CU-5 \times Patna-3 displayed maximum heterosis 23.0, 74.42 and 73.45% over better parent and 30.68, 78.78 and 15.93% over mid parents, respectively and were found to be the most promising hybrids.

Preethi et al. (2019) developed 25 F_1 hybrids using line \times tester technique (5 lines and 5 testers) for estimating heterosis for yield and its contributing traits. Cross combination IIHR 341 \times Phule Shubhangi displayed maximum heterosis for number of fruits over the check whereas, Pondicherry 1 \times Punjab Naveen and Green Long \times Kerala-2 exhibited maximum heterobeltiosis for number of fruits. Crosses including Long \times Poinsette, Green long \times Pusa Uday and Pondicherry 1 \times Punjab Naveen showed significant heterosis for fruit yield per plant over better parent and commercial check.

Arab et al. (2020) evaluated twenty-five F_1 hybrids developed by crossing five inbred lines in complete diallel cross. They observed significant heterosis for early yield, total yield, number of fruits, average fruit weight and fruit length. Hybrid combination $P_5 \times P_3$ exhibited maximum heterosis for days to first female flower over mid parent and better parent, respectively. Hybrid $P_3 \times P_1$ and $P_1 \times P_3$ displayed maximum heterosis for total yield and number of fruits per plant over mid and better parent.

Umeh et al. (2021) recorded significant and positive heterosis for yield and its component traits in cucumber over mid parent and better parent. Hybrid Cu 100 \times Cu 999 exhibited significant positive heterosis over mid parent and better parent for number of fruits per plant, fruit weight and fruit yield per hectare whereas, negative heterosis for days to first female flower was observed in hybrid combinations Cu 999 \times Cu 100, Cu 100 \times Songhai local, Cu 971 \times Cu 100 and Cu 971 \times Songhai local over better parent and Cu 100 \times Cu 999 for days to maturity. Cu 971 \times Songhai local was found best for vine length. Cu 100 \times Cu 999 and Cu 971 \times Cu 999 hybrids were found most promising for commercial exploitation in breeding programme.

3. MATERIALS AND METHODS

The present study entitled “Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)” was carried out at the Experimental Farm and Molecular Biology Laboratory of Vegetable Science and Floriculture department, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during spring-summer seasons of 2019-20 & 2020-21. The details of experimental site and methodologies employed in the present study are described below.

3.1 Experimental site

3.1.1 Location

The experimental farm is situated at 32° 6' North latitude and 76° 3' East longitude at an elevation of 1,290.8 meters above mean sea level. It is located in the mid hill regions of Himachal Pradesh. The soil of region is silty clay loam with a pH of 5.7 which are acidic in nature.

3.1.2 Climate

Agro-climatically, it is located in the mid hill regions having humid sub-temperate climate with 2,500 mm annual rainfall with 80% rainfall during June to September. The mean monthly meteorological data with regard to temperature and relative humidity inside the polyhouse during the cropping period in both the years (2020 and 2021) are presented in Appendix I and II (Fig 3.1 and 3.2)

3.2 Materials and layout of the experiment

3.2.1 Experimental material

(a) Diallele mating

The experimental material consists of eight diverse parthenocarpic gynoecious cucumber parental lines. The details of parental lines with their sources are described in Table 3.1

Fig. 3.1: Mean weekly meteorological data during the cropping season (March to August, 2020) inside the polyhouse

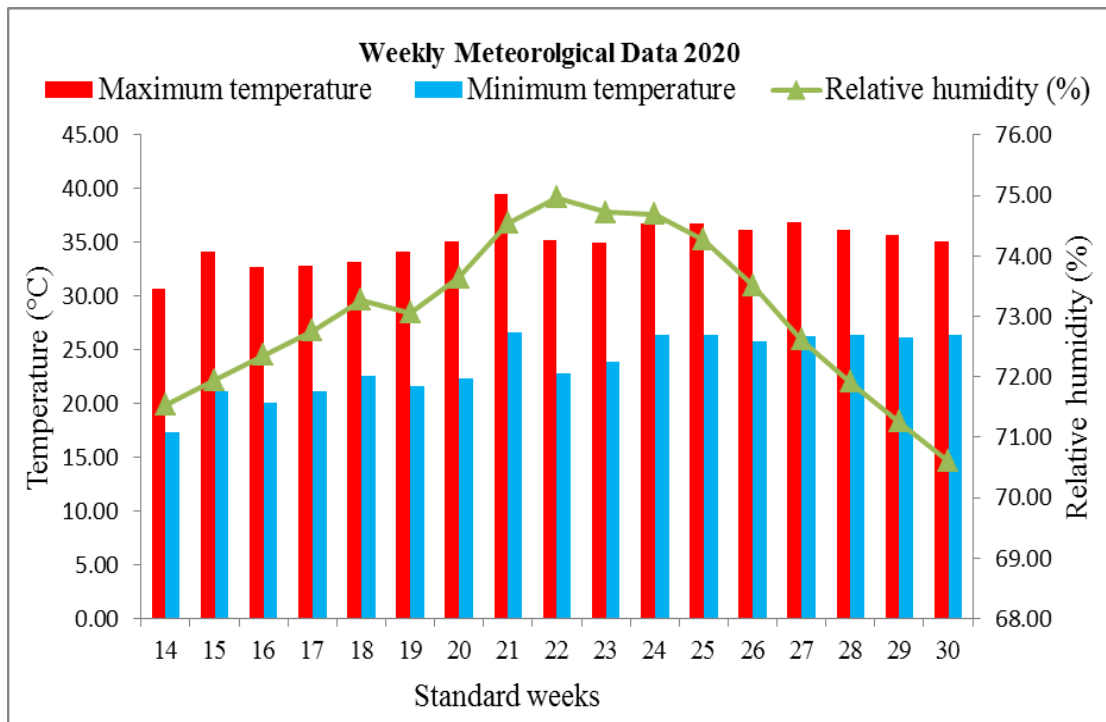


Fig. 3.2: Mean weekly meteorological data during the cropping season (March to August, 2021) inside the polyhouse

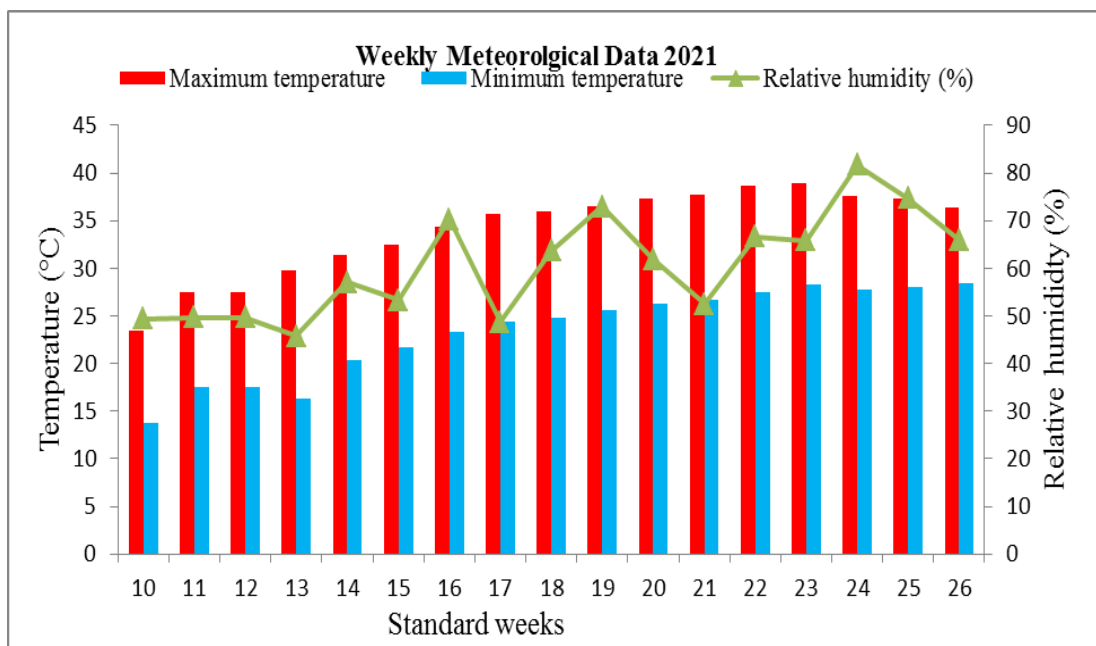


Table 3.1: List of cucumber (*Cucumis sativus* L.) genotypes used in the study and their sources

Code No.	Genotypes	Collection Source
P ₁	DDPCG4	CSKHPKV, Palampur
P ₂	DDPCG1	CSKHPKV, Palampur
P ₃	Punjab Kheera-1 (PK-1)	PAU, Ludhiana
P ₄	Pant Parthenocarpic Cucumber-2 (PPC-2)	GBPUA&T, Pantnagar
P ₅	Pant Parthenocarpic Cucumber-3 (PPC-3)	GBPUA&T, Pantnagar
P ₆	DDPCW1	CSKHPKV, Palampur
P ₇	DDPCG2	CSKHPKV, Palampur
P ₈	DDPCG5	CSKHPKV, Palampur
Standard Check	Kian	Nunhems India Private Limited

Table 3.2: Detail of cross combinations

Sr. No.	Hybrid combination (cross)	Code No.
1	DDPCG4 × DDPCG1	P ₁ × P ₂
2	DDPCG4 × Punjab Kheera-1 (PK-1)	P ₁ × P ₃
3	DDPCG4 × Pant Parthenocarpic Cucumber-2 (PPC-2)	P ₁ × P ₄
4	DDPCG4 × Pant Parthenocarpic Cucumber-3 (PPC-3)	P ₁ × P ₅
5	DDPCG4 × DDPCW1	P ₁ × P ₆
6	DDPCG4 × DDPCG2	P ₁ × P ₇
7	DDPCG4 × DDPCG5	P ₁ × P ₈
8	DDPCG1 × Punjab Kheera-1 (PK-1)	P ₂ × P ₃
9	DDPCG1 × Pant Parthenocarpic Cucumber-2 (PPC-2)	P ₂ × P ₄
10	DDPCG1 × Pant Parthenocarpic Cucumber-3 (PPC-3)	P ₂ × P ₅
11	DDPCG1 × DDPCW1	P ₂ × P ₆
12	DDPCG1 × DDPCG2	P ₂ × P ₇
13	DDPCG1 × DDPCG5	P ₂ × P ₈
14	Punjab Kheera-1 (PK-1) × Pant Parthenocarpic Cucumber-2 (PPC-2)	P ₃ × P ₄
15	Punjab Kheera-1 (PK-1) × Pant Parthenocarpic Cucumber-3 (PPC-3)	P ₃ × P ₅
16	Punjab Kheera-1 (PK-1) × DDPCW1	P ₃ × P ₆
17	Punjab Kheera-1 (PK-1) × DDPCG2	P ₃ × P ₇
18	Punjab Kheera-1 (PK-1) × DDPCG5	P ₃ × P ₈
19	Pant Parthenocarpic Cucumber-2 (PPC-2) × Pant Parthenocarpic Cucumber-3 (PPC-3)	P ₄ × P ₅
20	Pant Parthenocarpic Cucumber-2 (PPC-2) × DDPCW1	P ₄ × P ₆
21	Pant Parthenocarpic Cucumber-2 (PPC-2) × DDPCG2	P ₄ × P ₇
22	Pant Parthenocarpic Cucumber-2 (PPC-2) × DDPCG5	P ₄ × P ₈
23	Pant Parthenocarpic Cucumber-3 (PPC-3) × DDPCW1	P ₅ × P ₆
24	Pant Parthenocarpic Cucumber-3 (PPC-3) × DDPCG2	P ₅ × P ₇
25	Pant Parthenocarpic Cucumber-3 (PPC-3) × DDPCG5	P ₅ × P ₈
26	DDPCW1 × DDPCG2	P ₆ × P ₇
27	DDPCW1 × DDPCG5	P ₆ × P ₈
28	DDPCG2 × DDPCG5	P ₇ × P ₈

3.2.2 Planting of experimental material

3.2.2.1 Nursery sowing and transplanting

The seeds of eight parthenocarpic gynoecious cucumber parental lines were sown in soil-less media containing cocopeat: perlite: vermiculite (3:1:1) in February, 2019 for both molecular studies and hybrid development. For hybridization programme, seedlings were transplanted during March 2019 in naturally ventilated polyhouse number 7 of the Vegetable Research Farm of CSKHPKV, Palampur. Pollination work was done to generate F₁ hybrids in a half diallel fashion (excluding reciprocals). The list of hybrid combinations is presented in Table 3.2.

3.2.2.2 Selfing and Crossing programme

All the parental lines were gynoecious in nature; male flowers were induced with the application of silver thiosulphate (250-400ppm) at 2-3 true leaf stage in tagged plants of each genotype. These tagged plants were used as a male parent in crossing programme. Hybrids were obtained by hand pollinating the female flowers with the pollen of male flower of tagged parents. While the selfed seeds were developed by pollinating the female flowers with the male flowers of same parental line. Selfed seeds and F₁ of each cross was harvested separately during August 2019.

3.2.2.3 Harvesting and seed extraction

Ripened fruits of parental lines and crosses were harvested separately. The outer portion of fruits was cut off and flesh was cut down into small pieces having maximum number of seeds. Flesh was squeezed and fermented for overnight in water. Settled seeds were washed 2-3 times with water and dried under room temperature for 2-3 days. Dried seeds were stored in paper bags with labeling.

3.3 Molecular studies

For molecular studies, genomic DNA was extracted from 8 cucumber genotypes which were further subjected to Simple sequence repeats (SSR) marker.

3.3.1 Extraction of plant genomic DNA

Genomic DNA was extracted from the fresh leaf tissues from each parental line using cetyl trimethyl ammonium bromide (CTAB) method with few alterations (Clarke 2009). All the lines were maintained at Experimental farm, Department of



Plate 1 Nursery and transplanted crop

Vegetable Science and Floriculture, CSKHPKV, Palampur. Approximately 5 gm of fresh and tender leaf tissues were grinded using pestle and mortar. This extract was transferred into 2 ml of Eppendorf tube containing 2000 µl of 2X CTAB extraction buffer. These Eppendorf tubes were incubated at 60°C for 45 minutes in water bath with periodic shaking after 10 minutes. Add 800 µl of chloroform: isoamyl alcohol (24:1) in each tube and place the samples on shaker for 20-25 minutes for continuous shaking. Then, Centrifuge the tubes at 13000 rpm for 7 minutes. The supernatant (upper phase) was transferred to 1.5 ml tubes and 600 µl of chilled isopropanol was added and store the samples at -20°C for overnight. Next day, the samples were centrifuged at 13,000 rpm for 7 minutes. Discard the supernatant and rinse the pellet with 70% alcohol (200 µl) twice and centrifugation is done at 7000 rpm for 3 minutes. Then alcohol was decanted and pellet was air-dried at room temperature. Purified DNA pellet was re-suspended in Nuclease free water or 1 X TE buffer (70 µl) and stored at -20°C.

3.3.2 Assessment of quality and quantity of DNA

DNA concentration and purity was determined by Agarose gel electrophoresis or NanoDrop spectrophotometer.

3.3.2.1 Quantification by Nanodrop method:

DNA quantification was done with Thermo Scientific Nano drop spectrophotometer. Before sampling, set the blank with DEPC water. Place 1 ul of DNA sample in the instrument's receiving fibre optic cable and measure the concentration at Optical Density (OD) ratio of 260/280 value. If the OD value is between 1.8 and 2.0, DNA is considered to be pure whereas, low ratio (<1.8) indicates the RNA contamination and higher ratio (>2.0) shows protein contamination in a DNA sample.

3.3.2.2 Quantification by Agarose gel electrophoresis:

The quality of DNA was checked on Agarose gel electrophoresis (Lee et al. 2012). For agarose gel preparation, agarose powder (1.8 g) was dissolved in 1X TAE buffer (180 ml) and this mixture was heated in microwave until the solution became transparent. Complete solution was cooled for few minutes followed by addition of

ethidium bromide (12 μ l) to final concentration. Agarose gel was poured into gel mould with combs and allowed for solidification for 30-40 minutes. DNA samples were formulated by adding DNA (2 μ l), loading dye (1 μ l) and double distilled water (5 μ l). After agarose gel solidification, DNA samples were loaded into the separate wells. Known DNA concentration (100 bp) marker (ladder) was also loaded to determine the DNA concentration of each sample. The gel was visualized under UV transilluminator system. Each sample concentration was estimated by comparing the band intensity with ladder. Presence of single high intact band shows the good quality of DNA samples while; smear band indicates poor quality of DNA.

3.3.3 Stock solution preparation for DNA extraction (for 100 ml)-

a) 1M Tris: 12.11 g of Tris base was dissolved in 80 ml of distilled water. Adjust pH to 8.0 by using concentrated HCL. Total volume was made to 100 ml.

b) 0.5 M EDTA: 18.61 g of EDTA di sodium salt was dissolved in 80 ml of distilled water. Adjust pH of the solution to 8.0 using NaOH pellets and final volume was made to 100 ml.

c) 5M NaCl: 29.22 g of NaCl was dissolved in 75 ml of distilled water after complete dissolution of salt, final volume was brought to 100 ml.

d) 10% CTAB: 10 g of CTAB was dissolved in 80 ml of distilled water and final volume was made up to 100 ml.

e) 70% Ethanol: 70 ml of absolute ethanol mixed well with 30 ml of distilled water and stored at ambient temperature.

f) Chloroform: Isoamyl alcohol (24:1): 96 ml of chloroform and 4 ml of isoamyl alcohol were mixed well and stored in color reagent bottle at room temperature.

g) 10 X TAE Buffer: 48.5 g of Tris base, 20 ml of EDTA (0.5M) and 11.4 ml of Glacial acetic acid were mixed in 800 ml of distilled water. The pH of the buffer adjusted to 8.0 and final volume was brought to 1 L.

h) 1X TE Buffer: 1 ml of Tris base and 200 μ l of EDTA were dissolved in distilled water and final volume was made to 100 ml. Final composition of CTAB extraction buffer was prepared using different stock solutions (Table 3.3).

Table 3.3: Composition of CTAB extraction buffer for DNA isolation (for 100ml)

S. No.	Stock Reagent	Working Conc.	Quantity
1.	5M NaCl	1.4 M	28 ml
2.	1M Tris	100 Mm	20 ml
3.	0.5 M EDTA	20 Mm	4 ml
4.	10% CTAB	2.0%	20 ml
5.	Mercaptoethanol	1.0%	2 ml
6.	Double distilled water		26 ml

3.3.4 SSR amplification

3.3.4.1 Primers used for DNA amplification:

For the present investigation, 61 SSR primers were selected for assessment of genetic diversity (Table 3.4).

Table 3.4: List of SSR primers used for molecular studies

Sr. No	Oligo no.	Primer sequence forward	Primer sequence reverse
1	SSR 18362	CAAGTGGACAAATATGAGCCAA	TTCGTTTCGCAGAGTGATTG
2	SSR16028	TTACCTTCCCCACCCTAACC	TGACTTTTTGGGGAAACCCT
3	SSR12810	TTCCACAAAACAAATCTTGG	TTTTGGAGAGAAAAGGTTGGA
4	SSR11909	AATAATACCAGTGGCCCCATC	AAAGCTCCCTCCTCCCCTAC
5	SSR16183	GGAGAAATTTGATGGTGTAGCC	TGCAAATCTCTAATACTTTGCCTT
6	SSR12227	GGCATCGGTGAGTACCAACT	TTTCTCCTCCTTGGCCATAA
7	SSR12730	CGGTTTTTGAATTGTCTTCCC	ATCCCGACAGTCTCTGAAGG
8	SSR30665	AATTCCTGCTAAACCACCCC	GGTTTGTGAAGCCGAAAAA
9	SSR05830	TTTCGTTGTGCTCAGTGGAG	ACACCTTTCTTTCAC CCCCT
10	SSR22071	GCTGCTTGAATCGGTCTGT	GAGGAGGTAAATCATGCTCCA
11	SSR05737	TTGCCTTCGTAAGCAAAAA	GAAGTAAATGGGTTGGACGC
12	SSR07782	GGGTTTCGAGAAGTTGGTTGA	AAAGCTCTGCATCCACCATT
13	SSR 19493	AAGAGGCCAGAGATGGATGA	GCCAAAAATAGGCCAAAGT
14	SSR19430	TATGGCGAAGAAGCTTTGCT	AGGGGGATCTTGCTCTAAA
15	SSR05125	TGGCTCCTTCACATTGTTGT	TGGGAAAAAGGGTATGGAAA
16	SSR22172	CAACAATGAGTGGAAATGACATTTT	GACTTGGCTTTGGGATTCAA

17	SSR13340	GCTTTACATGGCTTCTCCCA	TTTCCTTGGCGACGATTAG
18	SSR06660	GATCGTTGCAAAACTCACGA	CGATTGACAGTTCGCTGAAA
19	SSR05819	AGATGCCAACTGATCTGCCT	CCAACCACGGTAGTTTCGAG
20	SSR03514	TAGGGTCCCCTTCCCTCATA	GGGTACCCAAAAGCAAGTGA
21	SSR16842	TGGGGTTAGGGTTCAAGTG	CAAGCTCTTCTCAACGGAC
22	SSR21186	TTTGAGCAAACTTCGCAAC	GCATGTTTTCATGTCATTGGA
23	SSR00973	TTGGGGCTGTTCTAATTTTCG	TCGTTGTTGAAGCCAAAAGAA
24	SSR13251	GGTCAATCCAAAAGAGAAAAGCA	ATCAACACCATTGACGACCA
25	SSR00083	GGCTGTGGAGTTCAAAGAGG	GGGAAGTCAAAATGTTTGCG
26	SSR13189	GCAGTCATTTTGGCGATACA	GCTGTGTCAGAAGCTCACAACT
27	SSR33278	GCAAACGCAATTAACACACG	GTTGGAATGAGGGAGTGAGC
28	SSR15477	CTGCCATTTCTGGGTTTGAT	AATTCTTCTGGGAATGGCCT
29	SSR11742	GCTATCCCCAAGGATGATGA	AGCTTGGCTTCGTCTTTTGA
30	SSR16226	TTAAAATTCCCAACGGAAACC	TGATGGGAGAAAGGTAAACAAGA
31	SSR13251	GGTCAATCCAAAAGAGAAAAGCA	ATCAACACCATTGACGACCA
32	UW020605	AACAGCTGTGCCATTCTCT	GGTTTGAAGTCCGCCATTAG
33	SSR11798,	TCCAAGCAAGTTCAATGCAA	CCCATTTTTCTCTCCATTTC
34	UW007281	GAGGAGGGTGGTGTGATTGAG	CCCTGTGGGTTCCACTCTAA
35	SSR15516	TGAGGGTTTAAAAGAAAAGGTG	GCCAATTCCCAATTCTTAAT
36	SSR18956	CGTATGTACGACAAAATGTGAACAG	TCGAAACCTTCAATACTTCTACCAA
37	CSWCT25	AAAGAAATTAAGTCAATCAAACCG	CCCACCAATAGTAAAATTATACAT
38	Cs-BCAT	CATTGTGTGAATGAAGACAAG	CTTCAACGCAAAACCTTCATC
39	Cs-Female1	TGGAGATAAAGCGTAAGGGAA	CCTCCAACGTCATAGAGTAAA
40	Cs-Female4	CGATCAGATATAACTGCAGCAGT	TAATAGTCGCTGCCAAGTAAAGC
41	Cs-Female7	TGGTTTGGTTTTTAGGGGAGA	CCCCACGTTACAAAATAGAAG
42	SSR22638	TGTGTAAGATTTTTATTGGATGCC	CTGAGCTTGATCAATTCCTTCA
43	SSR16695	CACAAATCCCACGAAGAACAA	TGCAATTATGGCAAATCAAAA
44	SSR00262	CCGTTGGTCTTGGACTCTCA	TGTA AAAAGTGATCAGGAGGGTCT
45	SSR00684	AAGGCCAAAAGACTATGCGA	CATCCCTTGCATCTCCACTT
46	SSR03070	GCTAACACTACCCGCTGCTT	AACAGAAAAGAGAATCGGGGG
47	SSR16226	TTAAAATTCCCAACGGAAACC	TGATGGGAGAAAGGTAAACAAGA
48	SSR13532	AAACCCAAGAATTGTAAACCCA	TGATCCATTTCTATTCTAACATTGA
49	SSR22083	TTATGCAACCATTGGAGAAGG	TGATTTGTTGTCTGTGCCAA
50	SSR07108	TAAGCAATTCCAGGAGAGGG	GTTCTTTGATGGGTGCCTGT
51	SSR17751	TCCAACGGAAAATTACAAGGA	TCAATTGTTGGATTTCATGTCAA
52	SSR00525	GGGCAGTGAAATTGGAGGTA	TTAAATAATGGGCTGGGCTG
53	SSR06210	TTGGAAAAGTCGCCAAACTT	TCCATGTCTGCTTTTGATTCC
54	SSR03621	CCCAGACACTTTTACACAACCC	TTCACCAACCCGTTTTCTTC
55	SSR16667	TTTGCAGAGGGCAAAGAAAG	TCGGTGGAGGGATTTCATAAC
56	SSR03341	TGCGAGTATTTCTGCATGTTG	TTCTTGGGAAAGGGAAGAT
57	SSR07057	CCATTTGGGTTCTCACACA	CCCATTTTACAGCTCCATT
58	SSR19178	CCGTTCTTAGAATAGCGTGT	CCCACGCCTTCTATTCTACA
59	SSR30647	GAAATGAGAGCAAGTTGCAAAA	AGGCGTAAATCTGACCGTTG
60	SSR14797	CCCTAAACCAGAAGTCACCAA	TGTGTTTGTAATGGTAAAGTCTTCAA
61	SSR04689	TCTCCGGCAGAAAGAAAAGA	TGCGTCTCCTTCTCCTCAT

Primer Dilution:

Nuclease free water was used for primer dilution at a concentration of 10 pmol.

3.3.4.2 PCR amplification:

For genomic DNA amplification, a reaction mixture of 10 μ l was prepared in 0.2 ml PCR tubes. Components used for PCR reaction contains 1 μ l of template DNA, 0.6 μ l of forward and 0.6 μ l of reverse primer, 3.5 μ l of master mix and 4.3 of double distilled water for each genotypes. Tubes comprising PCR reaction mixture were thoroughly mixed by using spinner. The DNA amplification were carried out in Thermal Cycler (BIO-RAD) using temperature profile given in Table 3.5

Table 3.5 Temperature profile used in PCR amplification

Primer Type	Steps	Temperature and time	Cycles
SSR	Initial denaturation	94 ⁰ C for 3-5 minutes	1
	Denaturation	94 ⁰ C for 30-60 seconds	} 35-36
	Annealing	50-60 ⁰ C for 30-60 seconds	
	Extension	72 ⁰ C for 60-80 seconds	
	Final extension	72 ⁰ C for 5-10 minutes	1
	Storage	4 ⁰ C for ∞	

3.3.5 SSR-PCR banding Profile

PCR products were resolved on 3% agarose gel electrophoresis. For the preparation of agarose gel (3%), 3g of agarose was dissolved in 100 ml 1X TE buffer and this mixture was heated in microwave until the solution became transparent. This solution was cooled for few minutes and then add ethidium bromide (5 μ l) for band visualization. Agarose gel was poured into gel mould along with combs and allowed for solidification for 30-40 minutes. 1 μ l of known DNA ladder (100 bp), 1 μ l of loading dye and 4 μ l of nuclease free water were mixed gently in PCR tubes for assessing the product size of SSR primers. Then 10 μ l of PCR products was loaded in

each well of the gel. Electrophoresis was carried out at 80V and current 120 for 2-3 hours and then gel was visualized under gel documentation unit (BIO-RAD).

3.3.6 Analysis of SSR profiles

The amplified DNA of 8 genotypes of cucumber developed SSR marker profiles. The SSR amplified bands of a particular molecular weight were confirmed as 1 (present) or 0 (absent) separately for each primer. The binary data were used to generate a similarity matrix using Jaccard's coefficient, $J_{ij} = C_{ij}/(n_i + n_j - c_{ij})$, where 'C_{ij}' is the number of positive matches between two genotypes, while n_i and n_j is the total number of band in genotype i and j, respectively, in SIMQUAL program of NTSYS-PC package (version 2.02) by Rohlf (1993).

$GD = 1 - [C_{ij}/(n_i+n_j- C_{ij})]$ was used to calculate Genetic distances (GD). The data were subsequently used to construct a dendrogram using the unweighted pair group method with arithmetical averages (UPGMA) in SAHN program of NTSYS – PC package (version 2.02).

I. Polymorphic information content (PIC)

The Polymorphic information content (PIC) values allows the estimation of the discriminatory potential of the locus by taking into concern not only expressed the number of alleles but also the relative frequency of those alleles. It also determines the informativeness of a given DNA marker (Anderson et al. 1993).

$$PIC = 1 - \sum_{i=1}^k P_i^2$$

Where, k is the total number of alleles identified for a given marker locus and P_i reveals the frequency of the ith allele among all the genotypes investigated. PIC value ranges from 0 (monomorphic) to 1 (very highly discriminative, with many alleles each in equal and low frequency).

II. Analysis of molecular variance (AMOVA)

The analysis of molecular variance was used to determine the components of variance on the basis of pair wise individual-by-individual genetic distance

matrix (Euclidean distance metric) generated for binary data by using the procedure as described in GenALEx 6.5 (Peakall and Smouse, 2012)

III. Principal coordinate analysis (PCoA)

Principal Coordinates Analysis (PCoA) was used to visualise the genetic relationship patterns in the matrix in GenALEx 6.5 (Peakall and Smouse, 2012).

IV. Clustering analysis

Binary data was used to estimate the genetic dissimilarity using the Jaccard dissimilarity index (d_{ij}) between pairs of accessions.

$$d_{ij} = \frac{(b+c)}{a+(b+c)}$$

where, d_{ij} represents the dissimilarity between units i and j .

From the dissimilarity matrix, a Neighbor-Joining tree (UnWeighted Neighbor Joining) was computed using the DARwin software version 5.0 (Perrier and Jacquemoud 2006). Branch robustness was tested using 1000 bootstraps.

V. Population structure

The number of populations (K) and subgroups within each gene pool were estimated using the software program STRUCTURE (Pritchard et al. 2000).

3.4 Evaluation of parents and hybrids

3.4.1 Nursery raising

For evaluation, the seeds of F_1 crosses and parental lines along with standard check (kian) were sown in February 19, 2020 and February 08, 2021. The nursery was raised in pro-trays containing mixture of cocopeat, perlite and vermiculite (3:1:1). Seedlings were raised using regular nursery practices. The seeds were treated with the fungicides Dithane M-45 and Bavistin before sowing to prevent fungal diseases.

3.4.2 Experimental layout and transplanting

The seedlings of eight parents and 28 F_1 crosses along with standard check were transplanted on April 05, 2020 (environment-1) and March 23, 2021 (environment-II). The experiment was carried out in Randomized Block Design (RBD) under modified naturally ventilated polyhouses (25 m × 10 m) number 8 and

9, respectively. The ten plants of each F₁ cross/parent were transplanted at a spacing of 70 cm × 30 cm in three replications and were trained on single stem. Five plants were randomly selected from each entry and were tagged. The observations were recorded from five tagged plants for the various characters.

3.4.3 Manure and fertilizer including fertigation

The recommended package of practices was followed to raise healthy crop. With the addition of vermicompost @ 5 tonnes per hectare, chemical fertilizers (50 kg each of Nitrogen, Phosphorus and Potassium per ha) were also added before transplanting in pits. After three weeks of transplanting, fertigation was done with liquid fertilizers (19:19:19) @ 5.0 g/litre of water thrice in a week and was stopped 15 days before the last fruit harvesting

3.4.4 Cultural practices

The intercultural operations viz., hoeing, irrigation, weeding, pruning and staking were carried out to ensure healthy crop growth and development. Both irrigation and fertigation were done with drip system. Staking is an important in cucumber and vines were trained on the nylon twines in a single stem

3.5 Observations recorded

The observations were recorded from five randomly selected parents/hybrids in each entry were listed below:

- 1. Days to first female flower:** The number of days taken from transplanting to opening of first female flower were counted and average number of days were calculated.
- 2. Nodal position of first female flower:** Node number was counted from the ground level at which first female flower appeared and mean value was calculated.
- 3. Number of female flowers per node:** Number of female flowers on each node were counted and mean value was calculated.
- 4. Days taken to first fruit picking:** Number of days were counted from transplanting date to first fruit picking date in each entry and average value was worked out.

5. **Fruit length (cm):** Polar length was measured with scale and mean value was calculated.
6. **Fruit diameter (cm):** Fruit diameter was recorded with the help of vernier caliper and mean value was calculated.
7. **Fruit weight (g):** Fruit weight was measured by using a weighing balance and mean value was worked out.
8. **Number of fruits per plant:** Number of fruits harvested in each picking from the selected plants were added to obtain total number of fruits per plant and average was worked out.
9. **Marketable yield per plant (kg):** Total weight of marketable fruits in different pickings were recorded and mean was worked out.
10. **Marketable yield per meter square area (kg):** Marketable yield per meter square area was calculated by counting the number of plants per meter square and multiplied by marketable yield per plant.
11. **Harvest duration (days):** Total number of days was counted from first fruit picking to last picking and average was calculated.
12. **Internodal length (cm):** Distance between two nodes was measured with the help of scale at three spots on vine and average value was calculated.
13. **Vine length (m):** Vine length was measured from basal to apical shoot at last fruit picking and mean was worked out.
14. **Flesh to seed cavity ratio:**

$$F/C \text{ ratio} = \frac{P \times E}{P' \times E'}$$

Where, P is the polar diameter of fruit, E is the equatorial diameter of fruit, P' is the polar diameter of fruit cavity, E' is the equatorial diameter of fruit cavity.

15. **Flesh thickness (mm):** Flesh thickness was measured with vernier calliper from an equatorial section of the fruits and average value was calculated.
16. **Color of the fruit:** The fruit color was observed at near maturity of fruits and was regarded as light, medium and dark green by using Royal Horticulture color chart (Fifth Edition)

17. Incidence of downy mildew disease (%)

At maturity stage when disease was at its peak level the observations were made for the incidence of downy mildew disease. On the basis of leaf area affected, ten leaves from top to bottom on the tagged plant were observed from different level of height and categorized according to the scale adopted by Reuveni (1983):

Scale to record downy mildew of cucumber

Disease rating	Per cent infection	Description	Disease reaction
0	0	No symptoms	Highly Resistant (HR)
1	1-10	Scattered small lesions per leaf. Less than 25% of leaf area turned yellowish.	Resistant (R)
2	11-20	Scattered small lesions per leaf. Yellowing covered > 25-50% of leaf area.	Moderate Resistant (MR)
3	21-40	Scattered or coalesced lesions per leaf. Greater than 50% of leaf area turned yellowish.	Moderate Susceptible (MS)
4	> 40	> 40% coalesced lesions per leaf. Yellowing covered > 75% of the leaf area. The infected area of leaf turned brown and died.	Susceptible (S)

18. Total soluble solids (°Brix):

The total soluble solids content was calculated using a 'Erma Hand Refractometer' at room temperature (20°C) by putting a drop of juice on the prism and taking a reading. The values recorded were expressed as a percentage of juice (AOAC 1970).

19. Ascorbic acid (mg/100g):

The ascorbic acid content was calculated from the cucumber fruits by 2,6-dichlorophenol Indophenol Visual Titration Method as suggested by Ranganna

(1979). 100 mg of L-ascorbic acid was dissolved in 100 ml of metaphosphoric acid (3%) for the preparation of standard ascorbic acid solution. 10 ml of this solution was diluted to 100 ml with 3% metaphosphoric acid. 15 g of metaphosphoric acid was dissolved in 500 ml distilled water for the metaphosphoric acid (3%) solution. For the preparation of dye, 50 mg of sodium salt of 2,6-dichlorophenol indophenol was dissolved in 150 ml of distilled water including 42 mg of sodium bicarbonate then cool it and made the final volume upto 200 ml. For the dye factor determination, 5 ml each of standard ascorbic acid and metaphosphoric acid (3%) solution were taken in a flask and titrated against the dye for pink colour development which persists for few seconds. Dye factor (mg of ascorbic acid per ml of dye) was estimated by using the following formula:

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

Blend 10 g of macerated sample with metaphosphoric acid (3%) to make up the volume to 100 ml and then pipette out 10 ml solution from this 100 ml solution for titration against 2, 6-dichlorophenol indophenol dye. The ascorbic acid content was estimated from the formula given below:

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

20. Total sugar (%):

Reagents:

1. Anthrone: Dissolve 0.2 g of anthrone in 100 ml of concentrated H₂SO₄ (95%).
2. Stock Solution: 100 mg of Glucose or Dextrose is dissolved in 100 ml of distilled water.
3. Working solution: 10 ml of stock solution is diluted and final volume was made 100 ml

Extraction of total sugar

1 g of sample was grinded in pestle mortar in 50 ml of 80% alcohol. After 15 minutes, samples were filtered with whatman filter paper. Discard the residue and

filtrate was boiled in water bath and content was reduced to half concentration to original volume. Add 10 ml of lead acetate and sodium oxalate crystals in each sample and sample turned milky. Filter the content and clear solution was obtained (Sadasivam and Manickam 1992).

Estimation of total sugars

1. Weigh 100 mg of dextrose and mix in 100 ml of distilled water for preparation of working solution.
2. Take 0.2, 0.4, 0.6, 0.8 and 1 ml of working solution in five different test tubes labelled as A, B, C, D and E.
3. Volume was made upto 1 ml with distilled water in each test tube.
4. In another test tube, add 0.2 ml of sample and volume was made with distilled water.
5. Add 4 ml of anthrone in each test tube.
6. Vortex and boil each test tube in boiling water bath for 10-15 minute. Cool it and take reading at 630 nm in spectrophotometer.

$$\text{Total sugar (\%)} = - \frac{\text{Sugar value from graph (mg)} \times \text{Total volume of extract (ml)}}{\text{Aliquot sample used (ml)} \times \text{weight of sample (mg)}} \times 100$$

21. Reducing sugar (%):

Reagents

1. DNS (Dinitrosalicylic acid) reagents- Add 1 g of Dinitrosalicylic acid, 200 mg of crystalline phenol, 20 mg of sodium sulphite in 100 ml of NaOH solution (1%). Mix all the reagents thoroughly.
2. 40% Rochelle salt solution
3. Standard sugar solution: Add 100 mg of glucose in 100 ml of distilled water
4. Working solution: From stock solution, add 10 ml of solution and make the final volume 100 ml with distilled water.

Extraction of reducing sugar

Weigh 1 gm of sample and add 5 ml of alcohol (80%) twice in each sample. Collect the supernatant and boil in water bath for evaporation of sample. Then add 10 ml of distilled water in each sample for dissolving the sugar (Sadasivam and Manickam 1992).

Estimation of reducing sugar

Add 1 ml of supernatant in each test tube and make the final volume of 3 ml with distilled water. Prepare working standard solution in five test tubes containing 0.2, 0.4, 0.6, 0.8 and 1 ml of solution and add 3 ml of DNS in each test tube and mix thoroughly. Also, prepare one blank containing 3 ml of DNS solution with all the samples. Boil the samples in water bath for 5 minutes for color development. Then add Rochelle salt solution (40%) in each sample and mix it properly. Keep the test tubes in water for 5 minutes. The absorbance was measured at 510 nm in spectrophotometer.

$$\text{Reducing sugar (\%)} = \frac{\text{Sugar value from graph } (\mu\text{g}) \times \text{total volume of extract (ml)} \times 1}{\text{Aliquot of extract used (ml)} \times \text{weight of sample (mg)} \times 1000}$$

3.6 Statistical analysis

Average values for each genotype (parental lines and hybrids and standard check) in each replication for the traits studied were used for further statistical analysis. A brief outline of the procedure adopted for estimation of different statistical parameters is given below:

3.6.1 Analysis of variance

The data for different characters were analyzed as per Panse and Sukhatme (1984):

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

where,

Y_{ij}	=	Phenotypic observation of i^{th} genotype grown in j^{th} replication
μ	=	General population mean
g_i	=	Effect of i^{th} genotype
r_j	=	Effect of j^{th} replication
e_{ij}	=	Error component of i^{th} genotype in j^{th} replication

On the basis of this model, the analysis of variance was done as follows:

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F ratio	Expected Mean Squares
Replications (r)	(r-1)	S_r	$M_r = S_r/(r-1)$	M_r/M_e	$\sigma^2_e + g\sigma^2_r$
Genotypes (g)	(g-1)	S_g	$M_g = S_g/(g-1)$	M_g/M_e	$\sigma^2_e + r\sigma^2_g$
Error (e)	(r-1)(g-1)	S_e	$M_e = S_e/(r-1)(g-1)$		σ^2_e
Total	(rg-1)	-			

where,

r	=	Number of replications
g	=	Number of genotypes
σ^2_r	=	Variance due to replication = M_r
σ^2_g	=	Variance due to genotypes = M_g
σ^2_e	=	Error variance = M_e

The replications and entries mean sum of squares were tested against error mean squares by 'F' test for (r-1), (r-1)(g-1) and (g-1), (r-1)(g-1) degree of freedom at P=0.05. From this analysis, the following standard errors were calculated, where the 'F' test was significant.

The pooled over environment was done as per following analysis of variance.

ANOVA

Source of variation	df	Mean sum of square	Expected mean sum of square
Replications (within environments)	E(r-1)	M_r	-
Environments	(E-1)	M_E	
Genotypes	(g-1)	M_g	$\sigma^2_e + r\sigma^2_g \times E + rE\sigma^2_g$
Genotypes × Environment	(g-1)(E-1)	$M_g \times E$	$\sigma^2_e + r\sigma^2_g \times E$
Pooled error	E(g-1)(r-1)	$M_e(C)$	σ^2_e

Where,

r	=	number of replicates
E	=	number of environments
g	=	number of genotypes
σ^2_e	=	Error variance
$\sigma^2_g \times E$	=	Variance due to genotypes \times environment interactions
σ^2_g	=	Variance due to genotypes

$$Me(C) = \frac{(\text{Error ss at Env. I} + \text{Error ss at Env. II})}{(\text{df at Env. I} + \text{df at Env. II})}$$

The replications (within environments), environments, genotypes, genotypes \times environment mean sum of square were tested against pooled error mean squares by 'F' test for E (r-1), E (g-1) (r-1); (E-1), E(g-1) (r-1); (g-1), E(g-1) (r-1) and (g-1) (E-1), E (g-1) (r-1) degree of freedom at P = 0.05, respectively.

From these analysis, the following standard errors were calculated where the 'F' test was significant.

Standard error for the entry mean:

$$\begin{aligned} SE(m) = \text{Individual environment} &= \pm (Me/r)^{1/2} \\ \text{Pooled environment} &= \pm (Me(C)/rE)^{1/2} \end{aligned}$$

Standard error for the difference of entry mean:

$$\begin{aligned} SE(d) \text{ for individual environment} &= \pm (2Me/r)^{1/2} \\ SE(d) \text{ for pooled environment} &= \pm (2Me(C)/rE)^{1/2} \end{aligned}$$

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

$$CD = SE(d) \times 't' \text{ value at error degree of freedom and } P = 0.05$$

$$\text{Coefficient of variation (CV) \%} = (Me^{1/2} \text{ or } Me(C)^{1/2} / \text{general mean}) \times$$

3.6.2 Estimation of heterosis

The estimates of heterosis were calculated as the deviation of F_1 mean (\bar{F}_1) from the mean values of better parent (\bar{BP}) and standard check (\bar{SC}) hybrid Kian.

1. Heterosis over better parent/ heterobeltiosis (%) = $[(\bar{F}_1 - \bar{BP})/\bar{BP}] \times 100$
2. Heterosis over standard check/economic heterosis (%) = $[(\bar{F}_1 - \bar{SC})/\bar{SC}] \times 100$

1. Calculation of standard errors

(i) SE for testing heterosis over BP:

$$\text{Individual environment} = \pm (2Me/r)^{1/2} = \text{SE (H}_1\text{)}$$

$$\text{Pooled environment} = \pm (2Me/rE)^{1/2} = \text{SE (H}_1\text{)}$$

(ii) SE for testing heterosis over SC:

$$\text{Individual environment} = \pm (2Me/r)^{1/2} = \text{SE (H}_2\text{)}$$

$$\text{Pooled environment} = \pm (2Me/rE)^{1/2} = \text{SE (H}_2\text{)}$$

2. **Test of significance for heterosis:** There are two methods:

Method-I

The difference of $(\bar{F}_1 - \bar{BP})$ or $(\bar{F}_1 - \bar{SC}) \geq [\text{SE}(H_1) \text{ or } \text{SE}(H_2)] \times \text{'t' tab}$, at error degree of freedom of individual environment analysis of variance or at error degree of freedom of pooled over environment analysis and $P=0.05$] were considered significant and the asterisk (*) was put on the per cent values only. This method is relatively less time consuming.

Method-II

't' calculated values were worked out as follow

1. 't' calculated values for heterosis over BP = $(\bar{F}_1 - \bar{BP})/\text{SE}(H_1)$

$$2. \quad 't' \text{ calculated value for heterosis over SC} = (\bar{F}_1 - \overline{SC})/SE(H_2)$$

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

't' calculated values \geq 't' tabulated values were marked as significant and asterisk was put on per cent values only (Dabholkar 1992).

3.6.3 Diallel cross analysis

A set of all possible mating procedure among a set of genotypes is designated a diallel cross and analysis of such a cross is known as diallel analysis. The analysis provides information on general and specific combining ability of parents and their crosses and also on the nature and magnitude of genetic parameters. The diallel analysis was carried out as per Method 2 (parents plus one set of crosses and no reciprocal), Model I (fixed effect model) as described by Griffing (1956b).

Combining ability analysis for individual environment/year

When the F-test revealed significant differences among the genotypes, combining ability analysis was followed. A linear mathematical model for an observation made on *ijth* genotype could be expressed as:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc} \sum_K \sum_L e_{ijKL}$$

where,

Y_{ij} = phenotype of the hybrid between i^{th} and j^{th} parents in K^{th} block

μ = population mean

g_i = general combining ability (GCA) effect of the i^{th} parent

g_j = general combining ability (GCA) effect of the j^{th} parent

s_{ij} = specific combining ability (SCA) effect of the hybrid between i^{th} and j^{th} parents

such that $s_{ij} = s_{ji}$

bc = block effect

e_{ijKL} = environment effect associated with $ijKL^{\text{th}}$ observation

$\frac{1}{bc} \sum_K \sum_L e_{ijKL}$ = is the mean error effect

The restrictions imposed on this model were:

$$\sum_i g_i = 0 \text{ and}$$

$$\sum_j s_{ii} + s_{ji} = 0 \text{ (for each } i\text{)}$$

Analysis of variance for combining ability Method 2 Model I (Griffing 1956b)

Source of variation	df	Sum of squares	Mean sum of squares	Expected mean sum of squares	F-ratio
General combining ability (GCA)	(p - 1)	Sg	Mg	$\sigma^2_e + \frac{(p+2)}{(p-1)} \sum_i g^2_i$	Mg/Me'
Specific combining ability (SCA)	$\frac{p(p-1)}{2}$	Ss	Ms	$\sigma^2_e + \frac{2}{p(p-1)} \sum_i \sum_j s^2_{ij}$	Ms/Me'
Error	(b-1)[$\frac{p(p-1)}{2} + (p-1)$]	Se	Me' (=Me/r)	σ^2_e	

where,

$$Sg = \frac{1}{p+2} \left[\sum_i (y_{i.} + y_{ii})^2 - \frac{4}{p} y^2_{..} \right] \text{ and}$$

$$Ss = \sum_{i \leq j} \sum_j y_{ij}^2 - \frac{1}{p+2} \sum_i (y_{i.} + y_{ii})^2 + \frac{2}{(p+1)(p+2)} y^2_{..}$$

p = number of parents

b = number of blocks or replications

$y_{i.}$ = total number of array of i^{th} parent

y_{ii} = value of i^{th} parent

$y_{..}$ = grand total of $[p(p-1)/2]$ progenies and (p) parental values

y_{ij} = progeny mean value in the diallel table

When the mean squares for GCA and SCA were found significant, their respective effects and standard errors were calculated.

3.6.4 Combining ability estimates per effects and their standard errors

General combining ability effects of i^{th} parent:

$$\hat{g}_i = \frac{1}{(p+2)} (y_{i.} + y_{ii}) - \frac{2}{p} y_{..}$$

Specific combining ability effect of ij^{th} crosses:

$$\hat{s}_{ij} = y_{ij} - \frac{1}{(p+2)}(y_{i.} + y_{.j} + y_{ij}) + \frac{2}{(p+1)(p+2)}y_{..}$$

where,

p = number of parents

$y_{i.}$ = total number of array i^{th} parent

$y_{.j}$ = total of array involving j^{th} parent

y_{ii} = value of the i^{th} parent

y_{jj} = value of j^{th} parent

$y_{..}$ = total of all the $\left[\frac{p(p+1)}{2}\right]$ items in the diallel table

y_{ij} = mean value of the cross involving i^{th} and j^{th} parent

Standard error to test the significance of general and specific combining ability and the standard error of difference between the two estimates were computed from the following formulae:

$$1. \text{ SE for testing GCA (gi) effects} = \pm \sqrt{\frac{Me'(p-1)}{p(p+2)}}$$

$$2. \text{ SE for testing difference between two GCA (gi - gj) effects} = \pm \sqrt{\frac{2Me'}{(p+2)}}$$

$$3. \text{ SE for testing SCA (sij) effects} = \pm \sqrt{\frac{Me'(p^2+p+2)}{(p+1)(p+2)}}$$

4. (i) SE for testing difference between two SCA effects in the same array ($S_{ij} - S_{ik}$)

$$= \pm \sqrt{\frac{2(p+1)Me'}{(p+2)}}$$

(ii) SE for testing difference between two SCA effects in the different arrays ($S_{ij} - S_{kl}$)

$$= \pm \sqrt{\frac{2p(Me')}{(p+2)}}$$

Test of significance for GCA and SCA effects

There are two methods

Method-I

GCA and SCA effects $\geq [(SE_{g_i}/SE_{s_{ij}}) \times 't'$ tab at error degree of freedom and $P = 0.05]$ were marked significant (*).

Method-II

$$(a) \quad t_i \text{ (cal) for GCA of parents} = (g_i - 0)/SE (g_i)$$

$$(b) \quad t_{ij} \text{ (cal) for SCA of crosses} = (S_{ij} - 0)/SE (S_{ij})$$

where,

t_i (cal) and t_{ij} (cal) are the calculated 't' values,

$$g_i = \text{GCA effect of } i^{\text{th}} \text{ parent}$$

$$s_{ij} = \text{SCA effect of } ij^{\text{th}} \text{ cross}$$

The GCA effects of parents and SCA effects of crosses were marked significant (*) when the values of t_i (cal) and t_{ij} (cal) were \geq 't' tabulated value at error degree of freedom of individual environment or pooled over environment and $P = 0.05$.

Critical differences (CD) for comparing GCA effects of parents and SCA effect of crosses

$$(a) \quad \text{CD for GCA} = SE (D1a) \times 't' \text{ tab (error df, } p=0.05)$$

$$(b) \quad \text{CD for SCA} = SE (D2a) \times 't' \text{ tab (error df, } p=0.05)$$

The difference between GCA of any two parents and SCA of any two crosses were considered significant when the differences were \geq respective CD values.

3.6.5 Combining ability analysis pooled over environments per years

The pooled analysis over environments for combining ability for experimental Method 2 Model I was carried out by following method of Singh (1973). The notations used by Singh (1973) are: p (number of parents), b (number of blocks), c (number of observations for each of the plot) and L (number of environments).

The model used is:

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + LK + (gL)_{ik} + (gL)_{jk} + (SL)_{ijk} + H = \frac{1}{bc} \sum_m \sum_{ijkmr}$$

where,

μ	=	population mean
g_i (g_j)	=	GCA effect of i^{th} (j^{th}) parent
S_{ij}	=	SCA effect of the crosses between the i^{th} and j^{th} parents
LK	=	effect of k^{th} environment
$(gL)_{ik}$ or $(gL)_{jk}$	=	interaction between GCA effects of the i^{th} and j^{th} parents with k^{th} environment
$(SL)_{ijk}$	=	the interaction between SCA effects of the ij^{th} cross and the k^{th} environment
H	=	0 for fixed effect model

Least square estimates of effects and their interaction with environment per year

The estimates are:

$$\hat{\mu} = 2x.../p(p+1)L$$

$$\hat{g}_i = [x_{i..} + x_{ii..} - (2/p)x...]/(p+2)L$$

$$\hat{S}_{ij} = (x_{ij}/L) - [(x_{i..} + x_{ii..} + x_{j..} + x_{jj..})/(p+2)L] + 2x.../(p+1)(p+2)L$$

$$\hat{L}K = [2x..K/p(p+1)] - 2x.../p(p+1)L$$

$$\hat{g}L = [\{x_{i..K} + x_{iiK} - (2/p)x..K\}/(p+2)] - \{x_{i..} - (2/p)x...\}/(p+2)L$$

$$\hat{S}L = x_{ijK} - \{(x_{i..K} + x_{iiK} + x_{j..K} + x_{jjK})/(p+2)\} + \{2x..K/(p+1)(p+2)\} - (x_{ij}/L + \{(x_{i..} + x_{ii..} + x_{j..} + x_{jj..})/(p+2)L\} + \{2x.../(p+1)(p+2)L\})$$

The sum of squares was calculated as follows:

$$SS_{\hat{\mu}} = 2x^2.../p(p+1)L$$

$$SS_{(\hat{g}_i)} = \{\sum_i (x_{i..} + x_{ii..})^2/(p+2)L\} - \{4x^2.../p(p+2)L\}$$

$$SS_{(\hat{S})} = \sum_i \leq \sum_j (x^2_{ij}/L) - \left\{ \sum_i (x_{i..} + x_{ii..})^2/(p+2)L \right\} + \{2x^2.../(p+1)(p+2)L\}$$

$$SS(\hat{L}) = \left\{ (2 \sum_K x \dots K) / p(p+1) \right\} - \{ (2x^2 \dots / p(p+1)L) \}$$

$$SS(\hat{g}L) = \left\{ \sum_K \sum_i (x_i \cdot K + x_{ii}K)^2 / (p+2) \right\}$$

$$- \left\{ 4 \sum_K x^2 \dots (K/p(p+2)) \right\}$$

$$- \left\{ \sum_i (x_{i.} + x_{ii.})^2 / ((p+2)L) + \{ 4x^2 \dots / p(p+2)L \} \right\}$$

$$SS(\hat{S}L) = \sum_K \sum_{i \leq j} x_{ijk}^2$$

$$- \left\{ \sum_K \sum_i \frac{(x_i \cdot K + x_{ii}K)^2}{(p+2)} \right\} + \left\{ 2 \sum_K x^2 \dots \frac{K}{(p+1)(p+2)} \right\}$$

$$- \left(\sum_{i \leq j} \frac{x_{ij}^2}{L} + \left\{ \sum_i \frac{(x_{i.} + x_{ii.})^2}{(p+2)} L \right\} - \frac{2x^2}{(p-1)(p+2)L} \right)$$

where,

$SS(\hat{g})$	=	Sum of squares due to GCA
$SS(\hat{S})$	=	Sum of squares due to SCA
$SS(\hat{L})$	=	Sum of squares due to location
$SS(\hat{g}L)$	=	Sum of squares due to GCA \times Location
$SS(\hat{S}L)$	=	Sum of squares due to SCA \times Location
x_i	=	Arrays total of i^{th} parent
x_{ii}	=	Mean values of the i^{th} parent
$x_{..}$	=	Grand total of $p(p-1)$ progenies and parental values

Analysis of variance for the design of experiment

Source	df	MS	Expectation of MS
GCA	$(p-1)$	Mg	$\sigma^2 e + \frac{(p+2)L}{(p-1)} \sum_i g^2 i$
SCA	$p(p-1)/2$	MS	$\sigma^2 e + \frac{2L}{(p-1)} \sum_{i \leq j} s^2 ij$
Location	$(L-1)$	ML	$\sigma^2 e + \frac{p(p+1)}{2(L-1)} \sum_k L^2 K$

GCA Environment	$\times (p-1)(L-1)$	MgL	$\sigma^2 e + \frac{(p+2)}{(p-1)} \sum_K \sum_i (gL)^2 iK$
SCA Environment	$\times p(p-1)(L-1)/2$	MsL	$\sigma^2 e + \frac{2}{p(p-1)} \sum_K \sum_{i \leq j} (sL)^2 ijK$
Error	$L(p-1)(b-1)$	Me'	$\sigma^2 e$

Variance of effects and their differences:

- i) Var. (μ) = $\{2/p(p+1)\} \sigma^2 e$
- ii) Var. (g_i) = $\{(p-1)/p(p+2)L\} \sigma^2 e$
- iii) Var. ($g_i - g_j$) = $\{2/(p+2)L\} \sigma^2 e \dots (i=j)$
- iv) Var. (S_{ij}) = $\{(p^2+p+2)/(p+1)(p+2)L\} \sigma^2 e \dots (i=j)$
- v) Var. ($S_{ij} - S_{iK}$) = $\{2(p+1)/(p+2)L\} \sigma^2 e \dots (i=j, K)$
- vi) Var. ($S_{ij} - S_{K_m}$) = $\{2p/(p+2)L\} \sigma^2 e \dots (i=j, K, m)$

where,

$\sigma^2 e$ is the estimate of $\sigma^2 e$ and given by $\sigma^2 e = Me$.

S.E. = (Var. of that estimate)^{1/2}

CD of the estimate:

Application to differences between any two mean values and to the difference between estimates involved in (ii) to (vi).

CD = SE \times 't'; where 't' is the tabulated value for ml degree of freedom and $p = 0.05$

Estimation of additive ($\sigma^2 A$) and dominance ($\sigma^2 D$) components of variance:

For computing the additive and dominance components of variance, following formulae have been used (Singh and Chaudhary 1985).

$$\sigma^2 gca = 1/(n+2) (Mg - Ms)$$

$$\sigma^2 sca = Ms - Me'$$

$$\sigma^2 A = 2 \sigma^2 gca$$

$$\sigma^2 D = \sigma^2 sca$$

where,

Mg = Mean squares due to gca

Ms = Mean squares due to sca

Me' = Mean squares due to error

Average degree of dominance

It was calculated by using the following formula:

$$\text{Average degree of dominance} = \sqrt{\frac{\sigma_D^2}{\sigma_A^2}}$$

4. RESULTS AND DISCUSSION

The present investigation entitled, “Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)” were carried out at the experimental farm of Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur to estimate the nature of combining ability, gene action, heterosis for yield and its component traits and to recognize the best cross combination(s) of parthenocarpic cucumber for protected conditions. To study the extent of combining ability, gene action and heterosis eight parental lines were selected and crossed in diallel fashion (excluding reciprocals) to develop 28 F₁ hybrids. In 2020 and 2021, 28 F₁ cross combinations and eight parental lines along with standard check were evaluated with three replications in Randomized Block Design under protected conditions. Genetic diversity of eight parental lines was assessed using SSR markers to identify the diverse parents. In this chapter, results pertaining to study are discussed in detail under the following headings:

4.1 Genetic diversity studies through molecular markers

4.2 Analysis of variance

4.3 Mean performance

4.4 Combining ability and gene action

4.5 Heterosis

4.1 Genetic diversity studies through molecular markers

Selection of suitable parent for hybridization depends upon the presence of genetic variation in the gene pool. Identification of the suitable parents is the most imperative for breeding programme. The D²-statistics are a powerful traditional tool for identification of divergent genotypes by intra and intergroup distance. Cluster composition alters with location and environmental location revealing that D²-statistics is affected by environmental variation ensuing inconsistent clustering of genotypes. Recent progress in plant genomics offers an opportunity for assessing genetic diversity through use of molecular markers. Molecular markers/DNA makers

are more advantageous than morphological characterization due to more stability under different environments. Different types of molecular markers like random amplified polymorphic DNA (RAPD), sequence characterized amplified regions (SCAR), amplified fragment length polymorphisms (AFLP) and simple sequence repeats (SSR) are available (Dar et al. 2017). Among all, SSR markers are widely used for genetic diversity analysis.

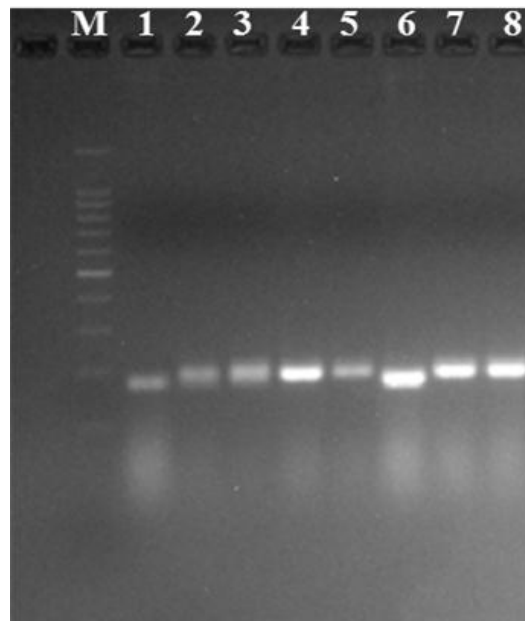
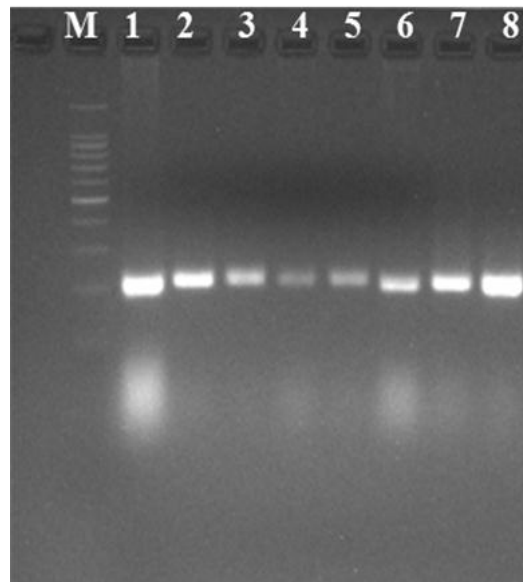
4.1.1 Genotyping

In the present investigation, 61 SSRs cucumber primers were screened for PCR amplification on eight genotypes. Out of 61 primers, 56 primers showed polymorphism (Table 4.1). For each 56 SSR primers in 8 genotypes, allele frequency per locus, polymorphic information content and heterozygosity was observed. A total of 160 amplicons were created with amplicon size ranging from 100 to 380 bp. Maximum four alleles per locus were amplified by UW007281, SSR11742 and SSR04689 (Table 4.1). The variation produced by SSR markers in the number of alleles per locus revealed presence of heterozygosity indicating huge variability in the germplasm. Major allele frequency includes recurrently occurrence of allele in single primer and it varied from 0.29 (UW007281) to 0.88 (SSR05830) with an average value of 0.53. The polymorphic information content (PIC), a measure associated with marker discriminating power varied from 0.19 (SSR05830) to 0.74 (UW007281) and heterozygosity ranged from 0.23 (SSR05830) to 0.84 (UW007281) with a mean of 0.62.

Similarly, Dar et al. (2017) and Lv et al. (2012) observed an average number of alleles 2.9 and 13.7 per locus, respectively. Our study revealed similar results of PIC (0.74) in comparison with previous reports on cucumber i.e. 0.664 and 0.69 (Hu et al. 2011; Normohamadi et al. 2017) while, PIC was lower in Indian cucumber (0.310), Chinese cucumber (0.388) and cucumber (0.33) (Hu et al. 2011; Pandey et al. 2013; Dar et al. 2017). A PIC value ranged from 0.12-0.44 for 15 primers with the mean value of 0.21 (Someh et al. 2016). Similarly, the results of expected heterozygosity are in accordance with earlier studies on cucumber with the range of 0.074-0.428 with the mean value of 0.255 (Pandey et al. 2018). Park et al. (2021) assessed the genetic diversity using a core set of single nucleotide polymorphisms (SNPs) in 280 cucumber accessions and reported a range of 0.04-0.82 per loci heterozygosity with the mean value of 0.32.

Table 4.1: Detail of polymorphic SSR primers used for the molecular characterization of eight parthenocarpic cucumber parental lines

Locus/SSR	Name	Band size (bp)	No. of alleles	PIC	Heterozygosity	Major allele frequency
1	Cs-Female-1	180-220	3	0.55	0.72	0.50
2	Cs-Female-4	200-250	2	0.31	0.40	0.75
3	UW007281	180-250	4	0.74	0.84	0.29
4	SSR15516	200-250	3	0.51	0.63	0.50
5	SSR 00083	100-150	3	0.52	0.63	0.56
6	Cs-Female-7	100-150	2	0.38	0.55	0.50
7	SSR33278	190-220	3	0.61	0.70	0.50
8	SSR15477	180-220	2	0.31	0.40	0.75
9	SSR22172	190-220	3	0.50	0.62	0.57
10	SSR06660	180-220	3	0.58	0.70	0.37
11	SSR18362	200-220	3	0.58	0.70	0.42
12	SSR11909	200-280	2	0.35	0.49	0.67
13	SSR16028	150-200	3	0.47	0.57	0.63
14	SSR30665	180-210	2	0.31	0.40	0.75
15	SSR05830	150-200	2	0.19	0.23	0.88
16	SSR13251	160-180	3	0.53	0.66	0.43
17	UW020605	200-230	3	0.56	0.67	0.50
18	SSR11798	200-280	2	0.38	0.55	0.50
19	SSR13189	150-250	3	0.67	0.77	0.38
20	SSR33278	200-220	2	0.33	0.44	0.71
21	SSR15477	200-230	3	0.52	0.63	0.38
22	SSR11742	200-250	4	0.71	0.80	0.37
23	SSR16226	100-180	3	0.61	0.70	0.50
24	SSR05125	100-140	3	0.56	0.67	0.50
25	SSR05819	120-160	3	0.67	0.79	0.33
26	SSR03514	100-130	2	0.36	0.50	0.63
27	SSR12730	100-180	3	0.57	0.66	0.57
28	SSR12810	150-200	3	0.64	0.75	0.43
29	SSR22071	200-300	3	0.67	0.77	0.37
30	SSR22172	150-180	2	0.31	0.43	0.75
31	SSR06660	130-270	3	0.58	0.70	0.37
32	SSR19493	200-250	3	0.37	0.43	0.75
33	SSR19430	170-200	3	0.56	0.71	0.40
34	SSR18956	350-380	3	0.54	0.67	0.50
35	SSR16842	250-320	3	0.54	0.67	0.50
36	SSR21186	150-200	3	0.50	0.62	0.57
37	SSR13251	150-220	3	0.54	0.67	0.50
38	SSR16183	150-200	2	0.36	0.50	0.63
39	SSR12227	130-150	2	0.38	0.55	0.50
40	SSR03341	150-200	3	0.54	0.67	0.50
41	SSR00684	160-200	3	0.52	0.60	0.62
42	SSR16226	160-200	3	0.37	0.43	0.75
43	SSR00525	200-250	3	0.67	0.77	0.38
44	SSR03621	150-190	3	0.67	0.77	0.38
45	SSR16667	190-230	3	0.52	0.60	0.63
46	SSR07057	200-260	3	0.63	0.73	0.37
47	SSR16695	130-180	3	0.61	0.70	0.50
48	SSR00262	190-220	3	0.31	0.40	0.75
49	SSR19178	200-260	3	0.61	0.70	0.50
50	SSR04689	120-190	4	0.70	0.79	0.38
51	SSR22638	100-150	3	0.58	0.70	0.37
52	SSR17751	200-230	4	0.67	0.77	0.38
53	SSR30647	160-190	3	0.54	0.67	0.50
54	SSR07108	190-240	3	0.37	0.43	0.75
55	SSR06210	150-200	3	0.54	0.67	0.50
56	SSR22083	150-210	3	0.41	0.48	0.71
	Mean		2.85	0.51	0.62	

**SSR 11742****UW007281**

1: DDPCG4, 2: DDPCG1, 3: Punjab Kheera-1 (PK-1), 4: Pant Parthenocarpic cucumber-2 (PPC-2), 5: Pant Parthenocarpic cucumber-3 (PPC-3), 6: DDPCW1, 7: DDPCG2, 8: DDPCG5

Plate 2: SSR profile of cucumber genotypes

4.1.2 Diversity analysis

Based on polymorphism demonstrated by SSR markers, Jaccard's similarity coefficient was used to construct dendrogram using UPGMA method of NTSYS software (version 2.02). Cluster analysis classified the cucumber genotypes into two main clusters. Cluster A and cluster B consists of 5 and 3 genotypes, respectively (Fig. 4.1). Cluster A was further divided into two sub-clusters A₁ comprised of 4 genotypes (DDPCG4, PK-1, PPC-2 and PPC-3) while, only one genotype (DDPCG1) in sub-cluster A₂ (Table 4.2). Cluster B comprised of 3 genotypes and was further divided into two sub-cluster B₁ and B₂. Sub cluster B₁ consists of only single genotype viz., DDPCW1 and sub-cluster B₂ comprised of 2 genotypes namely, DDPCG2 and DDPCG5. The genetic similarity coefficient was estimated between 0.56 to 0.70 among cucumber genotypes with mean value of 0.63. Clustering of population into two diverse groups indicates the genetic diversity among genotypes. Similar results were reported by Dar et al. (2017) which grouped cucumber germplasm into two main distinct clusters. Someh et al. (2016) and Normohamadi et al. (2017) reported Jaccard's similarity coefficient ranging from 0.56 to 0.88 and 0.51 to 0.92 in cucumber, respectively. Lower range of Jaccard's similarity coefficient viz., 0.01-0.44 and 0.35-0.51 was reported in cucumber by Valcarcel et al. (2018) and Park et al. (2021).

Table 4.2: Clustering of cucumber genotypes on the basis of SSR data (NTSYS 2.02)

Cluster No.	Sub-cluster	Number of genotypes in each cluster	Genotypes
A	A ₁	4	DDPCG4, PK-1, PPC-2, PPC-3
	A ₂	1	DDPCG1
B	B ₁	1	DDPCW1
	B ₂	2	DDPCG2, DDPCG5

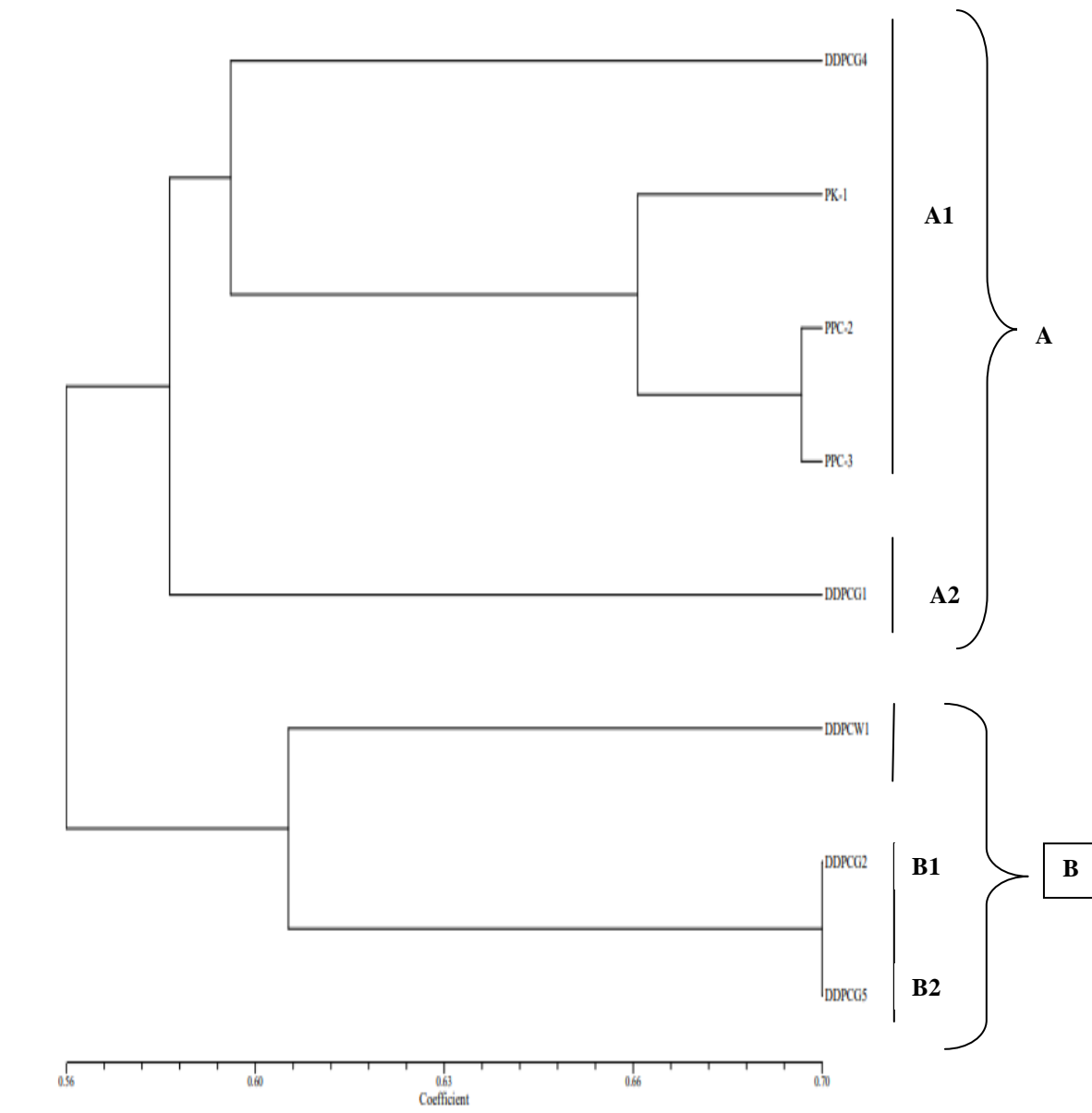


Fig. 4.1 Dendrogram of 8 cucumber genotypes generated by SSR data using the UPGMA method

Neighbour joining tree was constructed with marker data in cucumber to estimate the genetic identity using the DARwin software version 5.0.158 (Perrier and Jacquemoud 2006). Branch robustness was tested using 1000 bootstraps. Cluster tree constructed with marker data documented three major clusters (Table 4.3, Fig. 4.2). Cluster I (green) consists of 2 genotypes (DDPCG1, DDPCG4) while, cluster II (red) comprised of 3 genotypes which was further divided into two sub-clusters comprising single genotype (DDPCW1) and 2 genotypes (DDPCG2 and DDPCG5), respectively. Cluster III comprised of 3 genotypes namely, PK-1, PPC-2 and PPC-3. The variation between the two systems viz., NTSYS version 2.02 and DARwin 5 is might be due to differences in the method of clustering by two systems i.e. by computing similarity and dissimilarity coefficients, respectively.

Table 4.3: Clustering of cucumber genotypes on the basis of neighbour-joining tree SSR data

Cluster No.	Sub-cluster	No. of genotypes in each cluster	Genotypes
I	-	2	DDPCG1, DDPCG4
II	II ₁	1	DDPCW1
	II ₂	2	DDPCG2, DDPCG5
III	-	3	PK-1, PPC-2, PPC-3

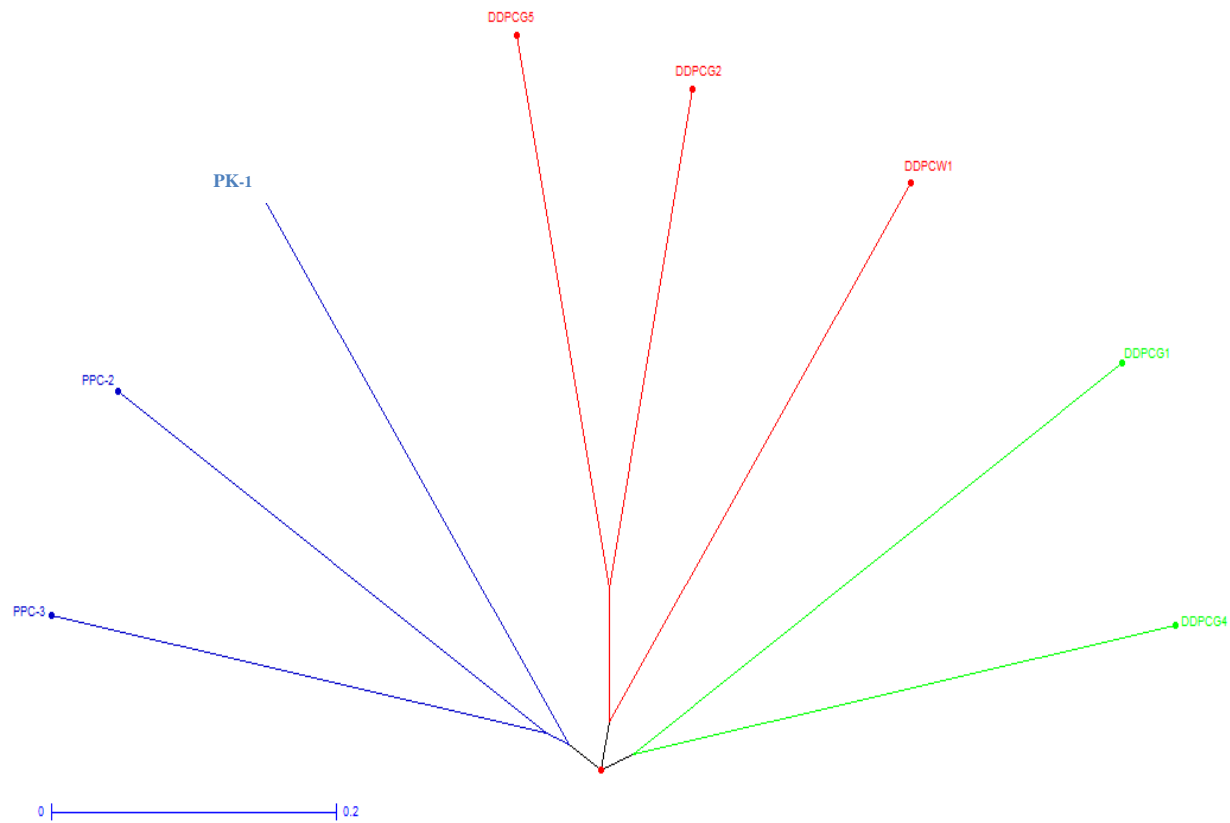


Fig 4.2 Neighbor joining tree of cucumber using SSR markers generated by DARwin software

4.1.3 Analysis of molecular variance (AMOVA)

AMOVA helps in analyzing the overall genetic variation into 2 different levels viz., between and within populations. Molecular analysis of variance (AMOVA) was computed to determine the genetic variation among cucumber genotypes using GenALEx 6 (Peakall and Smouse 2012). AMOVA reveals that variation within population was higher i.e. 92 per cent of total variation while, only 8 per cent among population in cucumber (Table 4.4). Valcarcel et al. (2018) observed 55 per cent variation among accessions while, 45 per cent within accessions. Castilla et al. (2019) observed 92% variation among population and 8% within population.

Table 4.4 Analysis of molecular variance (AMOVA)

Marker System	Source	Df	SS	MSS	Variation	% of total Variation
SSR	Among Populations	1	55.292	55.292	3.752	8%
	Within Populations	6	247.333	41.222	41.222	92%
	Total	7	302.625		44.974	100%

4.1.4 Principal Coordinate Analysis (PCoA)

PCoA is a multivariate approach for grouping based on similarity coefficients or variance-covariance values that provides more valuable information about major groups, but cluster analysis provides a higher level of resolution among closely related populations. PCoA examines relationships between several quantitative variables by assembling a small number of linear combinations that retain as much information in the original data. In cucumber genotypes, Principal Coordinate Analysis (PCoA) re-confirmed the genetic relationship as revealed by cluster analysis. PCoA divided 8 cucumber genotypes into two populations (Fig. 4.3). The per cent variation is justified by first three axes using SSR markers. Axis 1 contributes 21.10 per cent variation while, Axis 2 and Axis 3 contributes 17.66 and 15.28 per cent variation, respectively (Table 4.5). This reveals the presence of huge variation in cucumber germplasm.

Pandey et al. (2013) reported that first three principal coordinates accounted for 28 per cent variation by PC1, 22 per cent variation by PC2 while 15 per cent variation by PC3. According to Dar et al. (2017) a three-dimensional PCoA plot categorized the cucumber genotypes into two main clusters with maximum genotypes in cluster B. The analysis revealed that the first three coordinates accounted for 17% of the total variance. Valcarcel et al. (2018) reported that the first three axis contributes 40.8 per cent of total variation.

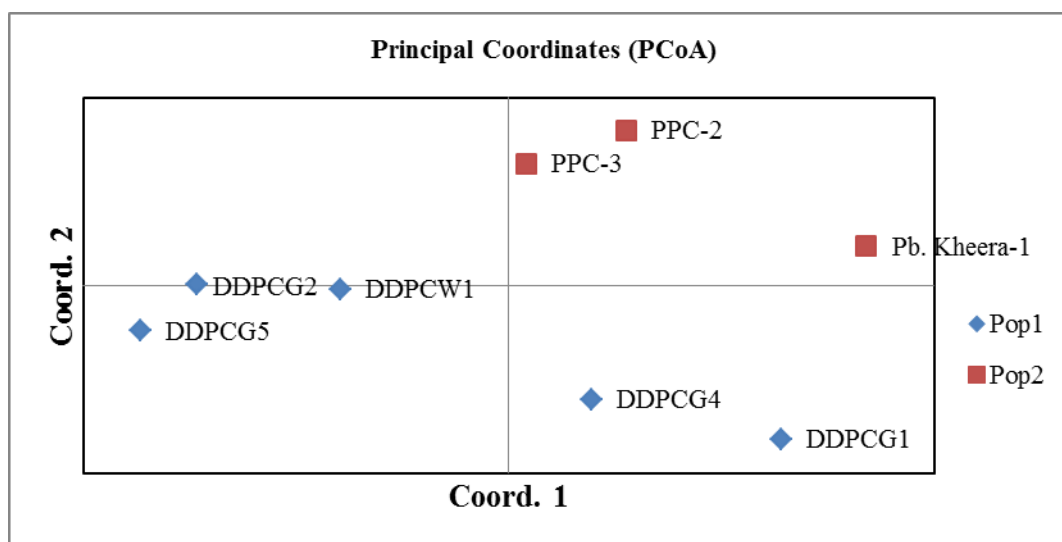


Fig. 4.3 Principal Coordinate Analysis (PCoA) used to analyze substructures of cucumber genotypes

Table 4.5: Percentage of variation explained by PCoA

Axis	1	2	3
%	21.10	17.66	15.28
Cum %	21.10	38.77	54.04

4.1.5 Population Structure

To evade spurious associations, meticulous information of genetic relatedness among individuals in an association panel is necessary. Estimation of population structure (Q matrix) using STRUCTURE (Falush et al. 2003) is the best way to evade fake connections due to genetic associations and expressed as membership probabilities. Estimating the true number of population (k) is very complex and hard. In general, k is regarded as the value with the highest estimated LnP (D) value

returned by STRUCTURE (Pritchard et al. 2000). In actual conditions, few data sets verify accurately to the STRUCTURE model and the LnP (D) value continues to increase as k achieves the true number. Evanno et al. (2005) recommended an ad hoc method, Δk the second-order rate of change of the likelihood value with regard to k proved efficient in demonstrating the real number.

The population structure in the panel comprises of 8 cucumber genotypes was assessed using 56 SSRs and a model based approach of STRUCTURE. Ten independent Ks (from K=2 to K=10 where, K is kinship matrix) were used to estimate the accurate population substructure (K). Based on STRUCTURE analysis populations were divided into two groups (Table 4.6, Fig. 4.4), where the differentiations at K = 2 were approximately corresponding with Pedigree information having minor differences. Therefore, pedigree knowledge and cluster membership was used to analyze the division of P₁ and P₂ groupings. P₁ consists of 6 genotypes while, only 2 genotypes in P₂. The structure bar plot reveals that P₁ showed maximum of 100% and minimum of 95% membership while maximum of 100% membership was observed in P₂. Dar et al. (2017) assessed the genetic diversity in 104 genotypes and based on population structure analysis 47 and 39 genotypes were grouped in population 1 and 2, respectively, while 18 genotypes were identified as admixtures.

Table 4.6: Grouping of cucumber genotypes using STRUCTURE software program

Population Groups	Number of genotypes	Genotypes
Group 1	6	‘DDPCG4’, ‘DDPCG1’, ‘PK-1’, ‘PPC-2’, ‘PPC-3’ and ‘DDPCW1’
Group 2	2	‘DDPCCG2’ and ‘DDPCG5’

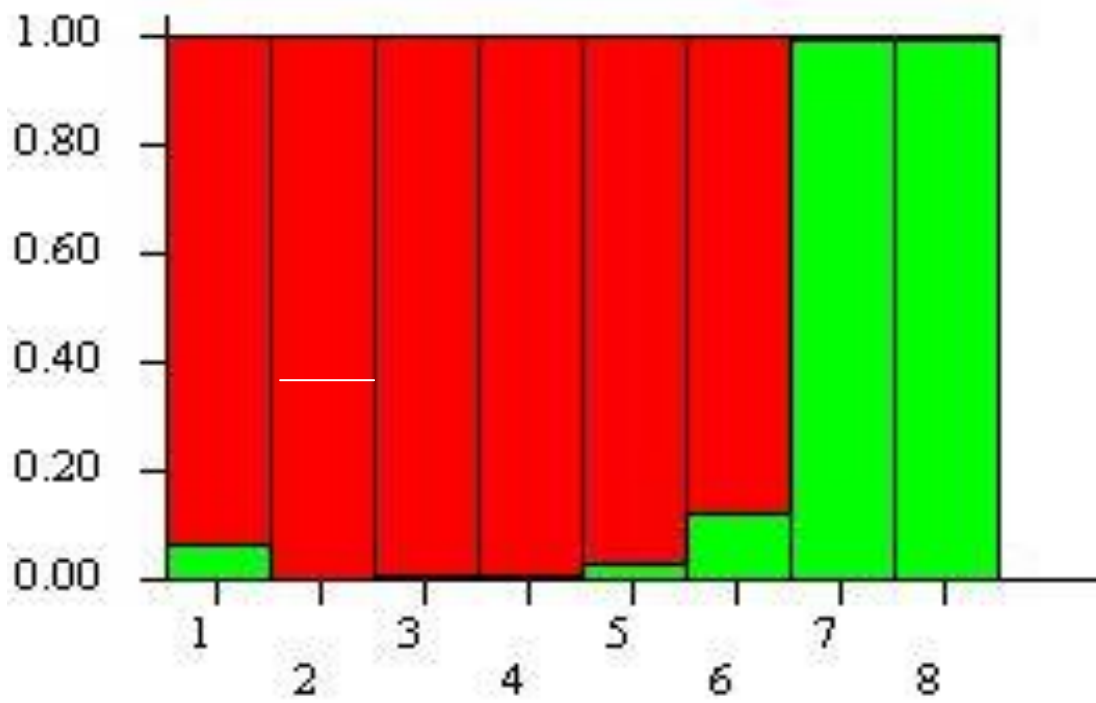


Fig. 4.4: Gene pool introgression based on population structure analysis at $k=2$

4.2 Analysis of variance

To test the significant differences among treatments, analysis of variance was worked out as described by Gomez and Gomez (1983) for randomized block design. Significant differences were observed for the traits among genotypes comprising parents, hybrids and standard check in analysis of variance (Table 4.7) during 2020, 2021 and pooled over environments. In analysis of variance under pooled environment, significant differences due to environment were observed for all the traits except number of female flowers per node, fruit length (cm), fruit diameter (cm), number of fruits per plant and flesh to seed cavity ratio which indicates the presence of huge genetic variability in the genetic material for exploitation of crop improvement. Similarly, significant differences were also revealed due to genotype \times environment interaction for nodal position of first female flower, number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square (kg), vine length (m), flesh to seed cavity ratio, flesh thickness (mm), total soluble solids ($^{\circ}$ Brix), ascorbic acid (mg/100g), total sugar (%) and reducing sugar (%). Significant differences among genotypes for all the traits allowed appropriate analysis of combining ability of these traits. Similar results for analysis of variances were reported by Singh et al. (2010), Jat et al. (2015), Kaur et al. (2016), Kaur and Dhall (2017), Singh and Tiwari (2018), Manggoel et al. (2021) and Umeh et al. (2021).

Combined analysis of variance:

Among parents and hybrids, significant differences were observed in combined analysis of variance (Table 4.8) for all the traits in 2020 and 2021 except flesh thickness (mm) in 2020. Significant differences were recorded in parents vs. hybrids for all the character studied except fruit diameter (cm) and flesh to seed cavity ratio in 2020 and fruit diameter (cm) in 2021. This indicates the presence of appreciable diversity in the genetic material for yield, yield related traits and quality parameters which can be further utilized for crop improvement. The results are in line with Sharma (2006), Sharma et al. (2016) and Singh and Tiwari (2018).

4.3 Mean performance

The mean performance illustrate the exact data of different parental lines for various traits studied. The estimates of mean values of 8 parental lines, 28 hybrid combinations along with the standard check (Kian) are discussed below:

Table 4.7: Analysis of variance for various traits in cucumber during 2020, 2021 and pooled over environments

Sr. No	Years→ Source of variation df→ Traits	2020			2021			Pooled				
		Replication	Genotype	Error	Replication	Genotype	Error	Replication	Genotype	Environment	Genotype × Environment	Error
		2	36	72	2	36	72	4	36	1	36	144
1.	Days to first female flower	43.97	20.05*	2.73	10.78	20.77*	2.38	27.38	37.18*	31.79*	3.63	2.56
2.	Nodal position of first female flower	0.09	1.37*	0.08	0.09	1.46*	0.03	0.09	2.64*	2.35*	0.18*	0.06
3.	Number of female flowers per node	0.005	0.41*	0.006	0.007	0.41*	0.01	0.006	0.81*	0.005	0.012	0.008
4.	Days taken to first fruit picking	181.14	68.56*	3.72	47.60	46.19*	8.95	114.37	107.71*	3.05*	7.05	6.33
5.	Fruit length (cm)	8.39	16.12*	2.39	7.11	13.00*	2.24	7.75	26.07*	6.19	3.05	2.31
6.	Fruit diameter (cm)	0.015	0.22*	0.02	0.05	0.14*	0.04	0.03	0.34*	0.04	0.02	0.03
7.	Fruit weight (g)	96.69	647.93*	71.22	13.25	729.25	66.22	54.96	1369.06*	3354.82*	8.12	68.72
8.	Number of fruits per plant	6.549	36.75*	4.04	6.513	15.93*	3.25	6.53	44.49*	12.05	8.18*	3.64
9.	Marketable yield per plant (kg)	0.002	1.43*	0.03	0.008	1.29*	0.05	0.005	2.63*	1.22*	0.09*	0.04
10.	Marketable yield per meter square (kg)	0.09	51.56*	1.31	0.31	46.37*	1.59	0.20	94.59*	43.95*	3.35*	1.45
11.	Harvest duration	44.84	126.38*	7.384	77.68	135.98*	5.19	61.26	256.61*	520.72*	5.77	6.29
12.	Internodal length (cm)	0.62	3.24*	0.59	0.49	2.79*	0.82	0.55	5.76*	2.82*	0.27	0.71
13.	Vine length (m)	0.02	0.65*	0.012	0.013	0.62*	0.012	0.017	1.26*	0.06*	0.02*	0.012
14.	Flesh to seed cavity ratio	0.022	0.13*	0.02	0.12	0.06*	0.02	0.07	0.16*	0.07	0.04*	0.02
15.	Flesh thickness (mm)	0.22	2.23	1.06	0.48	2.64	0.45	0.35	3.65*	38.39*	1.22*	0.75
16.	Total soluble solids (°B)	0.0007	1.61*	0.006	0.002	1.55*	0.006	0.002	3.13*	0.13*	0.02*	0.006
17.	Ascorbic acid (mg/100g)	10.52	1.13*	0.003	0.0006	1.11*	0.0003	5.26	2.16*	0.06*	0.09*	0.002
18.	Total sugar (%)	0.005	0.29*	0.005	0.005	0.31*	0.005	0.005	0.49*	0.06*	0.11*	0.005
19.	Reducing sugar (%)	0.0002	0.56*	0.0004	0.0003	0.39*	0.0003	0.0002	0.93*	0.71*	0.03*	0.0004

*Significant at ≤5% level of significance

Table 4.8: Combined analysis of variance for different traits in cucumber during 2020 and 2021

Sr. No	Years→ Source of variation df→ Traits	2020					2021				
		Replication	Parents	Hybrids	Parents vs Hybrids	Error	Replication	Parents	Hybrids	Parents vs Hybrids	Error
		2	7	27	1	70	2	7	27	1	70
1.	Days to first female flower	38.95	9.81	20.96*	83.82*	2.69	10.70	10.47*	23.74*	32.89*	2.378
2.	Nodal position of first female flower	0.10	0.66*	1.37*	2.05*	0.08	0.08	0.64*	1.49*	2.79*	0.04
3.	Number of female flowers per node	0.006	0.43*	0.37*	1.69*	0.006	0.005	0.38*	0.38*	1.69*	0.01
4.	Days taken to first fruit picking	180.33	18.85*	62.19*	644.29*	3.78	44.009	54.09*	25.79*	588.16*	9.04
5.	Fruit length (cm)	8.96	16.90*	15.50*	27.54*	2.39	7.65	12.74*	12.46*	27.71*	2.27
6.	Fruit diameter (cm)	0.02	0.12*	0.26*	0.00001	0.02	0.06	0.15*	0.14*	0.11	0.04
7.	Fruit weight (g)	87.93	272.35*	715.83*	2089.06*	72.40	19.73	277.60*	823.37*	2070.29*	67.31
8.	Number of fruits per plant	5.69	52.74*	26.12*	26.12*	4.12	5.65	7.93*	14.49*	105.65*	3.17
9.	Marketable yield per plant (kg)	0.003	1.16*	1.32*	7.86*	0.04	0.003	0.41*	1.39*	5.77*	0.04
10.	Marketable yield per meter square (kg)	0.13	41.73*	47.45*	283.04*	1.33	0.11	14.71*	50.11*	207.65*	1.56
11.	Harvest duration (days)	41.84	46.61*	101.59*	1438.91*	7.56	83.08	22.48*	110.18*	1697.36*	5.15
12.	Internodal length (cm)	0.67	2.64*	3.20*	8.37*	0.59	0.61	3.95*	2.25*	8.69*	0.84
13.	Vine length (m)	0.02	0.64*	0.59*	3.09*	0.01	0.02	0.45*	0.63*	2.27*	0.01
14.	Flesh to seed cavity ratio	0.03	0.10*	0.15*	0.04	0.02	0.12	0.08*	0.05*	0.29*	0.02
15.	Flesh thickness (mm)	0.20	1.99	1.37	19.80*	19.80	0.58	3.93*	2.17*	8.72*	0.45
16.	Total soluble solids (°Brix)	0.0006	1.34*	1.67*	1.16*	0.006	0.002	1.04*	1.65*	1.55*	0.006
17.	Ascorbic acid (mg/100g)	10.20	1.35*	1.15*	0.42*	0.003	0.0006	1.14*	1.18*	0.12*	0.0003
18.	Total sugar (%)	0.004	0.48*	0.27*	0.13*	0.005	0.007	0.29*	0.32*	0.33*	0.005
19.	Reducing sugar (%)	0.0002	0.21*	0.49*	5.19*	0.0004	0.0002	0.19*	0.34*	3.86*	0.0004

*Significant at ≤5% level of significance

1. Days to first female flower

Earliness is most desirable trait to get higher price in the market and therefore hybrids are more preferred by farmers over purelines in cucumber. Days to first female flower is the main character to predict the earliness in cucumber. The present investigation (Table 4.9) indicated that mean values for days to first female flower in parents ranged from 21.67 (P_5) to 27 days (P_8). Among parents, P_5 (21.67) took minimum number of days to first female flower which was statistically at par with P_1 (23.50) and P_4 (21.83) while, maximum days were recorded in P_8 (27).

Days to first female flower in cross combinations varied from 18 ($P_2 \times P_3$) to 27.33 days ($P_3 \times P_8$) in 2020, 19.33 ($P_2 \times P_4$ and $P_4 \times P_6$) to 32 days ($P_3 \times P_5$) in 2021 and 18.83 ($P_2 \times P_3$) to 28.67 days ($P_3 \times P_5$) in pooled over environments. For this trait, 14 hybrids each in 2020 and pooled over environments and 16 hybrids in 2021 were significantly superior to the standard check (kian). In 2020, 12 hybrids were statistically at par with $P_2 \times P_3$ (18.00). In 2021, $P_2 \times P_4$ (19.33) took minimum number of days to first female flower which was statistically at par with $P_1 \times P_3$ (21.33), $P_2 \times P_3$ (19.67), $P_2 \times P_5$ (21.33), $P_2 \times P_6$ (20.00), $P_2 \times P_7$ (21.00), $P_2 \times P_8$ (21.33), $P_4 \times P_7$ (20.33), $P_4 \times P_8$ (21.33) and $P_7 \times P_8$ (21.33). Similarly in pooled over environments, $P_2 \times P_3$ (18.83) took minimum days to first female flower which was statistically at par with $P_2 \times P_4$ (19.33), $P_2 \times P_5$ (20.33), $P_2 \times P_6$ (19.17), $P_2 \times P_8$ (20.17), $P_4 \times P_6$ (19.17) and $P_4 \times P_7$ (19.50). Jat et al. (2015), Kumar et al. (2016), Preethi et al. (2019), Manggoel et al. (2021) and Umeh et al. (2021) reported that hybrids were earlier in flowering as compared to the parents and standard check.

2. Nodal position of first female flower

Nodal position of first female flower showed significant variation among parents. The present study (Table 4.9) revealed that mean values for this trait ranged from 2.06 (P_8) to 3.57 (P_5). Among parents, P_8 (2.06) recorded lowermost nodal position of first female flower and none of the parents were found statistically at par with P_8 .

Table 4.9: Mean performance of yield attributing traits of cucumber viz., days to first female flower, nodal position of first female flower, number of female flowers/node and days to first fruit picking during 2020, 2021 and pooled over environments

Parental lines	Days to first female flower			Nodal position of first female flower			Number of female flowers/node			Days to first fruit picking		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	23.33	23.67	23.50	3.07	2.95	3.01	1.53	1.47	1.50	43.00	41.00	42.00
P ₂	24.33	24.67	24.50	2.59	2.89	2.74	1.46	1.56	1.51	48.33	44.67	46.50
P ₃	25.00	25.33	25.17	3.13	2.96	3.05	2.07	2.01	2.04	43.33	41.33	42.33
P ₄	22.00	21.67	21.83	3.03	2.33	2.68	1.21	1.29	1.25	50.33	52.00	51.17
P ₅	21.00	22.33	21.67	3.80	3.33	3.57	1.22	1.3	1.26	47.33	51.00	49.17
P ₆	24.33	23.33	23.83	2.57	2.67	2.62	1.05	1.03	1.04	44.67	46.67	45.67
P ₇	25.67	24.33	25.00	2.92	2.33	2.63	1.17	1.13	1.15	46.33	46.67	45.00
P ₈	26.33	27.67	27.00	2.24	1.88	2.06	1.96	1.94	1.95	45.67	49.33	47.50
P ₁ × P ₂	21.67	22.67	22.17	1.92	2.33	2.13	1.93	2.00	1.97	43.00	40.67	41.83
P ₁ × P ₃	20.00	21.33	20.67	3.53	3.00	3.27	2.40	2.06	2.23	37.33	38.67	38.00
P ₁ × P ₄	23.33	23.00	23.17	3.67	3.00	3.33	2.10	2.06	2.08	39.33	42.00	40.67
P ₁ × P ₅	24.67	23.00	23.83	3.07	3.00	3.03	1.17	1.2	1.19	40.33	40.67	40.50
P ₁ × P ₆	20.67	22.00	21.67	2.77	2.33	2.55	1.69	1.73	1.71	36.33	38.67	37.50
P ₁ × P ₇	23.00	23.67	23.33	1.54	1.60	1.57	1.85	1.8	1.83	45.33	43.33	44.33
P ₁ × P ₈	23.00	24.33	23.33	2.92	2.33	2.63	1.45	1.46	1.45	45.00	42.33	43.67
P ₂ × P ₃	18.00	19.67	18.83	3.07	3.33	3.20	1.67	1.66	1.66	33.67	36.67	35.17
P ₂ × P ₄	19.33	19.33	19.33	3.70	3.43	3.57	1.97	2.07	2.02	36.00	37.00	36.50
P ₂ × P ₅	19.33	21.33	20.33	2.87	2.67	2.77	1.76	1.8	1.78	37.33	39.00	38.17
P ₂ × P ₆	18.33	20.00	19.17	3.53	3.00	3.27	1.38	1.43	1.41	36.67	37.33	37.00
P ₂ × P ₇	20.33	21.00	20.67	4.27	4.33	4.30	2.01	2.06	2.04	34.33	37.00	35.67
P ₂ × P ₈	19.00	21.33	20.17	3.07	3.31	3.19	1.81	1.83	1.82	40.67	40.33	40.50
P ₃ × P ₄	23.67	23.00	23.33	3.18	2.87	3.02	1.86	1.81	1.84	38.33	39.33	38.83
P ₃ × P ₅	25.33	32.00	28.67	3.40	3.67	3.54	1.69	1.66	1.68	38.00	40.00	39.00
P ₃ × P ₆	19.67	22.00	20.83	2.43	2.67	2.55	2.16	2.35	2.26	37.67	39.33	38.50
P ₃ × P ₇	24.00	23.00	23.50	3.32	3.00	3.16	2.39	2.43	2.41	39.00	40.67	39.83
P ₃ × P ₈	27.33	26.67	27.00	3.40	3.33	3.37	2.09	2.08	2.08	48.00	45.33	46.67
P ₄ × P ₅	23.67	23.00	23.33	3.43	3.00	3.22	1.41	1.46	1.44	48.33	46.67	47.50
P ₄ × P ₆	19.00	19.33	19.17	4.48	4.00	4.24	1.36	1.33	1.34	35.33	36.33	35.83
P ₄ × P ₇	18.67	20.33	19.50	3.49	3.00	3.25	1.47	1.5	1.49	38.33	40.00	39.17
P ₄ × P ₈	21.33	21.33	21.33	2.69	2.33	2.51	2.12	2.06	2.09	48.67	46.33	47.50
P ₅ × P ₆	27.00	26.67	26.83	4.27	4.33	4.30	1.28	1.2	1.24	38.00	39.67	38.83
P ₅ × P ₇	25.00	28.67	26.83	3.59	3.00	3.29	1.15	1.13	1.14	44.67	42.00	43.33
P ₅ × P ₈	23.67	23.33	23.50	3.01	2.67	2.84	1.78	1.8	1.79	47.67	45.33	46.50
P ₆ × P ₇	22.67	22.33	22.50	4.03	4.67	4.34	2.06	2.27	2.16	45.00	43.67	44.33
P ₆ × P ₈	20.67	22.67	21.67	3.90	3.33	3.62	1.93	1.91	1.92	38.00	40.67	39.33
P ₇ × P ₈	20.33	21.33	20.83	2.47	2.00	2.23	1.33	1.36	1.35	36.67	37.67	37.17
Kian (check)	21.33	22.67	22.00	1.83	1.67	1.75	1.71	1.78	1.75	43.67	42.00	42.83
Mean	22.32	23.08	22.70	3.14	2.93	3.04	1.69	1.70	1.70	41.61	41.8	41.73
SE d	1.34	1.25	0.92	0.23	0.15	0.17	0.06	0.08	0.06	1.57	2.44	1.49
CV	7.4	6.68	5.01	9.01	6.42	7.92	4.52	6.23	4.56	4.63	7.14	4.4
CD	2.69	2.51	1.84	0.46	0.31	0.49	0.13	0.17	0.12	3.13	4.86	2.98

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5



Plate 3 Vegetative and fruiting stages of cucumber crop

Nodal position of first female flower in crosses ranged from 1.54 ($P_1 \times P_7$) to 4.48 ($P_4 \times P_6$) in 2020, 1.60 ($P_1 \times P_7$) to 4.67 ($P_6 \times P_7$) in 2021 and 1.57 ($P_1 \times P_7$) to 4.34 ($P_6 \times P_7$) in pooled over environments. The standard check recorded 1.83, 1.67 and 1.75 values for nodal position of first female flower during 2020, 2021 and pooled over environments, respectively. For this trait, only one hybrid ($P_1 \times P_7$) in 2020, 2021 and pooled over environments was found significantly superior over standard check (Kian). Based on the mean performance of hybrids, hybrid combination $P_1 \times P_8$ (1.54) recorded minimum values for nodal position of first female flower in 2020, however, it was statistically at par with $P_1 \times P_7$ (1.92) and standard check (1.83). Cross combination $P_1 \times P_8$ in 2021 (1.60) and pooled over environments (1.57) recorded lower most nodal position of first female flower which was statistically at par with standard check. The results are in congruous with the findings of Bairagi et al. (2005), Bairagi et al. (2013), Jat et al. (2015), Preethi et al. (2016), Kumar et al. (2016), Malav et al. (2018), Preethi et al. (2019) and Thakur and Kumar (2020) who reported that hybrids bear fruits at lower node as compared to parents.

3. Number of female flowers per node

Marketable yield per plant is positively correlated with number of female flowers per plant. The perusal of data (Table 4.9) revealed that mean values among parents for number of female flowers per node varied from 1.04 (P_6) to 2.04 (P_3). Among parents, maximum number of female flowers per node was noticed in genotype P_3 (2.04) which was statically at par with P_8 (1.95) while, minimum number of female flowers per node was observed in P_6 (1.04).

Among cross combinations, mean values for number of female flowers per node varied from 1.15 to 2.40, 1.13 to 2.43 and 1.14 to 2.41 in 2020, 2021 and pooled over environments, respectively. For this trait, 16 hybrids each in 2020, 2021 and pooled over environment were observed significantly outstanding than the standard check (kian). In 2020, maximum number of female flowers per node was recorded in $P_1 \times P_3$ (2.40) which was statically at par with $P_3 \times P_7$ (2.39). Similarly in 2021, $P_3 \times P_7$ (2.43) exhibited highest

values for number of female flowers per node, which was statically at par with $P_3 \times P_6$ (2.35), while in pooled over environment, maximum values for this trait was noticed in $P_3 \times P_7$ (2.41) and none of the cross combination was statically at par. Similar results are also reported by Dogra and Kanwar (2011), Singh et al. (2016b), Mehta (2019) and Mehta and Sharma (2020) for number of female flowers per node

4. Days taken to first fruit picking

Days taken to first fruit picking is the most desirable trait to identify early maturing parents or hybrids for early produce and high price in the market. The perusal of data (Table 4.9) indicated that mean values among parents for days to first fruit picking ranged from 42 (P_1) to 51.17 days (P_4). For this trait, minimum number of days to first fruit picking was recorded in P_1 (42) which was statistically at par with P_3 (42.33) while, maximum days were exhibited in P_4 (51.17).

Days to first fruit picking in hybrids ranged from 33.67 to 48.67 days, 36.33 to 46.67 days and 35.17 to 47.50 days in 2020, 2021 and pooled over environments, respectively. For this trait, standard check (kian) took 43.67, 42.00 and 42.83 days during 2020, 2021 and pooled over environments, respectively. Among 28 cross combinations, 20 hybrids each in 2020 and pooled over environments and 19 hybrids in 2021 were observed significantly outstanding over standard check (kian). Earlier researchers (Kumar et al. 2010; Tiwari and Singh 2016; Kumar et al. 2016; Malav et al. 2018; Preethi et al. 2019; Umeh et al. 2021) have identified that hybrids are earlier in fruit maturity than the parents and standard check.

5. Fruit length (cm)

Fruit length and diameter have direct effect on marketable yield and cylindrical fruit shape with tenderness is mainly preferred by consumers to get high returns. Among parents, significant variation was recorded for fruit length ranging from 14.61 (P_3) to 21.02 cm (P_4) (Table 4.10). The maximum values for fruit length was observed in P_4 (21.02) which was statistically at par with P_2 (20.04) and P_5 (19.72) while P_3 (14.61) recorded minimum values for fruit length.

In cross combinations, fruit length ranged from 15.75 to 22.31 cm, 15.35 to 22.55 cm and 15.88 to 22.12 cm in 2020, 2021 and pooled over environments, respectively. For this trait, 22 hybrids in 2020, 23 hybrids in 2021 and 24 hybrids in pooled over environments outperformed over the standard check. In 2020, cross combination $P_2 \times P_7$ (22.31) executed maximum fruit length which was statistically at par with 10 other hybrids viz., $P_1 \times P_8$ (21.40), $P_2 \times P_3$ (20.55), $P_2 \times P_4$ (21.53), $P_2 \times P_5$ (20.71), $P_2 \times P_6$ (21.62), $P_2 \times P_8$ (21.37), $P_4 \times P_6$ (19.89), $P_4 \times P_8$ (20.94), $P_5 \times P_6$ (21.28) and $P_5 \times P_7$ (20.21). In 2021, hybrid combination $P_2 \times P_8$ (22.55) recorded maximum fruit length which was statistically at par with 12 other hybrids. Similarly in pooled over environments, 11 hybrids were found statistically at par with $P_2 \times P_7$ (22.12). The present findings are in agreement with earlier researchers (Yadav et al. 2007; Singh et al. 2010; Airina et al. 2013; Singh et al. 2016b; Kaur and Dhall 2017 and Manggoel et al. 2021) who reported increase in fruit length in hybrids over parents and standard check.

6. Fruit diameter (cm)

The perusal of data (Table 4.10) indicated that mean values for fruit diameter ranged for 3.62 (P_3) to 4.19 cm (P_8). Among parents, P_8 (4.19) recorded maximum fruit diameter which was statistically at par with P_1 (4.16), P_2 (4.06), P_4 (4.06), P_5 (4.08) and P_6 (4.18) whereas, minimum value was noticed in P_3 (3.62).

Fruit diameter in hybrids ranged from 3.47 to 4.56 cm, 3.59 to 4.42 cm and 3.53 to 4.47 cm in 2020, 2021 and pooled over environments, respectively. For this trait, 22 hybrids in 2020, 19 hybrids each in 2021 and pooled over environments were observed significantly outstanding than the standard check (kian). In 2020, maximum fruit diameter was noticed in $P_1 \times P_7$ (4.56) which was statistically at par with $P_1 \times P_4$ (4.45), $P_2 \times P_6$ (4.35), $P_3 \times P_4$ (4.43) and $P_4 \times P_7$ (4.53). Similarly in 2021, highest value for this trait was recorded in $P_4 \times P_7$ (4.42) which was statistically at par with $P_1 \times P_3$ (4.11), $P_1 \times P_4$ (4.41), $P_1 \times P_7$ (4.29), $P_1 \times P_8$ (4.16), $P_2 \times P_4$ (4.27), $P_2 \times P_5$

(4.17), $P_2 \times P_6$ (4.35), $P_2 \times P_7$ (4.15), $P_2 \times P_8$ (4.18), $P_3 \times P_4$ (4.21), $P_4 \times P_5$ (4.10) and $P_6 \times P_8$ (4.14). In pooled over environments, 5 hybrids *viz.*, $P_1 \times P_4$ (4.43), $P_1 \times P_7$ (4.42), $P_2 \times P_4$ (4.29), $P_2 \times P_6$ (4.35) and $P_3 \times P_4$ (4.32) were found statistically at par with $P_4 \times P_7$ (4.47). Similar results are also reported by Bairagi et al. (2013), Jat et al. (2015) and Arab et al. (2020) that hybrids perform better than the parents and standard check for fruit diameter.

7. Fruit weight (g)

Fruits having maximum weight are preferred by consumers and farmers to enhance the marketable yield. The present investigation (Table 4.10) revealed that mean values for this trait ranged from 91.75 (P_3) to 116.20 g (P_2). Among parents, P_2 (116.20) recorded maximum fruit weight which was statistically at par with P_1 (115.17), P_5 (110.17), P_6 (113.00) and P_7 (114.98).

Among crosses, mean values for fruit weight varied from 88.07 to 138.57 g in 2020, 96.73 to 146.62 g in 2021 and 92.40 to 142.45 g in pooled over environments. Fifteen hybrids each in 2020 and pooled over environments and 16 hybrids in 2021 recorded significantly maximum fruit weight than the standard check. Among cross combinations, maximum fruit weight was observed in $P_2 \times P_6$ (138.57), which was statistically at par with $P_1 \times P_6$ (130.13), $P_1 \times P_7$ (128.57), $P_1 \times P_8$ (136.69), $P_2 \times P_4$ (129.14), $P_2 \times P_5$ (130.27), $P_2 \times P_7$ (138.29), $P_2 \times P_8$ (134.00) in 2020. Similarly in 2021, maximum fruit weight was recorded in $P_2 \times P_7$ (146.62), which was statistically at par with $P_1 \times P_6$ (138.48), $P_1 \times P_7$ (135.57), $P_1 \times P_8$ (143.69), $P_2 \times P_4$ (145), $P_2 \times P_5$ (141.27), $P_2 \times P_6$ (145.57) and $P_2 \times P_8$ (144.14). In pooled over environments, $P_2 \times P_7$ (142.45) exhibited maximum fruit weight which was statistically at par with seven cross combinations. The results are in line with the study of Jat et al. (2015), Singh et al. (2016b), Kumar et al. (2016), Kaur and Dhall (2017), Singh and Tiwari (2018), Manggoel et al. (2021) and Umeh et al. (2021) who reported that many of the cross combinations are superior over standard check for fruit weight in cucumber.

8. Number of fruit per plant

Number of fruits per plant is directly related with yield which is the main objective of breeding programme for crop improvement. The present investigation (Table 4.10) revealed that mean values among parents for number of fruits per plant ranged from 20.13 (P₄) to 27.86 (P₂). Genotype P₂ (27.86) recorded maximum number of fruits per plant which was statistically at par with P₇ (26.39) while, minimum values was noticed in P₄ (20.13).

Number of fruits per plant for cross combinations varied from 19.49 to 32.45 in 2020, 22.80 to 31.20 in 2021 and 21.15 to 31.19 in pooled over environments. Among 28 cross combinations, 17 hybrids in 2020, 5 hybrids in 2021 and 7 hybrids in pooled over environments were significantly superior over standard check (kian). For this trait, maximum number of fruits were recorded in P₂ × P₄ (32.45), which was statistically at par with P₂ × P₅ (31.91), P₂ × P₇ (30.68) and P₂ × P₈ (31.85) in 2020. Similarly in 2021, maximum number of fruits per plant were observed in cross combination P₂ × P₇ (31.20), which was statistically at par with P₂ × P₄ (29.93), P₂ × P₅ (29.87), P₂ × P₆ (28.53) and P₂ × P₈ (30). In pooled over environments, 3 hybrids *viz.*, P₂ × P₅ (30.89), P₂ × P₇ (30.94) and P₂ × P₈ (30.93) were found statistically at par with P₂ × P₄ (31.19). Earlier researchers (Yadav et al. 2007; Airina et al. 2013; Bairagi et al. 2013; Singh et al. 2016b; Singh and Tiwari 2018 and Arab et al. 2020) also observed that some of hybrids are excelling over standard check for number of fruits per plant.

9. Marketable yield per plant (kg)

The main aim of breeding programme is to achieve higher yield for crop improvement. This is the main factor for adoption or rejection of genotypes by consumers or farmers. The perusal of data (Table 4.11) revealed that fruit yield per plant among parents ranged from 1.88 (P₃) to 3.24 kg (P₂). For fruit yield, maximum value was observed in P₂ (3.24), which was statistical at par with P₇ (3.03) while, minimum value was noticed in P₃ (1.88).

Table 4.10 Mean performance of yield attributing traits of cucumber viz., fruit length (cm), fruit diameter (cm), fruit weight (g) and number of fruits/plant during 2020, 2021 and pooled over environments

Parental lines	Fruit length (cm)			Fruit diameter (cm)			Fruit weight (g)			Number of fruits/plant		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	16.69	17.07	16.88	4.2	4.11	4.16	111.00	119.33	115.17	22.87	25.07	23.97
P ₂	19.56	20.51	20.04	4.12	3.99	4.06	112.20	120.20	116.20	28.91	26.80	27.86
P ₃	15.25	13.98	14.61	3.68	3.55	3.62	88.25	95.25	91.75	18.50	22.23	20.42
P ₄	20.39	21.65	21.02	4.18	3.93	4.06	95.00	103.33	99.17	17.92	22.23	20.13
P ₅	20.57	18.87	19.72	4.13	4.02	4.08	106.67	113.67	110.17	26.28	23.24	24.76
P ₆	17.36	19.12	18.24	4.11	4.25	4.18	108.83	117.17	113.00	22.48	22.14	22.31
P ₇	15.73	17.44	16.59	3.79	3.74	3.77	111.32	118.65	114.98	28.44	24.34	26.39
P ₈	17.48	17.09	17.29	4.23	4.14	4.19	93.53	101.87	97.70	21.41	24.24	22.82
P ₁ × P ₂	16.39	15.38	15.88	3.97	4.05	4.01	95.73	102.73	99.23	26.31	24.73	25.52
P ₁ × P ₃	16.21	18.20	17.21	4.23	4.11	4.17	99.53	97.87	98.70	28.41	25.53	26.97
P ₁ × P ₄	16.36	15.71	16.04	4.45	4.41	4.43	113.80	120.80	117.30	28.94	25.87	27.40
P ₁ × P ₅	17.77	19.33	18.55	3.91	4.03	3.97	122.57	130.90	126.73	24.41	26.47	25.44
P ₁ × P ₆	19.00	19.83	19.41	3.62	3.76	3.69	130.13	138.47	134.30	26.45	25.73	25.99
P ₁ × P ₇	16.29	18.59	17.44	4.56	4.29	4.42	128.57	135.57	132.07	26.74	28.20	27.47
P ₁ × P ₈	21.40	22.19	21.80	4.26	4.16	4.21	136.69	143.69	140.19	28.50	27.07	27.68
P ₂ × P ₃	20.55	18.77	19.66	3.96	4.09	4.03	120.23	128.56	124.39	27.96	27.20	27.58
P ₂ × P ₄	21.53	22.39	21.96	4.31	4.27	4.29	129.14	145.00	137.07	32.45	29.93	31.19
P ₂ × P ₅	20.71	21.37	21.04	4.23	4.17	4.20	130.27	141.27	135.77	31.91	29.87	30.89
P ₂ × P ₆	21.62	21.83	21.22	4.35	4.35	4.35	138.57	145.57	142.07	29.05	28.53	28.79
P ₂ × P ₇	22.31	21.92	22.12	4.27	4.15	4.21	138.29	146.62	142.45	30.68	21.30	30.94
P ₂ × P ₈	21.37	22.55	21.96	4.29	4.18	4.24	134.00	144.14	139.07	31.85	30.00	30.93
P ₃ × P ₄	18.46	16.32	17.39	4.43	4.21	4.32	117.44	125.10	121.27	24.15	26.85	25.51
P ₃ × P ₅	19.71	21.24	20.48	3.75	3.89	3.82	118.93	126.93	122.93	28.03	25.67	26.85
P ₃ × P ₆	19.41	18.11	18.76	3.87	3.83	3.85	93.07	100.40	96.73	22.62	24.74	23.68
P ₃ × P ₇	15.75	16.13	15.94	3.93	3.79	3.86	98.53	102.87	100.70	25.53	24.33	24.93
P ₃ × P ₈	16.67	15.86	16.27	3.97	3.83	3.90	94.33	101.67	98	25.87	25.27	25.57
P ₄ × P ₅	19.71	20.96	20.34	4.18	4.10	4.14	116.13	123.13	119.63	21.77	24.60	23.18
P ₄ × P ₆	19.89	20.19	20.04	4.15	4.09	4.12	104.20	112.53	108.36	27.06	24.00	25.53
P ₄ × P ₇	16.53	17.63	17.08	4.53	4.42	4.47	108.54	115.54	112.04	26.36	25.93	26.15
P ₄ × P ₈	20.94	20.85	20.90	3.72	3.85	3.79	90.13	98.47	94.30	27.04	23.67	25.36
P ₅ × P ₆	21.28	21.33	21.31	3.65	3.79	3.72	103.06	110.06	106.56	19.49	22.80	21.15
P ₅ × P ₇	20.21	20.66	20.43	3.71	3.81	3.76	108.40	116.73	112.57	24.57	23.40	23.98
P ₅ × P ₈	19.87	21.13	20.50	3.87	3.91	3.89	105.73	114.07	109.90	26.76	23.40	25.08
P ₆ × P ₇	16.99	18.25	19.41	3.47	3.59	3.53	88.07	96.73	92.40	27.58	25.27	26.42
P ₆ × P ₈	18.04	17.32	17.68	4.07	4.14	4.11	116.00	124.33	120.17	27.68	26.34	27.01
P ₇ × P ₈	19.73	17.50	18.62	3.86	3.97	3.91	109.93	118.27	114.10	28.03	26.66	27.35
Kian (check)	16.59	16.83	16.71	3.87	3.95	3.91	110.66	117.66	114.16	26.71	28.33	27.52
Mean	18.77	19.03	18.93	4.05	4.02	4.04	111.55	119.33	115.44	26.20	25.73	25.96
SE d	1.26	1.22	0.89	0.11	0.16	0.09	6.89	6.64	6.66	1.64	1.47	1.04
CV	7.96	8.09	5.8	3.25	4.88	3.01	7.56	6.81	7.07	7.67	6.99	4.94
CD	2.43	2.51	1.78	0.21	0.32	0.19	13.71	13.22	13.26	3.26	2.92	2.08

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5



DDPCG4



DDPCG1



Punjab Kheera-1 (PK-1)



PPC-2



DDPCG3



DDPCW1



DDPCG2



DDPCG5

Plate 4 Fruit shape of parents used in the present study



DDPCG4 × DDPCG1



DDPCG4 × PK-1



DDPCG4 × PPC-2



DDPCG4 × PPC-3



DDPCG4 × DDPCW1



DDPCG4 × DDPCG2

**DDPCG4 × DDCPG5****DDPCG1 × PK-1****DDPCG1 × PPC-2****DDPCG1 × PPC-3****DDPCG1 × DDPCW1****DDPCG1 × DDPCG2**



DDPCG1 × DDPCG5



PK-1 × PPC-2



PK-1 × PPC-3



PK-1 × DDPCW1



PK-1 × DDPCG2



PK-1 × DDPCG5



PPC-2 × PPC-3



PPC-2 × DDPCW1



PPC-2 × DDPCG2



PPC-2 × DDPCG5



PPC-3 × DDPCW1



PPC-3 × DDPCG2

**PPC-3 × DDPCG5****DDPCW1 × DDPCG2****DDPCW1 × DDPCG5****DDPCG2 × DDPCG5**

Plate 5 Fruit shape of 28 cross combinations developed using half diallel mating design (without reciprocals)

Fruit yield in hybrid combinations varied from 2.02 to 4.28 kg, 2.33 to 4.57 kg and 2.26 to 4.41 kg in 2020, 2021 and pooled over environments, respectively. The standard check exhibited 2.95 kg fruit yield in 2020, 3.33 kg in 2021 and 3.14 kg in pooled over environments. Fourteen hybrids in 2020, 11 hybrids in 2021 and 13 hybrids in pooled over environments gave significantly higher fruit yield per plant than the standard check (kian). In 2020, hybrid combination $P_2 \times P_8$ (4.28) exhibited maximum fruit yield, which was statistical at par with other cross combinations viz., $P_2 \times P_4$ (4.18), $P_2 \times P_5$ (4.15), $P_2 \times P_6$ (4.03) and $P_2 \times P_7$ (4.24). In 2021, $P_2 \times P_7$ (4.57) gave maximum fruit yield, which was statistically at par with $P_2 \times P_4$ (4.35). In pooled over environments, maximum fruit yield was noticed in hybrid $P_2 \times P_7$ (4.41), which was statistically at par with $P_2 \times P_4$ (4.26) and $P_2 \times P_5$ (4.18). Similarly various scientists Sood et al. (2011), Bairagi et al. (2013), Jat et al (2015), Kaur et al. (2016), Preethi et al. (2016), Kaur and Dhall (2017) and Umeh et al. (2021) have also reported that hybrids outperformed for fruit yield per plant over the standard check.

10. Marketable yield per meter square (kg)

The data analysis (Table 4.11) showed that mean values for this trait varied from 11.27 (P_3) to 19.42 kg (P_2) in pooled over environments. Maximum fruit yield per meter square area was observed in P_2 (19.42), which was statistical at par with P_7 (18.17) whereas, P_3 (11.27) exhibited minimum values among parents.

In cross combinations, fruit yield per meter square ranged from 12.11 to 25.66 kg in 2020, 13.98 to 27.45 kg in 2021 and 13.58 to 26.44 kg in pooled over environments. Fourteen hybrids, 11 hybrids and 13 hybrids in 2020, 2021 and pooled over environments were observed significantly superior than the standard check (Kian) for fruit yield per meter square, respectively. Maximum fruit yield per meter square was observed in hybrid combination $P_2 \times P_8$ (25.66), which was statistical at par with $P_2 \times P_4$ (25.10), $P_2 \times P_5$ (24.93), $P_2 \times P_6$ (24.15) and $P_2 \times P_7$ (25.43) in 2020. In 2021, hybrid combination $P_2 \times P_7$ (27.45) exhibited maximum value for this trait which was statistical at par with $P_2 \times P_4$ (26.07), $P_2 \times P_5$ (25.29) and $P_2 \times P_8$ (25.96). In pooled over

environments, $P_2 \times P_7$ (26.44) recorded highest fruit yield per meter square, which was statistical at par with $P_2 \times P_4$ (25.59), $P_2 \times P_5$ (25.11) and $P_2 \times P_8$ (25.81). Similar results are also reported by Bairagi et al. (2013), Jat et al. (2015), Mehta (2019), Preethi et al. (2019), Mehta and Sharma (2020) and Umeh et al. (2021) who reported that hybrids are superior for fruit yield per meter square over the standard check.

11. Harvest duration (days)

In parthenocarpic cucumber, prolonged availability of fruits is a more desirable trait and genotypes with longer harvest periods are often favoured to be cultivated in polyhouse for higher returns. The perusal of data (Table 4.11) revealed a range of 34.67 (P_8) to 44.83 days (P_1) for harvest duration among parents. Maximum harvest duration was recorded in P_1 (44.83) and none of parent was found statistically at par with P_1 while, minimum harvest duration was observed in P_8 (34.67).

Harvest duration in the cross combinations varied from 38 ($P_3 \times P_5$) to 57.67 days ($P_2 \times P_8$) in 2020, 35.67 ($P_3 \times P_5$) to 55.33 days ($P_3 \times P_6$) in 2021 and 36.83 ($P_3 \times P_5$) to 56.17 days ($P_2 \times P_8$) in pooled over environments. The standard check recorded 43.67, 39.67 and 41.67 days for harvest duration during 2020, 2021 and pooled over environments, respectively. Among 28 cross combinations, 23 hybrids each in 2020, 2021 and pooled over environments significantly outperformed than the standard check. In 2020, maximum harvest duration was observed in $P_2 \times P_8$ (57.67), which was statistically at par with $P_1 \times P_4$ (56.00), $P_2 \times P_3$ (55.00), $P_2 \times P_4$ (54.00), $P_2 \times P_5$ (54.33), $P_2 \times P_6$ (56.67), $P_2 \times P_7$ (56.33), $P_3 \times P_6$ (56.33), $P_4 \times P_6$ (57.00) and $P_4 \times P_7$ (52.33). Similarly in 2021, $P_3 \times P_6$ (55.33) recorded maximum harvest duration which was statistically at par with $P_2 \times P_4$ (54.33), $P_2 \times P_5$ (53.33), $P_2 \times P_6$ (53), $P_2 \times P_7$ (55.00), $P_2 \times P_8$ (54.67) and $P_4 \times P_6$ (52.33). In pooled over environments, maximum harvest duration was noticed in $P_2 \times P_8$ (56.17) which was statistically at par with $P_2 \times P_4$ (54.17), $P_2 \times P_5$ (53.83), $P_2 \times P_6$ (54.83), $P_2 \times P_7$ (55.67), $P_3 \times P_6$ (55.83) and $P_4 \times P_6$ (54.67). Kumar et al. (2016), Mehta and Sharma (2020), Thakur and Kumar (2020) and Kumar et al. (2021) also reported prolonged availability of fruits in hybrids as compared to parents and standard check.

Table 4.11: Mean performance of yield attributing traits of cucumber viz., marketable yield per plant (kg), marketable yield per meter square (kg), harvest duration (days) and internodal length (cm) during 2020, 2021 and pooled over environments

Parental lines	Marketable yield per plant (kg)			Marketable yield per meter square (kg)			Harvest duration (days)			Internodal length (cm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	2.54	3.00	2.79	15.43	18.02	16.72	47.00	42.67	44.83	11.36	10.96	11.16
P ₂	3.24	3.23	3.24	19.46	19.38	19.42	43.33	38.00	40.67	11.30	10.74	11.02
P ₃	1.64	2.12	1.88	9.81	12.73	11.27	41.33	37.67	39.50	10.88	10.04	10.46
P ₄	1.71	2.32	2.01	10.23	13.91	12.07	42.00	36.33	39.17	11.75	10.89	11.32
P ₅	2.82	2.68	2.75	16.93	16.06	16.49	36.67	36.00	36.33	12.81	13.04	12.92
P ₆	2.46	2.56	2.51	14.76	15.35	15.06	36.33	35.00	35.67	12.66	13.07	12.86
P ₇	3.15	2.91	3.03	18.90	17.44	18.17	42.33	37.00	39.67	10.99	10.63	10.81
P ₈	1.99	2.47	2.23	11.93	14.85	13.39	36.00	33.33	34.67	9.97	10.63	10.3
P ₁ × P ₂	2.52	2.55	2.54	15.11	15.32	15.21	45.00	41.33	43.17	9.70	9.89	9.80
P ₁ × P ₃	2.84	2.51	2.67	17.06	15.03	16.04	48.00	42.67	45.33	11.06	10.33	10.70
P ₁ × P ₄	3.30	3.12	3.21	19.81	18.70	19.26	56.00	51.33	53.67	11.03	10.11	10.57
P ₁ × P ₅	2.98	3.47	3.22	17.86	20.84	19.35	48.00	48.33	48.17	12.23	12.07	12.15
P ₁ × P ₆	3.42	3.57	3.51	20.73	21.42	21.07	50.00	50.00	50.00	10.66	10.63	10.65
P ₁ × P ₇	3.43	3.83	3.63	20.57	22.96	21.77	52.67	44.67	48.67	10.89	10.59	10.74
P ₁ × P ₈	3.86	3.89	3.88	23.18	23.37	23.27	51.00	46.00	48.50	11.20	10.78	10.99
P ₂ × P ₃	3.35	3.50	3.43	20.13	20.98	20.55	55.00	50.67	52.83	11.02	10.81	10.92
P ₂ × P ₄	4.18	4.35	4.26	25.10	26.07	25.59	54.00	54.33	54.17	10.36	10.00	10.18
P ₂ × P ₅	4.15	4.21	4.18	24.93	25.29	25.11	54.33	53.33	53.83	10.62	10.48	10.55
P ₂ × P ₆	4.03	4.15	4.09	24.15	24.91	24.53	56.67	53.00	54.83	13.11	12.55	12.83
P ₂ × P ₇	4.24	4.57	4.41	25.43	27.45	26.44	56.33	55.00	55.67	9.97	10.26	10.12
P ₂ × P ₈	4.28	4.33	4.30	25.66	25.96	25.81	57.67	54.67	56.17	10.29	10.07	10.18
P ₃ × P ₄	2.82	3.36	3.09	16.95	20.16	18.55	48.67	48.33	48.50	10.64	10.22	10.43
P ₃ × P ₅	3.33	3.26	3.30	19.98	19.57	19.77	38.00	35.67	36.83	9.82	10.22	10.02
P ₃ × P ₆	2.11	2.48	2.30	12.65	14.90	13.77	56.33	55.33	55.83	10.08	9.78	9.93
P ₃ × P ₇	2.52	2.51	2.52	15.16	15.07	15.11	48.33	44.67	46.50	9.84	9.33	9.59
P ₃ × P ₈	2.42	2.57	2.50	14.54	15.43	14.99	45.33	42.33	43.83	9.88	9.63	9.76
P ₄ × P ₅	2.53	3.03	2.78	15.18	18.19	16.68	43.33	39.00	41.17	12.27	11.33	11.80
P ₄ × P ₆	2.82	2.70	2.76	16.89	16.22	16.56	57.00	52.33	54.67	12.24	12.01	12.13
P ₄ × P ₇	2.86	3.00	2.93	17.17	17.98	17.57	52.33	51.00	51.67	10.70	10.59	10.65
P ₄ × P ₈	2.44	2.33	2.38	14.63	13.98	14.31	46.33	41.33	43.83	8.65	9.44	9.05
P ₅ × P ₆	2.02	2.51	2.26	12.11	15.04	13.58	40.33	37.33	38.83	11.09	10.59	10.84
P ₅ × P ₇	2.66	2.73	2.70	15.97	16.39	16.18	45.67	43.00	44.33	13.18	12.78	12.98
P ₅ × P ₈	2.82	2.67	2.75	16.95	16.02	16.48	38.00	37.00	37.50	9.96	10.19	10.08
P ₆ × P ₇	2.43	2.44	2.43	14.56	14.66	14.61	49.67	46.00	47.83	10.70	10.22	10.46
P ₆ × P ₈	3.20	3.27	3.24	19.20	19.64	19.42	42.67	39.00	40.83	10.51	10.85	10.68
P ₇ × P ₈	3.08	3.15	3.12	18.48	18.93	18.70	46.67	45.33	46.00	10.63	10.19	10.41
Kian (check)	2.95	3.33	3.14	17.71	19.99	18.85	43.67	39.67	41.67	9.89	9.62	9.76
Mean	2.95	3.10	3.03	17.71	18.60	18.16	47.35	44.29	45.82	10.92	10.69	10.80
SE d	0.15	0.17	0.12	0.93	1.03	0.73	2.21	1.86	1.02	0.62	0.74	0.48
CV	6.45	6.78	4.93	6.45	6.78	4.93	5.74	5.14	5.47	7.01	8.49	5.48
CD	0.3	0.34	0.24	1.86	2.05	1.45	4.42	3.70	2.86	1.24	1.47	0.96

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

12. Internodal length (cm)

In parthenocarpic cucumber, plants with less internodal length with more number of nodes are preferred for high returns because plants bear fruits at almost every node. The perusal of data (Table 4.11) revealed that internodal length in parents ranged from 10.30 (P₈) to 12.92 cm (P₅). The minimum internodal length was observed in P₈ (10.30), which was statistically at par with P₁ (11.16), P₂ (11.02), P₃ (10.46) and P₇ (10.81), while maximum values were recorded in P₅ (12.92).

Among cross combinations, internodal length ranged from 8.65 to 13.18 cm in 2020, 9.33 to 12.78 cm in 2021 and 9.05 to 12.98 cm in pooled over environments. The standard check recorded 9.89 cm internodal length in 2020, 9.62 cm in 2021 and 9.76 cm in pooled over environments. In 2020, minimum internodal length was exhibited by hybrid combination P₄ × P₈ (8.68), which was statistically at par with P₁ × P₂ (9.70), P₃ × P₅ (9.82), P₃ × P₇ (9.84) and P₃ × P₈ (9.88). In 2021, hybrid combination P₃ × P₇ (9.33) recorded minimum internodal length which was statistically at par with P₁ × P₂ (9.89), P₂ × P₄ (10.00), P₂ × P₈ (10.07), P₃ × P₆ (9.78), P₃ × P₈ (9.63), P₄ × P₈ (9.44) and standard check (9.89). Similarly in pooled over environments, P₄ × P₈ (9.05) recorded minimum internodal length, which was statistically at par with P₁ × P₂ (9.80), P₃ × P₆ (9.93), P₃ × P₇ (9.59), P₃ × P₈ (9.76) and standard check (9.76). Similar findings are also reported by Golabadi et al. (2015), Ahirwar et al. (2018), Mehta (2019) and Mehta and Sharma (2020) for internodal length.

13. Vine length (m)

Indeterminate types of genotypes or hybrids are more preferred with longer vine length in high rainfall areas over the semi-determinate and determinate types. The present study (Table 4.12) revealed that mean values for vine length among parents varied from 2.54 (P₃) to 3.89 m (P₈). Among parents, maximum vine length was exhibited by P₈ (3.89), which were statistically at par with P₅ (3.79), while minimum vine length was recorded in P₃ (2.54).

Vine length in hybrids ranged from 3.04 to 4.57 m in 2020, 3.09 to 4.66 m in 2021 and 3.07 to 5.49 m in pooled over environments. The

corresponding vine length of the standard check (kian) was 3.71 in 2020, 3.85 in 2021 and 3.78 in pooled over environments. Among 28 cross combinations, 18 hybrids in 2020 and 16 hybrids each in 2021 and pooled over environments were significantly superior over standard check (kian). In 2020, $P_2 \times P_7$ (4.57) cross combination exhibited maximum vine length, which was statistically at par with $P_4 \times P_8$ (4.52), $P_5 \times P_8$ (4.45) and $P_6 \times P_7$ (4.43). Similarly in 2021 and pooled over environments, $P_2 \times P_7$ recorded maximum vine length, which was statistically at par with 2 cross combinations. The results of the study are in congruous with the findings of Yadav et al. (2007), Singh et al. (2010), Singh et al. (2016b), Kaur and Dhall (2017), Singh and Tiwari (2018) and Umeh et al. (2021) who reported increase in vine length in hybrids as compared to parents.

14. Flesh to seed cavity ratio

Flesh firmness and seed cavity affects the firmness, quality and shelf life of fruits. The present investigation (Table 4.12) indicated that mean values for flesh to seed cavity ratio among parents varied from 1.79 (P_3 and P_4) to 2.21 (P_6). Among parents, maximum flesh to seed cavity ratio was observed in P_6 (2.21) which was statistically at par with P_1 (2.00), P_2 (2.15) and P_5 (2.15) while, minimum flesh to seed cavity ratio in P_3 and P_4 i.e. 1.79.

Flesh to seed cavity ratio in cross combination ranged from 1.74 to 2.50 in 2020, 1.83 to 2.38 in 2021 and 1.78 to 2.43 in pooled over environments. Among 28 cross combinations, 18 hybrids in 2020, 12 hybrids in 2021 and 16 hybrids in pooled over environments significantly outperformed over standard check (kian). In 2020, maximum flesh to seed cavity ratio was recorded in $P_2 \times P_6$ (2.50) which was statistically at par with $P_1 \times P_3$ (2.33), $P_1 \times P_4$ (2.36), $P_3 \times P_6$ (2.33) and $P_4 \times P_5$ (2.34). Similarly in 2021, $P_1 \times P_3$ (2.38) recorded maximum flesh to seed cavity ratio which was statistically at par with $P_1 \times P_5$ (2.16), $P_1 \times P_6$ (2.21), $P_2 \times P_3$ (2.17), $P_2 \times P_5$ (2.20), $P_2 \times P_6$ (2.36), $P_2 \times P_8$ (2.26), $P_4 \times P_5$ (2.22), $P_4 \times P_6$ (2.22) and $P_6 \times P_7$ (2.22). In pooled over environment, maximum flesh to seed cavity ratio was exhibited in $P_2 \times P_6$ (2.43) which was statistically at par with $P_1 \times P_3$ (2.36), $P_1 \times P_4$ (2.24), $P_2 \times P_8$ (2.26) and $P_4 \times P_5$ (2.28). Dogra and Kanwar (2011), Kaur

et al. (2016) and Thapliyal (2017) also reported similar results for flesh to seed cavity ratio.

15. Flesh thickness (mm)

Among parents, flesh thickness ranged from 8.09 (P₃) to 10.63 mm (P₄) (Table 4.12). The maximum flesh thickness was recorded in P₄ (10.63), which was statistically at par with P₅ (10.25), P₆ (9.85) and P₈ (10.15), while minimum was in P₃ (8.09).

In the hybrid combinations, flesh thickness varied from 8.73 to 11.89 mm in 2020, 8.20 to 11.10 mm in 2021 and 9.29 to 11.49 mm in pooled over environments. The standard check recorded 8.73, 9.93 and 9.33 mm flesh thickness in 2020, 2021 and pooled over environments, respectively. The maximum flesh thickness was recorded in P₄ × P₆ which was statistically at par with 22 hybrids in 2020, 13 hybrids in 2021 and 11 hybrids in pooled over environments. Similarly, Munshi et al. (2006), Pandey et al. (2005) and Simi et al. (2017) also reported more flesh thickness in cross combinations than parents.

16. Fruit color

Fruit color is one of the main characteristic for determination of economic value and consumer preference. Fruit color study revealed that 4 genotypes exhibited dark green color, 3 genotypes were found green and only one genotype was white in color among parents (Table 4.12).

Among hybrid combinations, 16 hybrids revealed dark green color, 6 hybrids were found green while 6 cross combinations were light green in color. Light green color was observed due to crossing between white and green or dark green color. Similarly, Verma (2003) and Kumar et al. (2013) also reported variation in fruit color.

17. Incidence of downy mildew disease (%)

Downy mildew is a serious disease of cucumber. Incidence of downy mildew disease ranged from 15.98 (P₂) to 23.19% (P₈) in parents (Table 4.12). Percent disease infection showed that 2 parents namely, P₁ and P₂ were moderately resistant while 6 parents were moderately susceptible to downy mildew disease.

Among hybrid combinations, incidence of downy mildew disease ranged from 16.55 ($P_2 \times P_3$) to 23.31% ($P_1 \times P_8$). Out of 28 cross combinations, 9 hybrids showed 11-20% disease incidence which were categorized under moderate resistant while, 19 hybrids exhibited 21-40% disease incidence which were grouped under moderate susceptible. Minimum incidence of downy mildew was recorded in $P_2 \times P_3$ (16.55%), $P_1 \times P_3$ (16.77%), $P_6 \times P_7$ (17.45%) and $P_2 \times P_6$ (17.56%). Among hybrids, 9 hybrids were superior over the standard check (Kian). Similarly, Gaikwad et al. (2011), Dogra (2012), Mehta (2019) and Mehta and Sharma (2020) also reported similar results for incidence of downy mildew disease.

18. Total soluble solids (°Brix)

The perusal of data (Table 4.13) revealed that total soluble solids in the parents varied from 2.08 (P_7) to 4.38 °Brix (P_8). Among parents, P_8 (4.06 °Brix) exhibited maximum total soluble solids and none of the parents were found statistically at par with P_8 while, minimum total soluble solids was recorded in P_7 (2.08). Total soluble solids (°Brix) in hybrids ranged from 2.09 to 4.45 °Brix in 2020, 2.13 to 4.30 °Brix in 2021 and 2.13 to 4.38 °Brix in pooled over environments. The standard check recorded 2.35 (2020), 2.27 (2021) and 3.31 °Brix (pooled over environments) of total soluble solids. Among 28 cross combinations, 24 hybrids each in 2020 and 2021 and 23 hybrids in pooled over environments were observed significantly outstanding for total soluble solids over standard check (Kian). In 2020 and pooled over environments, $P_4 \times P_8$ recorded maximum total soluble solids, which was statistically at par with $P_6 \times P_7$. Similarly in 2021, maximum total soluble solids was observed in $P_4 \times P_8$ (4.30°B), which was statistically at par with $P_2 \times P_7$ (4.23°B) and $P_6 \times P_7$ (4.28°B). These findings are in close conformity with Dogra and Kanwar (2011), Kumar et al. (2016), Kumar et al. (2019) and Kumar et al. (2021) who reported that hybrids had significantly higher TSS as compared to the standard check.

Table 4.12: Mean performance of cucumber for vine length (m), flesh to seed cavity ratio flesh thickness (mm), fruit color and Incidence of downy mildew disease (%) during 2020, 2021 and pooled over environments

Parental lines	Vine length (m)			Flesh to seed cavity ratio			Flesh thickness (mm)			Fruit color	Incidence of downy mildew disease (%)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled		-	2020	2021
P ₁	3.40	3.52	3.46	2.05	1.95	2.00	9.43	8.30	8.87	Green	24.57	21.44	23.01
P ₂	3.66	3.71	3.69	2.18	2.13	2.15	9.70	8.33	9.02	Dark green	15.37	16.58	15.98
P ₃	2.45	2.64	2.54	1.74	1.83	1.79	8.05	8.13	8.09	Green	24.57	21.58	23.08
P ₄	3.64	3.77	3.71	1.77	1.82	1.79	10.10	11.17	10.63	Dark green	19.52	22.97	21.25
P ₅	3.85	3.73	3.79	2.14	2.16	2.15	10.24	10.27	10.25	Dark green	20.74	23.57	22.16
P ₆	3.33	3.49	3.41	2.23	2.19	2.21	10.54	9.17	9.85	White	24.34	20.58	22.46
P ₇	3.54	3.66	3.60	1.88	1.93	1.91	9.55	8.10	8.82	Dark green	23.96	20.43	22.20
P ₈	3.92	3.85	3.89	2.05	1.81	1.93	10.57	9.73	10.15	Green	21.49	24.89	23.19
P ₁ × P ₂	3.90	4.09	3.99	1.78	1.92	1.85	11.21	10.07	10.64	Dark green	20.54	18.56	19.55
P ₁ × P ₃	4.02	3.89	3.96	2.33	2.38	2.36	10.10	9.10	9.60	Dark green	15.67	17.87	16.77
P ₁ × P ₄	4.35	4.51	4.43	2.36	2.12	2.24	11.12	10.17	10.65	Dark green	23.29	19.67	21.48
P ₁ × P ₅	3.06	3.24	3.15	1.92	2.16	2.04	10.57	9.30	9.93	Green	22.57	20.78	21.68
P ₁ × P ₆	4.09	3.91	4.00	2.11	2.21	2.16	11.37	10.60	10.99	Light green	23.48	21.22	22.35
P ₁ × P ₇	3.92	4.00	3.96	1.87	2.01	1.94	10.37	8.93	9.65	green	24.17	19.37	21.77
P ₁ × P ₈	3.54	3.40	3.47	2.22	1.93	2.08	11.65	10.87	11.26	Dark green	24.47	22.15	23.31
P ₂ × P ₃	3.82	3.67	3.75	2.20	2.17	2.18	10.47	9.30	9.89	Dark green	17.23	15.87	16.55
P ₂ × P ₄	4.37	4.42	4.39	1.99	2.14	2.06	11.49	11.07	11.28	Dark green	19.57	20.68	20.13
P ₂ × P ₅	3.66	3.77	3.72	2.10	2.20	2.15	10.44	8.53	9.49	Dark green	19.25	21.59	20.42
P ₂ × P ₆	3.72	3.83	3.77	2.50	2.36	2.43	9.91	10.50	10.21	Light green	16.78	18.34	17.56
P ₂ × P ₇	4.57	4.48	4.53	1.77	1.94	1.85	10.19	8.53	9.39	Green	22.57	19.57	21.07
P ₂ × P ₈	4.02	4.16	4.09	2.26	2.26	2.26	11.25	9.53	10.39	Dark green	18.67	20.35	19.51
P ₃ × P ₄	3.87	4.06	3.96	2.09	2.07	2.08	11.79	10.67	11.23	Dark green	22.48	20.53	21.51
P ₃ × P ₅	3.53	3.45	3.49	2.13	2.08	2.11	11.06	10.27	10.66	Dark green	19.35	24.67	22.01
P ₃ × P ₆	4.11	4.26	4.18	2.33	2.01	2.17	9.59	9.60	9.60	Light green	24.18	22.35	23.27
P ₃ × P ₇	4.28	4.12	4.20	2.08	2.09	2.09	8.94	10.37	9.65	Dark green	22.75	19.67	21.21
P ₃ × P ₈	4.17	4.22	4.20	1.80	2.04	1.92	10.99	9.37	10.18	Dark green	23.18	22.48	22.83
P ₄ × P ₅	4.14	3.98	4.06	2.34	2.22	2.28	10.73	9.03	9.88	Dark green	23.79	21.67	22.73
P ₄ × P ₆	3.31	3.44	3.37	2.08	2.22	2.15	11.89	11.10	11.49	Green	18.34	19.67	19.01
P ₄ × P ₇	3.66	3.60	3.63	1.95	2.07	2.01	11.14	10.93	11.04	Green	21.57	20.78	21.18
P ₄ × P ₈	4.52	4.66	4.59	1.74	2.00	1.87	10.40	10.50	10.45	Dark green	23.62	22.46	23.04
P ₅ × P ₆	3.21	3.18	3.19	2.18	2.01	2.09	11.07	10.33	10.70	Light green	24.83	21.61	23.22
P ₅ × P ₇	3.37	3.27	3.32	1.74	1.83	1.78	10.75	9.07	9.91	Dark green	20.92	19.57	20.25
P ₅ × P ₈	4.45	4.41	4.43	1.80	2.15	1.98	11.34	9.73	10.54	Dark green	22.34	18.26	20.30
P ₆ × P ₇	4.43	4.56	4.49	2.18	2.22	2.20	10.39	8.20	9.29	Light green	19.23	15.67	17.45
P ₆ × P ₈	3.54	3.47	3.50	1.79	2.06	1.92	10.98	8.97	9.97	Light green	17.65	18.65	18.15
P ₇ × P ₈	3.04	3.09	3.07	1.84	1.95	1.90	11.17	10.70	10.93	Green	23.78	20.67	22.23
Kian (check)	3.71	3.85	3.78	1.92	2.12	2.02	8.73	9.93	9.33	Green	21.98	24.86	23.42
Mean	3.79	3.82	3.80	2.04	2.07	2.06	10.52	9.69	10.10		21.43	20.58	21.01
SE d	0.08	0.08	0.06	0.11	0.11	0.08	0.83	0.55	0.48		-	-	-
CV	2.84	2.88	2.09	6.59	6.87	6.73	9.77	6.92	5.86		-	-	-
CD	0.17	0.17	0.12	0.22	0.23	0.23	1.67	1.09	0.96		NS	NS	NS

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

19. Ascorbic acid (mg/100g)

Ascorbic acid is a vital nutrient required by humans, so cucumber fruits rich in ascorbic acid improve the fruit quality. Among parents, mean values for ascorbic acid ranged from 4.80 (P₄) to 6.42 mg/100g (P₈) (Table 4.13). Maximum ascorbic acid was recorded in P₈ (6.42) and none of the parents were at par with the maximum values while, minimum in P₄ (4.80).

Among cross combinations, ascorbic acid values varied from 4.45 to 6.71 mg/100g, 4.71 to 6.43 mg/100g and 4.58 to 6.57 mg/100g in 2020, 2021 and pooled over environments, respectively. The standard check recorded 5.62, 5.71 and 5.66 mg/100 g ascorbic acid in 2020, 2021 and pooled over environments, respectively. Among 28 crosses, 11 hybrids in all the years were significantly superior over the standard check (Kian). Cross combination P₁ × P₇ exhibited maximum values for ascorbic acid which was statistically at par with P₄ × P₅ in 2021 and pooled over environments while, none of hybrid was at par in 2020. Kaur et al. (2016) and Das et al. (2018) also observed similar results for ascorbic acid.

20. Total sugar (%)

The perusal of data (Table 4.13) revealed that total sugar in parents ranged from 2.20 (P₄) to 3.16% (P₈). Maximum total sugar was recorded in P₈ (3.16) and none of the parent was found at par with P₈ while, minimum value was observed in P₄ (2.20).

Among cross combinations, total sugar ranged from 2.14 to 3.15% in 2020, 1.93 to 3.15% in 2021 and 2.04 to 3.06% in pooled over environments. In standard check, total sugar recorded was 2.72, 2.53 and 2.64 in 2020, 2021 and pooled over environments, respectively. As many as, 10 hybrids each in 2020 and pooled over environments while, 18 hybrids in 2021 outperformed over standard check. In 2020 and 2021, maximum total sugar (3.15) was exhibited by hybrid P₁ × P₇ which was statistically at par with P₁ × P₃. Similarly in pooled environments also, maximum value was recorded in P₁ × P₇ (3.06) which was statistically at par with P₁ × P₃ (3.10) and P₂ × P₃ (3.01). Das et al. (2018) and Tamang et al. (2018) have also reported that total sugar was higher in few hybrids.

Table 4.13: Mean performance of cucumber for quality traits during 2020, 2021 and pooled over environments

Parental lines	Total Soluble Solids (°B)			Ascorbic acid (mg/100g)			Total sugars (%)			Reducing sugar (%)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	2.78	2.89	2.84	6.03	6.25	6.14	2.90	2.51	2.71	0.78	0.81	0.79
P ₂	2.54	2.48	2.51	5.51	5.15	5.33	2.30	2.68	2.49	0.75	0.62	0.69
P ₃	2.52	2.45	2.49	5.92	5.67	5.79	2.50	2.67	2.59	0.35	0.26	0.30
P ₄	3.02	2.91	2.97	4.67	4.93	4.80	2.02	2.38	2.20	0.15	0.20	0.17
P ₅	3.50	3.43	3.47	6.42	6.11	6.26	2.90	2.60	2.75	0.12	0.07	0.10
P ₆	3.38	3.13	3.25	5.05	4.70	4.88	2.50	2.27	2.39	0.35	0.27	0.31
P ₇	2.05	2.11	2.08	5.18	5.44	5.31	2.87	3.16	3.01	0.68	0.54	0.61
P ₈	4.16	3.95	4.06	6.53	6.31	6.42	3.26	3.07	3.16	0.34	0.26	0.30
P ₁ × P ₂	2.36	2.21	2.28	6.30	6.03	6.17	2.27	2.56	2.41	0.37	0.42	0.39
P ₁ × P ₃	3.68	3.84	3.76	6.16	6.41	6.29	3.05	3.14	3.10	0.68	0.54	0.61
P ₁ × P ₄	4.16	3.97	4.07	5.72	5.49	5.61	2.82	2.69	2.76	1.41	1.22	1.32
P ₁ × P ₅	3.24	3.37	3.30	5.27	5.32	5.29	2.53	2.88	2.70	1.75	1.39	1.57
P ₁ × P ₆	2.35	2.28	2.32	6.00	5.84	5.92	2.25	2.64	2.44	0.84	0.42	0.63
P ₁ × P ₇	2.65	2.78	2.72	6.71	6.43	6.57	3.15	2.81	2.98	0.37	0.44	0.40
P ₁ × P ₈	2.21	2.13	2.17	5.21	5.49	5.35	2.57	2.73	2.65	1.35	1.11	1.23
P ₂ × P ₃	3.74	3.62	3.68	5.23	5.08	5.16	3.15	2.88	3.01	0.72	0.92	0.82
P ₂ × P ₄	2.58	2.65	2.62	5.89	6.18	6.04	2.34	2.07	2.20	1.15	0.82	0.99
P ₂ × P ₅	2.97	2.82	2.89	5.51	5.78	5.65	2.86	2.67	2.77	1.35	1.11	1.23
P ₂ × P ₆	2.41	2.20	2.30	5.76	5.95	5.86	2.97	3.15	3.06	0.85	0.72	0.78
P ₂ × P ₇	4.15	4.23	4.19	5.04	4.81	4.92	2.76	2.57	2.66	0.63	0.58	0.61
P ₂ × P ₈	2.09	2.17	2.13	4.76	4.93	4.84	2.75	2.34	2.54	0.48	0.53	0.50
P ₃ × P ₄	2.52	2.63	2.58	5.06	4.95	5.01	2.25	2.42	2.34	1.25	1.04	1.15
P ₃ × P ₅	3.62	3.55	3.58	5.25	5.34	5.29	2.62	2.24	2.43	0.87	0.73	0.80
P ₃ × P ₆	4.13	4.00	4.07	4.75	4.72	4.73	2.18	1.97	2.07	1.37	1.12	1.25
P ₃ × P ₇	3.43	3.51	3.47	5.58	5.22	5.40	2.27	2.58	2.42	0.87	0.75	0.81
P ₃ × P ₈	3.44	3.25	3.35	4.45	4.71	4.58	2.49	2.69	2.59	0.96	0.89	0.93
P ₄ × P ₅	2.63	2.50	2.57	6.61	6.48	6.54	2.25	1.93	2.09	1.37	1.11	1.24
P ₄ × P ₆	3.62	3.79	3.71	5.25	4.64	4.94	2.36	2.56	2.46	1.15	1.32	0.23
P ₄ × P ₇	4.26	4.12	4.19	4.69	4.77	4.73	2.34	2.59	2.46	0.75	0.60	0.67
P ₄ × P ₈	4.45	4.30	4.38	5.50	5.30	5.40	2.78	2.50	2.64	0.37	0.40	0.39
P ₅ × P ₆	3.87	3.75	3.81	4.85	5.01	4.93	2.45	2.66	2.56	0.17	0.09	0.13
P ₅ × P ₇	3.19	3.06	3.12	6.06	6.37	6.22	2.59	2.69	2.64	1.57	1.33	1.45
P ₅ × P ₈	3.68	3.75	3.72	5.56	5.63	5.59	2.47	2.15	2.31	1.17	0.90	1.04
P ₆ × P ₇	4.33	4.28	4.31	4.76	4.52	4.64	2.14	1.93	2.04	0.87	0.75	0.81
P ₆ × P ₈	2.25	2.32	2.29	5.95	6.1	6.03	2.85	2.69	2.77	1.35	1.23	1.29
P ₇ × P ₈	2.85	2.71	2.78	6.46	6.22	6.34	2.57	2.26	2.41	1.05	0.84	0.95
Kian (check)	2.35	2.27	2.31	5.62	5.71	5.66	2.74	2.53	2.64	0.55	0.62	0.58
Mean	3.17	3.12	3.14	5.55	5.51	5.53	2.60	2.56	2.58	0.84	0.73	0.79
SE d	0.06	0.06	0.06	0.04	0.01	0.02	0.06	0.05	0.04	0.01	0.01	0.01
CV	2.51	2.46	2.49	1.07	0.32	0.51	2.78	2.72	1.85	2.45	2.53	1.55
CD	0.13	0.12	0.17	0.09	0.02	0.04	0.12	0.11	0.07	0.03	0.03	0.02

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

21. Reducing sugar (%)

The present investigation (Table 4.13) indicated that reducing sugar in parents ranged from 0.10 to 0.79%. For this trait, maximum value was recorded in P₁ (0.79) with none of the parent was at par while, minimum value in P₅ (0.10).

Reducing sugar in hybrids ranged from 0.17 to 1.75% in 2020, 0.09 to 1.39% in 2021 and 0.13 to 1.57% in pooled over environments. Reducing sugar values in the standard check were 0.55% (2020), 0.62% (2021) and 0.58% (pooled over environments). Out of 28 cross combinations, 23 hybrids in 2020, 19 hybrids in 2021 and 22 hybrids in pooled over environments were promising over standard check. Among hybrid combinations, P₁ × P₅ recorded maximum value for reducing sugar in all years and none of hybrid was found at par with P₁ × P₅ while, minimum value was observed in P₁ × P₃. Similarly, Das et al. (2018) and Tamang et al. (2018) also reported higher concentration of reducing sugar in hybrids in cucumber as compared to standard check.

4.4 Combining ability and gene action

The effectiveness of a breeding programme is determined by the selection of suitable parents and then use of those parents in an appropriate breeding procedure. The combining ability analysis has been widely utilized to select suitable parents for use in hybrid development. Estimation of this analysis helps in partitioning the total genotypic variation of hybrid combination into general combining ability (GCA) and specific combining ability (SCA). Additive gene action is measured by GCA effects which represents the fixed genetic variation components and are also exploited to categorize parents in hybrids for breeding behavior while, non-fixed components of genetic variation are measured by SCA effects which indicates the non-additive gene action (Sprague 1966). Due to parental differential abilities, the technique of selecting parents based on performance, adaption and genetic diversity does not always provide useful results. Due to the interaction of complex genes, capability of parents get changed so, parents cannot be selected based on their performance (Allard 1960). Therefore, it is necessary to estimate the general combining ability and specific

combining ability for selection of suitable parents and successful breeding programme. In the present study, diallel mating design (method 2) excluding reciprocals (Griffing 1956b) has been used and 8 parents, 28 crosses and one standard check were evaluated in 2020 and 2021. The results pertaining to combining ability are discussed below:

4.4.1 Analysis of variance for combining ability

For combining ability, analysis of variance is presented in Table 4.14. The results indicated that mean squares due to general combining ability were highly significant for all the characters in 2020, 2021 and pooled over environments. Mean squares due to specific combining ability were highly significant for all the traits in 2021 and pooled over environments and except for flesh thickness in 2020. In $GCA \times$ environment interaction, mean sum of squares were significant for nodal position of first female flower, total soluble solids ($^{\circ}$ brix), ascorbic acid (mg/100g), total sugar (%) and reducing sugar (%) while, mean squares due to $SCA \times$ environment interaction were highly significant for days to first female flower, nodal position of first female flower, number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square (kg), vine length (m), flesh to seed cavity ratio, total soluble solids ($^{\circ}$ brix), ascorbic acid (mg/100 g), total sugar (%) and reducing sugar (%). The highly significant results of mean squares due to general combining ability and specific combining ability suggested the role of both additive and non-additive gene action in controlling the expression of these traits. Similar results are also reported by Sarkar and Sirohi (2010), Bairagi et al. (2013), Vidhya and Kumar (2014), Moradipour et al. (2016), Singh et al. (2016b), Malav et al. (2018), Thakur and Kumar (2020) and Manggoel et al. (2021).

4.4.2 Estimates of genetic components of variance

Once the suitable parents and promising cross combinations have been selected in a breeding programme, then appropriate breeding strategy should be adopted which mainly relies on the nature of gene action of a particular trait in a population (Cockerham 1961; Sprague 1966). Among different mating designs, diallel mating design method 2 excluding reciprocals not only aids in assessing combining

Table 4.14: Analysis of variance for combining ability for various traits in cucumber during 2020, 2021 and pooled over environments

Years→ Source of variation Traits df→	2020			2021			Pooled					
	GCA	SCA	Error	GCA	SCA	Error	GCA	SCA	Environment	GCA × Environment	SCA × Environment	Error
	7.00	28.00	70.00	7.00	28.00	70.00	7	28	1	7	28	140
Days to first female flower	8.05*	6.54*	0.90	11.81*	5.94*	0.79	19.02*	11.14*	14.81*	0.85	1.34*	0.84
Nodal position of first female flower	0.46*	0.40*	0.03	0.59*	0.42*	0.01	0.94*	0.77*	1.16*	0.11*	0.05*	0.02
Number of female flowers per node	0.29*	0.10*	0.002	0.24*	0.12*	0.004	0.53*	0.21*	0.002	0.005	0.004	0.003
Days taken to first fruit picking	23.26*	23.41*	1.26	24.23*	13.74*	3.02	45.74*	34.64*	2.22	1.76	2.517	2.14
Fruit length (cm)	11.53*	3.84*	0.79	10.99*	2.65*	0.76	21.39*	5.46*	3.06*	1.13	1.02	0.78
Fruit diameter (cm)	0.12*	0.06*	0.006	0.08*	0.04*	0.01	0.18*	0.09*	0.02	0.01	0.006	0.01
Fruit weight (g)	331.22*	194.85*	24.13	392.72*	214.25*	22.44	719.59*	406.72*	1641.12*	4.344	2.383	23.28
Number of fruits per plant	24.74*	9.55*	1.37	11.79*	3.63*	1.06	34.46*	10.28*	7.41*	2.07	2.91*	1.22
Marketable yield per plant (kg)	0.99*	0.37*	0.01	0.82*	0.35*	0.014	1.79*	0.68*	0.54*	0.013	0.036*	0.01
Marketable yield per meter square (kg)	35.63*	13.19*	0.44	29.51*	12.43*	0.52	64.68*	24.33*	19.57*	0.47	1.29*	0.48
Harvest duration	71.37*	35.82*	2.52	52.30*	44.42*	1.72	121.74*	78.27*	249.04*	1.94	1.97	2.12
Internodal length (cm)	2.06*	0.83*	0.20	2.13*	0.62*	0.28	4.03*	1.38*	1.36*	0.15	0.08	0.24
Vine length (m)	0.13*	0.25*	0.004	0.16*	0.23*	0.004	0.28*	0.47*	0.02*	0.006	0.008*	0.004
Flesh to seed cavity ratio	0.06*	0.04*	0.006	0.03*	0.02*	0.007	0.08*	0.05*	0.03*	0.005	0.02*	0.006
Flesh thickness (mm)	1.10*	0.57	0.36	1.61*	0.73*	0.15	2.31*	0.94*	21.30*	0.40	0.35	0.25
Total soluble solids (°B)	0.35*	0.586	0.002	0.31*	0.56*	0.002	0.65*	1.13*	0.06*	0.006*	0.008*	0.002
Ascorbic acid (mg/100g)	0.43*	0.38*	0.0012	0.61*	0.32*	0.0001	1.03*	0.67*	0.04*	0.011*	0.04*	0.0007
Total sugar (%)	0.15*	0.09*	0.002	0.09*	0.11*	0.0016	0.22*	0.16*	0.021*	0.02*	0.04*	0.002
Reducing sugar (%)	0.026*	0.23*	0.0002	0.01*	0.17*	0.0001	0.03*	0.39*	0.38*	0.004*	0.01*	0.0001

*Significant at 5% level of significance

ability of parents and cross combinations but offers information on the type of gene action governing the traits under consideration (Griffing 1956b). The type of gene action has been estimated from GCA and SCA variances which are presented in Table 4.15.

The present investigation (Table 4.15) revealed that the estimates of $\sigma^2\text{SCA}$ were higher for all the traits *viz.*, days to first female flower, nodal position of first female flower, number of female flowers per node, days taken to first fruit picking (days), fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square (kg), harvest duration (days), internodal length (cm), vine length (m), flesh to seed cavity ratio, flesh thickness (mm), total soluble solids ($^{\circ}\text{B}$), ascorbic acid (mg/100g), total sugar (%) and reducing sugar (%) in all the environments indicating the predominance of non-additive gene action in controlling these traits. Therefore, hybrid vigour could be exploited for above traits.

The outcomes of analysis of variance were also assured from additive ($\sigma^2\text{A}$) and dominant ($\sigma^2\text{D}$) component of variances and average degree of dominance. The magnitude of dominant component ($\sigma^2\text{D}$) were higher than the additive component ($\sigma^2\text{A}$) for the all traits studied in all the environments except fruit length and internodal length in 2021 indicating the predominance of non-additive gene action in controlling all these traits. The higher estimates of non-additive components ($\sigma^2\text{D}$) revealed that average degree of dominance values were more than 1.00 for all the traits in all the environments. For the two traits fruit length and internodal length in 2021, though SCA variances were higher but the value of $\sigma^2\text{A}$ (additive component) estimates were also higher. This could be due to the fact that statistically GCA variance exploits the additive component of variability (Matzinger and Kempthorne 1956) however it also includes additive \times additive and higher order of epistatic interactions. GCA include the portion of dominance or epistasis or both with additive genetic effects in the presence of SCA as suggested by Hayman (1960).

Table 4.15: Estimation of genetic components of variance and degree of dominance for different traits during 2020, 2021 and pooled over environments

Traits	2020				2021				Pooled			
	σ^2 GCA	σ^2 SCA= σ^2 D	σ^2 A=2 σ^2 GCA	Average degree of dominance	σ^2 GCA	σ^2 SCA= σ^2 D	σ^2 A=2 σ^2 GCA	Average degree of dominance	σ^2 GCA	σ^2 SCA= σ^2 D	σ^2 A=2 σ^2 GCA	Average degree of dominance
Days to first female flower	0.72	5.65	1.43	1.99	1.10	5.15	2.20	1.53	0.91	5.13	1.81	1.68
Nodal position of first female flower	0.06	0.32	0.13	1.58	0.06	0.39	0.13	1.77	0.05	0.38	0.09	2.03
Number of female flowers per node	0.03	0.10	0.06	1.32	0.02	0.11	0.05	1.54	0.03	0.11	0.05	1.42
Days taken to first fruit picking (days)	2.20	22.15	4.40	2.24	2.12	10.72	4.24	1.59	2.17	16.18	4.35	1.93
Fruit length (cm)	1.07	3.04	2.15	1.19	1.02	1.89	2.05	0.96	1.03	2.33	2.06	1.06
Fruit diameter (cm)	0.01	0.06	0.02	1.63	0.01	0.03	0.01	1.45	0.01	0.04	0.02	1.61
Fruit weight (g)	30.71	170.71	61.42	1.67	37.03	191.82	74.06	1.61	33.72	180.79	67.45	1.64
Number of fruits per plant	2.34	8.18	4.67	1.32	1.07	2.57	2.15	1.09	1.67	4.58	3.34	1.17
Marketable yield per plant (kg)	0.10	0.35	0.20	1.35	0.08	0.33	0.16	1.43	0.09	0.33	0.18	1.36
Marketable yield per meter square (kg)	3.52	12.75	7.04	1.35	2.06	13.99	4.13	1.84	3.57	12.56	7.14	1.33
Harvest duration (days)	6.89	33.30	13.77	1.55	5.06	42.70	10.12	2.05	6.01	38.39	12.03	1.79
Internodal length (cm)	0.19	0.64	0.37	1.31	0.19	0.34	0.37	0.96	0.24	0.71	0.48	1.22
Vine length (m)	123.65	2446.05	247.31	3.14	157.88	2232.03	315.77	2.66	139.71	2316.12	279.41	2.88
Flesh to seed cavity ratio	0.01	0.04	0.01	1.84	0.0022	0.0124	0.0044	1.68	0.004	0.02	0.008	1.605
Flesh thickness (mm)	0.001	0.002	0.001	1.22	0.0015	0.0057	0.003	1.38	0.001	0.004	0.002	1.32
Total Soluble Solids ($^{\circ}$ B)	0.03	0.57	0.07	2.89	0.0303	0.55	0.06	3.03	0.03	0.56	0.06	2.96
Ascorbic acid (mg/100g)	0.04	0.38	0.09	2.10	0.06	0.31	0.12	1.61	0.05	0.33	0.10	1.80
Total sugar (%)	0.01	0.08	0.02	2.00	0.009	0.10	0.018	2.35	0.01	0.07	0.02	1.87
Reducing sugar (%)	0.02	0.023	0.05	2.40	0.01	0.16	0.02	2.83	0.01	0.19	0.02	3.08

These results for predominance of non-additive gene action are in line with the findings of Sharma (2006), Tiwari et al. (2009), Kumar et al. (2013), Pati et al. (2015), Thakur and Kumar (2020) for days to first female flower, Sharma (2006), Tiwari et al. (2009), Kumar et al. (2013), Pati et al. (2015), Kaur and Dhall (2017), Thakur and Kumar (2020) for nodal position of first female flower, Manggoel et al. (2021) for number of female flowers per node, Munshi et al. (2006), Sarkar and Sirohi (2006), Sharma (2006), Tiwari et al. (2009), Kumar et al. (2013), Pati et al. (2015), Thapliyal (2017), Malav et al. (2018), Thakur and Kumar (2020) for days taken to first fruit picking (days), Sharma (2006), Kaur and Dhall (2017) for fruit length (cm), Sharma (2006), Bairagi et al. (2013), Kaur and Dhall (2017), Thapliyal (2017), Thakur and Kumar (2020) for fruit diameter (cm), Sharma (2006), Kaur and Dhall (2017), Malav et al. (2018), Thakur and Kumar (2020) for fruit weight (g), Munshi et al. (2006), Sharma (2006), Tiwari et al. (2009), Kumar et al. (2013), Pati et al. (2015) for number of fruits per plant, Munshi et al. (2006), Sharma (2006), Tiwari et al. (2009), Kumar et al. (2013), Pati et al. (2015), Kaur and Dhall (2017), Thapliyal (2017), Rai et al. (2018), Thakur and Kumar (2020) for marketable yield per plant (kg), Kumar et al. (2013), Thakur and Kumar (2020) for marketable yield per meter square (kg), Sarkar and Sirohi (2006), Thapliyal (2017) for vine length (m), Thapliyal (2017) for flesh to seed cavity ratio, Rai et al. (2018) for flesh thickness (mm) and Thapliyal (2017) for total soluble solids ($^{\circ}$ B).

4.4.3 Estimation of general combining ability (GCA)

General combining ability estimation effects for various traits including growth, fruit yield and its component traits during 2020, 2021 and pooled over environments are described below:

1. Days to first female flower

For days to first female flower, negative GCA effects were more desirable for indication of earliness. The GCA effects varied from -1.65 to 0.95 in 2020, -1.52 to 1.48 in 2021 and -1.48 to 1.22 in pooled over environments (Table 4.16). The significant GCA effects were observed in P₂, P₃, P₄, P₅ and P₈ in all environments while P₆ in 2021. The best general combiner for days to first female flower was P₂ and P₄ in all the environments and P₆ in pooled over environments while P₃, P₅ and P₈ were poor combiner for days to first female flower. The results are in line

with findings of earlier scientists (Yadav et al. 2007; Bairagi et al. 2013; Kumar et al. 2013; Reddy et al. 2014; Malav et al. 2018; Arab et al. 2020; Thakur and Kumar 2020; Manggoel et al. 2021) who reported good general combiner parents in their studies for days to first female flower.

2. Nodal position of first female flower

The GCA effects for nodal position of first female flower ranged from -0.33 to 0.41, -0.37 to 0.29 and -0.31 to 0.25 in 2020, 2021 and pooled over environments, respectively (Table 4.16). Among seven parents, P₁, P₅, P₆ and P₈ in all environments, P₂ in 2020 and 2021, P₄ in 2020 and pooled over environment, P₃ in 2021 and pooled over environments showed significant GCA effects for this trait. Among parents, P₁ and P₈ in all environments and P₂ in 2020 were found to be the best combiners due to significant negative GCA effects. Parents *viz.*, P₅ and P₆ in all environments, P₄ in 2020 and pooled over environments, P₂ and P₃ in 2021 and pooled over environments were poor general combiners as revealed from their significant positive GCA effects. The results of the study are supported by Mule et al. (2012), Bairagi et al. (2013), Kumar et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kaur and Dhall (2017), Malav et al. (2018), Arab et al. (2020) and Kumar et al. (2021) who also revealed significant GCA effects for nodal position of first female flower.

3. Number of female flowers per node

For number of female flowers per node, GCA effects ranged from -0.26 to 0.32 in 2020, -0.25 to 0.28 in 2021 and -0.25 to 0.30 in pooled over environments (Table 4.16). The analysis revealed significant GCA effects for parents namely, P₃, P₄, P₅, P₆, P₇ and P₈ in all environments, P₁ in 2020 and P₂ in 2021 and pooled over environments. The best general combiners for this trait were P₃ and P₈ in all environments, P₁ in 2020 and P₂ in 2021 and pooled over environments while, P₄, P₅, P₆ and P₇ were observed poor general combiner. Yadav et al. (2007) and Moradipour et al. (2016) also reported significant GCA effects for number of female flowers per node.

4. Days taken to first fruit picking

The negative GCA effects for days taken to first fruit picking were considered more desirable as it reveals earliness. The GCA effects ranged from -1.77 to 2.20,

-1.92 to 2.01 and -1.75 to 2.10 in 2020, 2021 and pooled over environments, respectively (Table 4.16). The significant GCA effects were observed in P₂, P₃, P₄, P₅ and P₈ in all environments, P₆ in 2020 and pooled over environments. The best general combiners for days taken to first fruit picking were P₂ and P₃ in all environments and P₆ in 2020 and pooled over environments observed from their significant negative GCA effects while, parents *viz.*, P₄, P₅ and P₈ were found to be poor combiners. The results are in line with the study of Sarkar and Sirohi (2010), Kumar et al. (2013), Reddy et al. (2014), Jat et al. (2015), Singh et al. (2016b), Thapliyal (2017), Thakur and Kumar (2020) and Kumar et al. (2021) revealing significant GCA effects for days taken to first picking in their respective studies.

5. Fruit length (cm)

For fruit length, GCA effects ranged from -1.99 to 1.18, -1.26 to 1.42 and -1.60 to 1.30 in 2020, 2021 and pooled over environments, respectively (Table 4.16). The analysis revealed significant GCA effects for P₁, P₂, P₃ and P₅ in all environments, P₄ in pooled over environments and P₇ in 2021 and pooled over environments. The best combiners for fruit length were P₂ and P₅ in all environments and P₄ in pooled over environments revealed from their significant positive GCA effects. Parents namely, P₃ in all environments, P₁ in 2020 and pooled over environments and P₇ in 2021 and pooled over environments were found to be poor combiners for fruit length (cm). Significant GCA effects for fruit length are earlier reported by Yadav et al. (2007), Sarkar and Sirohi (2010), Singh et al. (2010), Mule et al. (2012), Singh et al. (2012), Kumar et al. (2013), Thapliyal (2017), Malav et al. (2018), Thakur and Kumar (2020) and Manggoel et al. (2021).

6. Fruit diameter (cm)

For fruit diameter, GCA effects varied from -0.11 to 0.16 in 2020, -0.14 to 0.10 in 2021 and -0.12 to 0.13 in pooled over environments (Table 4.16). The significant GCA effects were observed for P₁, P₂, P₃, P₄ and P₇ in all environments and P₅ and P₆ in 2020 and pooled over environments. Parents namely, P₁, P₂ and P₄ were found best general combiners in all environments while, P₃ and P₇ in all

Table 4.16: Estimates of general combining ability effects of parents for days to first female flower, nodal position of first female flower, number of female flowers/node, days to first fruit picking, fruit length (cm) and fruit diameter (cm) in cucumber during 2020, 2021 and pooled over environments

Parental lines	Days to first female flower			Nodal position of first female flower			Number of female flowers/node			Days to first fruit picking			Fruit length (cm)			Fruit diameter (cm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	0.18	-0.05	0.07	-0.33*	-0.32*	-0.31*	0.04*	-0.01	0.02	-0.13	-0.82	-0.48	-0.91*	-1.26*	-1.09*	0.09*	0.08*	0.08 *
P ₂	-1.65*	-1.32*	-1.48*	-0.13 *	0.15*	0.02	0.02	0.07*	0.04*	-1.57*	-1.92*	-1.75*	1.18*	1.42*	1.30*	0.11 *	0.10*	0.11 *
P ₃	0.68*	1.05*	0.87*	-0.03	0.11*	0.05*	0.32*	0.28*	0.30*	-1.53*	-1.39*	-1.46*	-1.99*	-1.22*	-1.60*	-0.10*	-0.14*	-0.12 *
P ₄	-0.82*	-1.52*	-1.17*	0.18*	-0.04	0.08*	-0.05*	-0.04*	-0.05*	1.10*	1.51*	1.30*	0.49	0.48	0.48*	0.16*	0.10*	0.13 *
P ₅	0.95*	1.48*	1.22*	0.23*	0.23*	0.25*	-0.26*	-0.25*	-0.25*	1.50*	1.88*	1.69*	1.13*	1.10*	1.11*	-0.09*	-0.05	-0.07 *
P ₆	-0.45	-0.38	-0.50*	0.41*	0.29*	0.24*	-0.13*	-0.10*	-0.11*	-1.77*	-0.76	-1.26*	0.52	0.15	0.34	-0.11*	-0.02	-0.06 *
P ₇	0.42	0.12	0.27	-0.04	-0.05	-0.03	-0.06 *	-0.05*	-0.06*	0.20	-0.49	-0.15	-0.33	-1.02*	-0.67*	-0.06*	-0.07*	-0.07 *
P ₈	0.68*	0.62*	0.73*	-0.30*	-0.37*	-0.31*	0.12 *	0.11*	0.11*	2.20*	2.01*	2.10*	-0.09	0.36	0.13	-0.00	0.01	0.00
SE(gi)±	0.28	0.26	0.27	0.05	0.03	0.04	0.01	0.02	0.01	0.33	0.51	0.42	0.26	0.26	0.26	0.02	0.03	0.02
SE(gi-gj) ±	0.42	0.40	0.41	0.07	0.04	0.06	0.02	0.03	0.02	0.50	0.78	0.64	0.39	0.39	0.39	0.03	0.05	0.04
CD (gi)	0.66	0.62	0.64	0.12	0.08	0.09	0.03	0.04	0.03	0.79	1.21	1.51	0.62	0.61	0.62	0.05	0.08	0.06
CD (gi-gj)	1.01	0.94	0.97	0.17	0.12	0.14	0.05	0.06	0.05	1.19	1.83	1.00	0.94	0.92	0.93	0.08	0.12	0.10

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

environments, P₅ and P₆ in 2020 and pooled over environments were poor combiners for fruit diameter. The results are in conformity with respect to GCA effects for fruit diameter with earlier studies of Sarkar and Sirohi (2010), Singh et al. (2010), Bairagi et al. (2013), Kumar et al. (2013), Reddy et al. (2014), Vidhya and Kumar (2014), Singh et al. (2016), Thapliyal (2017) and Thakur and Kumar (2020).

7. Fruit weight (g)

For fruit weight, GCA effects ranged from -8.56 to 10.64 in 2020, -10.05 to 11.99 in 2021 and -9.31 to 11.32 in pooled over environments (Table 4.17). The analysis of GCA revealed significant effects for P₁, P₂ and P₃ in all environments, P₄ and P₈ in 2020 and pooled over environments. Among parents, P₁ and P₂ were observed good general combiners due to their significant positive GCA effects in all environments while, P₃ in all environments and P₄ and P₈ in 2020 and pooled over environments were found as poor general combiners for fruit weight. Significant GCA effects for this trait are reported by Sarkar and Sirohi (2010), Sharma (2006), Singh et al. (2010), Singh et al. (2012), Bairagi et al. (2013), Reddy et al. (2014), Pati et al. (2015), Moradipour et al. (2016), Kaur and Dhall (2017), Malav et al. (2018) and Manggoel et al. (2021).

8. Number of fruits per plant

Number of fruits per plant is an economically important trait which contributes to the yield per plant. For this trait, GCA effects ranged from -1.61 to 3.24 in 2020, -0.93 to 2.41 in 2021 and -1.14 to 2.83 in pooled over environments (Table 4.17). The significant GCA effects were observed in P₂, P₃ and P₆ in all environments, P₄ in 2020 and pooled over environments, P₅ in 2021 and pooled over environments and P₇ in 2020 and pooled over environments. The best general combiners were found to be P₂ in all environments, P₆ in 2020 and P₇ in 2021 and pooled over environments while, P₃, P_{4,Z} P₆ in all environments and P₅ in pooled over environments were poor combiners for number of fruits per plant.

The results are in agreement with the previous findings of Yadav et al. (2007), Mule et al. (2012), Bairagi et al. (2013), Kumar et al. (2013), Reddy et al. (2014), Pati et al. (2015), Singh et al. (2016), Tiwari et al. (2016), Thapliyal (2017), Thakur and Kumar (2020) and Manggoel et al. (2021) for significant GCA effects for fruit diameter (cm).

9. Marketable yield per plant (kg)

For marketable yield per plant (kg), GCA effects ranged from -0.39 to 0.67 in 2020, -0.34 to 0.63 in 2021 and -0.36 to 0.65 in pooled over environments (Table 4.17). The analysis indicated significant GCA effects for parents *viz.*, P₁, P₂, P₃, P₄ and P₆ in all environments, P₇ in 2020 and pooled over environments, P₈ in pooled over environments. Parents *viz.*, P₁ and P₂ in all environments, P₇ in 2020 and pooled over environments were best general combiners while, P₃, P₄ and P₆ were poor general combiners for marketable yield per plant (kg). The significant GCA effects for marketable yield per plant (kg) are also reported by Sushir et al. (2005), Yadav et al. (2007), Sarkar and Sirohi (2010), Mule et al. (2012), Bairagi et al. (2013), Kumar et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kumar et al. (2016), Singh et al. (2016b), Kaur and Dhall (2017), Malav et al. (2018), Thakur and Kumar (2020) and Kumar et al. (2021).

10. Marketable yield per meter square area (kg)

The GCA effects for marketable yield per meter square area (kg) ranged from -2.33 to 4.00 in 2020, -1.47 to 3.19 in 2021 and -1.62 to 4.21 in pooled over environments (Table 4.17). Among parents, P₁, P₂, P₃ and P₆ in all environments, P₄ in 2020 and pooled over environments, P₅ in pooled over environments, P₇ in 2020 and P₈ in 2021 and pooled over environments showed significant GCA effects. The best general combiners were P₁ and P₂ in all environments and P₇ in 2020 while, P₃ and P₆ in all environments, P₄ in 2020 and pooled over environment and P₈ in 2021 and pooled over environments were poor general combiners for marketable yield per meter square area (kg).

The results are in line with the findings reported by Sarkar and Sirohi (2010), Mule et al. (2012), Bairagi et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kumar et al. (2016), Kaur and Dhall (2017), Malav et al. (2018), Thakur and Kumar (2020) and Kumar et al. (2021).

Table 4.17: Estimates of general combining ability effects of parents fruit weight (g), number of fruits/plant, marketable yield per plant (kg), marketable yield per meter square (kg), harvest duration (days) and internodal length (cm) in cucumber during 2020, 2021 and pooled over environments

Parental lines	Fruit weight (g)			Number of fruits/plant			Marketable yield per plant (kg)			Marketable yield per meter square (kg)			Harvest duration (days)			Internodal length (cm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	4.48*	3.43*	3.96*	-0.06	0.28	0.11	0.10*	0.11*	0.10*	0.58*	0.66*	0.89*	1.76*	1.00*	1.38*	0.10	-0.02	0.15
P ₂	10.64*	11.99*	11.32*	3.24*	2.41*	2.83*	0.67*	0.63*	0.65*	4.00*	3.19*	4.21*	3.86*	3.87*	3.86*	-0.08	-0.10	-0.10
P ₃	-8.56*	-10.05*	-9.31*	-1.61*	-0.67*	-1.14*	-0.39*	-0.34*	-0.36*	-2.33*	-1.47*	-1.62*	-0.47	-0.47	-0.47	-0.44*	-0.61*	-0.53*
P ₄	-3.48*	-2.71	-3.10*	-1.20*	-0.54	-0.87*	-0.22*	-0.13*	-0.18*	-1.32*	-0.21	-1.31*	1.46*	1.07*	1.26*	0.09	-0.10	0.11
P ₅	1.42	1.61	1.51	-0.62	-0.83*	-0.72*	-0.04	-0.06	-0.05	-0.26	-0.36	-0.40*	-4.61*	-3.40*	-4.01*	0.63*	0.73*	0.67*
P ₆	-1.34	-1.19	-1.27	-1.10*	-0.93*	-1.01*	-0.16*	-0.16*	-0.16*	-0.96*	-0.96*	-1.15*	-0.18	0.27	0.08	0.52*	0.63*	0.60*
P ₇	-0.12	-0.47	-0.30	1.07*	0.27	0.67*	0.10*	0.02	0.06*	0.57*	0.13	0.24	0.92	0.40	0.66*	-0.06	-0.13	-0.12
P ₈	-3.03*	-2.60	-2.82*	0.27	-0.01	0.13	-0.05	-0.07	-0.06*	-0.29	-0.98*	-0.88*	-2.74*	-2.73*	-2.74*	-0.75*	-0.41*	-0.78*
SE(gi)±	1.45	1.40	1.42	0.35	0.30	0.33	0.03	0.03	0.03	0.20	0.21	0.21	0.47	0.39	0.42	0.13	0.16	0.14
SE(gi-gj) ±	2.19	2.12	2.15	0.52	0.46	0.49	0.04	0.05	0.05	0.29	0.32	0.31	0.71	0.59	0.65	0.20	0.24	0.22
CD (gi)	3.43	3.31	3.37	0.82	0.72	0.77	0.08	0.08	0.08	0.47	0.51	0.48	1.11	0.92	1.01	0.31	0.37	0.34
CD (gi-gj)	5.19	5.01	5.10	1.23	1.09	1.16	0.11	0.12	0.12	0.70	0.76	0.73	1.68	1.39	1.53	0.47	0.56	0.52

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

11. Harvest duration (days)

For harvest duration (days), GCA effects varied from -4.61 to 3.86, -3.40 to 3.87 and -4.01 to 3.86 in 2020, 2021 and pooled over environments, respectively (Table 4.17). The analysis indicated significant GCA effects for P₁, P₂, P₄, P₅ and P₈ in all environments. The best general combiners were P₁, P₂ and P₄ in all environments while, P₅ and P₈ were poor general combiners for harvest duration (days). Kumar et al. (2016), Kumari et al. (2019) and Thakur and Kumar (2020) also reported significant GCA effects for harvest duration in their respective parents.

12. Internodal length (cm)

The GCA effects for internodal length varied from -0.75 to 0.63 in 2020, -0.61 to 0.73 in 2021 and -0.78 to 0.67 in pooled over environments (Table 4.17). Among parents, P₃, P₅, P₆ and P₈ showed significant GCA effects in all environments. The best combiners for internodal length were P₃ and P₈ in all environments while, P₅ and P₆ were poor general combiners. The significant GCA effects for internodal length are reported by Golabadi et al. (2015) and Kumari et al. (2018).

13. Vine length (m)

For vine length (m), GCA effects ranged from -0.14 to 0.13 in 2020, -0.16 to 0.18 in 2021 and -0.14 to 0.16 in pooled over environments (Table 4.18). The analysis revealed significant GCA effects for P₂, P₃, P₄, P₅, P₆ and P₈ in all environments and P₁ in 2020 and pooled over environments. In all environments, P₂, P₄ and P₈ exhibited significant positive GCA effects revealing best general combiners. The poor general combiners were P₃, P₅ and P₆ in all environments and P₁ in 2020 and pooled over environments due to negative GCA effects. Similar findings for vine length are reported by Sushir et al. (2005), Sharma (2006), Singh et al. (2010), Jat et al. (2011), Mule et al. (2012), Singh et al. (2016), Thapliyal (2017), Malav et al. (2018) and Manggoel et al. (2021).

14. Flesh to seed cavity ratio

For flesh to seed cavity ratio, GCA effects ranged from -0.12 to 0.12, -0.07 to 0.08 and -0.09 to 0.10 in 2020, 2021 and pooled over environments,

Table 4.18: Estimates of general combining ability effects of parents vine length (m), flesh to seed cavity ratio and flesh thickness (mm) in cucumber during 2020, 2021 and pooled over environments

Parental lines	Vine length (m)			Flesh to seed cavity ratio			Flesh thickness (mm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	-0.04*	-0.03	-0.04*	0.03	-0.00	0.01	0.01	-0.15	-0.07
P ₂	0.13*	0.14*	0.13*	0.05*	0.06*	0.06*	-0.07	-0.29*	-0.19
P ₃	-0.14*	-0.14*	-0.14*	0.01	-0.01	-0.00	-0.61*	-0.22	-0.41*
P ₄	0.13*	0.18*	0.16*	-0.03	-0.02	-0.02	0.36*	0.87*	0.61*
P ₅	-0.10*	-0.16*	-0.13*	0.01	0.03	0.02	0.13	-0.03	0.05
P ₆	-0.10*	-0.07*	-0.09*	0.12*	0.08*	0.10*	0.12	0.05	0.08
P ₇	0.02	0.007	0.02	-0.12*	-0.07*	-0.09*	-0.31	-0.42*	-0.36*
P ₈	0.10*	0.07*	0.08*	-0.08*	-0.07*	-0.07*	0.38*	0.20	0.29*
SE(gi)±	0.02	0.02	0.01	0.02	0.02	0.02	0.17	0.11	0.14
SE(gi-gj) ±	0.03	0.03	0.03	0.03	0.04	0.04	0.27	0.17	0.22
CD (gi)	0.04	0.04	0.04	0.05	0.06	0.05	0.42	0.27	0.34
CD (gi-gj)	0.07	0.07	0.07	0.08	0.09	0.08	0.63	0.41	0.52

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

respectively (Table 4.18). The significant GCA effects were observed for P₂, P₆, P₇ and P₈ in all environments. The best general combiners for flesh to seed cavity ratio were P₇ and P₈ in all environments due to their significant positive GCA effects while, P₂ and P₆ were poor combiners as indicated by their significant negative GCA effects. Kaur et al. (2016) and Thapliyal (2017) also reported significant GCA effects in their respective lines for flesh to seed cavity ratio.

15. Flesh thickness (mm)

The GCA effects for flesh thickness ranged from -0.61 to 0.38, -0.42 to 0.87 and -0.41 to 0.61 in 2020, 2021 and pooled over environments, respectively (Table 4.18). The analysis indicated significant GCA effects for parents viz., P₄ in all environments, P₃ and P₈ in 2020 and pooled over environments, P₂ in 2021 and P₇ in 2021 and pooled over environments. The best general combiners were P₄ in all environments and P₈ in 2020 and pooled over environments while, P₃ in 2020 and pooled over environments, P₂ in 2021 and P₇ in 2021 and pooled over environments were found to be poor general combiners for flesh thickness (mm). These results are in line with

earlier studies reported by Pandey et al. (2005), Munshi et al. (2006), Yoshioka et al. (2010) and Arab et al. (2020)

16. Total soluble solids (°Brix)

The GCA effects for total soluble solids (°Brix) varied from -0.33 to 0.16 in 2020, -0.34 to 0.15 each in 2021 and pooled over environments (Table 4.19). The significant GCA effects were recorded in P₁, P₂, P₃, P₄, P₅ and P₆ in all environments, P₇ in 2021 and pooled over environments and P₈ in 2020 and pooled over environments. Parents namely, P₃, P₄, P₅ and P₆ in all environments, P₇ in 2021 and pooled over environments and P₈ in 2020 and pooled over environments were observed to be the best general combiners while, P₁ and P₂ in all environments were poor general combiners. Sharma (2006), Vidhya and Kumar (2014), Kaur et al. (2016) and Thapliyal (2017) also reported similar results for significant GCA effects for total soluble solids (°Brix).

17. Ascorbic acid (mg/100g)

The GCA effects for ascorbic acid (mg/100g) varied from -0.25 to 0.35 in 2020, -0.34 to 0.39 in 2021 and -0.29 to 0.37 in pooled over environments (Table 4.19). The analysis indicated significant GCA effects for all the parents in all the environments. The best general combiners for ascorbic acid were P₁, P₅ and P₈ in all the environments due to their significant positive GCA effects. The poor combiners for ascorbic acid were P₂, P₃, P₄, P₆ and P₇ in all the environments. The results are in agreement with the findings of Kaur et al. (2016) who reported significant GCA effects in their respective lines for ascorbic acid.

18. Total sugar (%)

The GCA effects for total sugar varied from -0.22 to 0.17 in 2020, -0.16 to 0.14 in 2021 and -0.19 to 0.13 in pooled over environments (Table 4.19). The significant GCA effects were recorded for parents P₁, P₂, P₄, P₆ and P₈ in all the environments, P₃ in 2020 and P₅ and P₇ in 2021 and pooled over environments. The best general combiners for total sugar were P₁, P₂ and P₈ in all the environments and P₇ in 2021 and pooled over environments while, P₄ and P₆ in all the environments, P₃ in 2020, P₅ in 2021 and pooled over environments were poor general combiners for this trait.

19. Reducing sugar (%)

For reducing sugar (%), GCA effects varied from -0.06 to 0.08, -0.04 to 0.06 and -0.04 to 0.06 in 2020, 2021 and pooled over environments, respectively (Table 4.19). The analysis indicated significant GCA effects for all the parents in all the environments. Among parents, P₁, P₄ and P₅ were found to be best general combiners for reducing sugar in all the environments while P₂, P₃, P₆, P₇ and P₈ were poor general combiners in all the environments.

The trait wise list of good general combiners has been shown in Table 4.20. It can be revealed that the parent P₂ (DDPCG1) was found to be the best general combiner for a 12 traits namely, days to first female flower, number of female flowers per node, days taken to first fruit picking, fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square area (kg), harvest duration (days), vine length (m), flesh to seed cavity ratio in pooled over environments. P₈ (DDPCG5) also exhibited good general combining ability effects for nodal position of first female flower, number of female flowers per node, internodal length (cm), vine length (m), flesh thickness (mm), total soluble solids (°B), ascorbic acid (mg/100g) and total sugar (%) in pooled over environments which can also be included in breeding programme. P₇ (DDPCG2) exhibited significant desirable GCA effects for number of fruits per plant, harvest duration and total sugar (%) in pooled over environments and marketable yield per plant (kg) and marketable yield per meter square area (kg) in 2020. P₁ (DDPCG4) was found as a best general combiner for 9 traits viz., nodal position of first female flower, fruit diameter (cm), fruit weight (g), marketable yield per plant (kg), marketable yield per meter square area (kg), harvest duration (days), ascorbic acid (mg/100g), total sugar (%) and reducing sugar in pooled over environments. Similarly, P₄ (PPC-2) exhibited significant high GCA effects for days to first female flower, fruit length (cm), fruit diameter (cm), harvest duration (days), vine length (m), flesh thickness (mm) and total soluble solids (°B) in pooled over environments while P₅ (PPC-3) for fruit length (cm), total soluble solids (°B) and ascorbic acid (mg/100g) in pooled over environments.

Table 4.19: Estimates of general combining ability effects of parents on quality traits in cucumber during 2020, 2021 and pooled over environments

Parental lines	Total Soluble Solids (°B)			Ascorbic acid (mg/100g)			Total sugars (%)			Reducing sugar (%)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁	-0.25*	-0.19*	-0.22*	0.35*	0.39*	0.37*	0.11*	0.14*	0.13*	0.07*	0.06*	0.06*
P ₂	-0.33*	-0.34*	-0.34*	-0.04*	-0.05*	-0.04*	0.04*	0.05*	0.04*	-0.06*	-0.02*	-0.04*
P ₃	0.09*	0.10*	0.10*	-0.16*	-0.18*	-0.17*	-0.03*	0.02	-0.01	-0.02*	-0.008*	-0.02*
P ₄	0.16*	0.15*	0.15*	-0.19*	-0.19*	-0.19*	-0.22*	-0.16*	-0.19*	0.01*	0.00*	0.02*
P ₅	0.15*	0.14*	0.14*	0.20*	0.26*	0.23*	0.03	-0.07*	-0.02*	0.08*	0.02*	0.05*
P ₆	0.10*	0.06*	0.08*	-0.25*	-0.34*	-0.29*	-0.11*	-0.09*	-0.10*	-0.04*	-0.04*	-0.04*
P ₇	0.03	0.06*	0.04*	-0.03*	-0.03*	-0.03*	0.02	0.07*	0.05*	-0.02*	-0.02*	-0.02*
P ₈	0.06*	0.02	0.04*	0.10*	0.14*	0.12*	0.17*	0.04*	0.10*	-0.02*	-0.02*	-0.02*
SE(gi)±	0.01	0.01	0.01	0.01	0.03	0.01	0.01	0.01	0.01	0.003	0.03	0.003
SE(gi-gj) ±	0.02	0.02	0.02	0.02	0.04	0.01	0.02	0.02	0.02	0.005	0.04	0.005
CD (gi)	0.03	0.03	0.03	0.02	0.07	0.02	0.03	0.02	0.03	0.008	0.07	0.008
CD (gi-gj)	0.05	0.04	0.04	0.04	0.01	0.02	0.04	0.04	0.04	0.012	0.01	0.01

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

Table 4.20: Good general combiners for different traits during 2020, 2021 and pooled over environments

Trait	2020	2021	Pooled
Days to first female flower	P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₂ (DDPCG1), P ₄ (PPC-2) and P ₆ (DDPCW1)
Nodal position of first female flower	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₈ (DDPCG5)	P ₁ (DDPCG4) and P ₈ (DDPCG5)	P ₁ (DDPCG4) and P ₈ (DDPCG5)
Number of female flowers per node	P ₁ (DDPCG4), P ₃ (PK-1) and P ₈ (DDPCG5)	P ₂ (DDPCG1), P ₃ (PK-1) and P ₈ (DDPCG5)	P ₂ (DDPCG1), P ₃ (PK-1) and P ₈ (DDPCG5)
Days taken to first picking (days)	P ₂ (DDPCG1), P ₃ (PK-1) and P ₆ (DDPCW1)	P ₂ (DDPCG1) and P ₃ (PK-1)	P ₂ (DDPCG1), P ₃ (PK-1) and P ₆ (DDPCW1)
Fruit length (cm)	P ₂ (DDPCG1) and P ₅ (PPC-3)	P ₂ (DDPCG1) and P ₅ (PPC-3)	P ₂ (DDPCG1), P ₄ (PPC-2) and P ₅ (PPC-3)
Fruit diameter (cm)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₄ (PPC-2)
Fruit weight (g)	P ₁ (DDPCG4) and P ₂ (DDPCG1)	P ₁ (DDPCG4) and P ₂ (DDPCG1)	P ₁ (DDPCG4) and P ₂ (DDPCG1)
Number of fruits per plant	P ₂ (DDPCG1) and P ₇ (DDPCG2)	P ₂ (DDPCG1)	P ₂ (DDPCG1) and P ₇ (DDPCG2)
Marketable yield per plant (kg)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₇ (DDPCG2)	P ₁ (DDPCG4) and P ₂ (DDPCG1)	P ₁ (DDPCG4) and P ₂ (DDPCG1)
Marketable yield per meter square area (kg)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₇ (DDPCG2)	P ₁ (DDPCG4) and P ₂ (DDPCG1)	P ₁ (DDPCG4) and P ₂ (DDPCG1)
Harvest duration (days)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₄ (PPC-2)	P ₁ (DDPCG4), P ₂ (DDPCG1), P ₄ (PPC-2) and P ₇ (DDPCG2)
Internodal length (cm)	P ₃ (PK-1) and P ₈ (DDPCG5)	P ₃ (PK-1) and P ₈ (DDPCG5)	P ₃ (PK-1) and P ₈ (DDPCG5)
Vine length (m)	P ₂ (DDPCG1), P ₄ (PPC-2) and P ₈ (DDPCG5)	P ₂ (DDPCG1), P ₄ (PPC-2) and P ₈ (DDPCG5)	P ₂ (DDPCG1), P ₄ (PPC-2) and P ₈ (DDPCG5)
Flesh to seed cavity ratio	P ₂ (DDPCG1) and P ₆ (DDPCW1)	P ₂ (DDPCG1) and P ₆ (DDPCW1)	P ₂ (DDPCG1) and P ₆ (DDPCW1)
Flesh thickness (mm)	P ₄ (PPC-2) and P ₈ (DDPCG5)	P ₄ (PPC-2)	P ₄ (PPC-2) and P ₈ (DDPCG5)
Total soluble solids (°B)	P ₃ (PK-1), P ₄ (PPC-2), P ₅ (PPC-3), P ₆ (DDPCW1) and P ₈ (DDPCG5)	P ₃ (PK-1), P ₄ (PPC-2), P ₅ (PPC-3), P ₆ (DDPCW1) and P ₇ (DDPCG2)	P ₃ (PK-1), P ₄ (PPC-2), P ₅ (PPC-3), P ₆ (DDPCW1), P ₇ (DDPCG2) and P ₈ (DDPCG5)
Ascorbic acid (mg/100g)	P ₁ (DDPCG4), P ₅ (PPC-3) and P ₈ (DDPCG5)	P ₁ (DDPCG4), P ₅ (PPC-3) and P ₈ (DDPCG5)	P ₁ (DDPCG4), P ₅ (PPC-3) and P ₈ (DDPCG5)
Total sugars (%)	P ₁ (DDPCG4), P ₂ (DDPCG1) and P ₈ (DDPCG5)	P ₁ (DDPCG4), P ₂ (DDPCG1), P ₇ (DDPCG2) and P ₈ (DDPCG5)	P ₁ (DDPCG4), P ₂ (DDPCG1), P ₇ (DDPCG2) and P ₈ (DDPCG5)
Reducing sugars (%)	P ₁ (DDPCG4), P ₄ (PPC-2) and P ₅ (PPC-3)	P ₁ (DDPCG4) and P ₅ (PPC-3)	P ₁ (DDPCG4), P ₄ (PPC-2) and P ₅ (PPC-3)

4.4.4. Estimates of specific combining ability effects

Specific combining ability is a deviation in the performance of a cross combination which is predicted on the basis of general combining abilities of the parents involved in this cross. Specific combining ability effects depends more on dominance and epistatic gene effects. Specific combining ability (SCA) effects of different traits are presented below:

1. Days to first female flower

The SCA effects for days to first female flower ranged from -3.39 to 4.15 in 2020, -2.76 to 6.37 in 2021 and -3.27 to 3.86 in pooled over environments (Table 4.21). A total of 13 crosses in 2020, 15 crosses each in 2021 and pooled over environments exhibited significant negative SCA effects thus indicating good specific combining ability. Among cross combinations, P₂ (good) × P₃ (poor), P₄ (good) × P₇ (average), P₁ (average) × P₃ (poor), P₇ (average) × P₈ (poor) and P₃ (poor) × P₆ (average) in 2020, P₁ (average) × P₃ (poor), P₇ (average) × P₈ (poor), P₂ (good) × P₅ (poor), P₄ (good) × P₆ (average) and P₅ (poor) × P₈ (poor) in 2021, P₂ (good) × P₃ (poor), P₁ (average) × P₃ (poor), P₇ (average) × P₈ (poor), P₄ (good) × P₇ (average) and P₃ (poor) × P₆ (average) in pooled over environments were the best five good combinations based on SCA effects. Nine crosses in 2020 and 8 crosses each in 2021 and pooled over environments exhibited significant positive SCA effects indicating poor specific combining ability for days to first female flower. These results are in consonance with earlier reports of Bairagi et al. 2013; Kumar et al. 2013; Reddy et al. 2014; Malav et al. 2018; Arab et al. 2020; Thakur and Kumar 2020 and Manggoel et al. 2021 who reported significant SCA effects in their respective hybrid combinations.

2. Nodal position of first female flower

For nodal position of first female flower, SCA effects ranged from -1.30 to 1.22 in 2020, -1.00 to 1.45 in 2021 and -1.16 to 1.23 in pooled over environments (Table 4.21). A total of 10 crosses in 2020, 12 crosses in 2021 and 11 crosses in pooled over environments exhibited significant negative SCA effects indicating good specific combining ability. The best five cross combinations observed were P₁ (good) × P₇ (average), P₃ (average) × P₆ (poor), P₁ (good) × P₂ (good), P₁ (good) × P₆ (poor) and P₂ (good) × P₅ (poor) in 2020, P₁ (good) × P₇ (average), P₃ (poor) ×

P_6 (poor), P_2 (poor) \times P_5 (poor), P_1 (good) \times P_6 (poor) and P_7 (average) \times P_8 (good) in 2021, P_1 (good) \times P_7 (average), P_3 (poor) \times P_6 (poor), P_1 (good) \times P_2 (average), P_2 (average) \times P_5 (poor) and P_7 (average) \times P_8 (good) in pooled over environments. The significant positive SCA effects were recorded for 14 crosses each in 2020 and 2021 and 13 crosses in pooled over environments. The results are in close resemblance with Mule et al. (2012), Bairagi et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kaur and Dhall (2017), Malav et al. (2018), Arab et al. (2020) and Kumar et al. (2021) who revealed significant SCA effects for nodal position of first female flower.

3. Number of female flowers per node

The SCA effects for number of female flowers per node ranged from -0.42 to 0.55 in 2020, -0.39 to 0.72 in 2021 and -0.41 to 0.64 in pooled over environments (Table 4.21). The significant positive SCA effects were recorded in 14 crosses in 2020 and 15 crosses each in 2021 and pooled over environments. Among cross combinations, P_6 (poor) \times P_7 (poor), P_3 (good) \times P_7 (poor), P_1 (good) \times P_4 (poor), P_2 (average) \times P_7 (poor) and P_4 (poor) \times P_8 (good) in 2020, P_6 (poor) \times P_7 (poor), P_3 (good) \times P_7 (poor), P_3 (good) \times P_6 (poor), P_1 (average) \times P_4 (poor) and P_2 (good) \times P_4 (poor) in 2021 and P_6 (poor) \times P_7 (poor), P_3 (good) \times P_7 (poor), P_1 (average) \times P_4 (poor), P_3 (good) \times P_6 (poor) and P_2 (good) \times P_7 (poor) in pooled over environments were the top five combinations exhibiting good specific combining ability. Similarly, 11 crosses in all the environments displayed significant negative SCA effects revealing poor specific combiners. Yadav et al. (2007) and Moradipour et al. (2016) also reported significant SCA effects for number of female flowers per node.

4. Days taken to first fruit picking

The SCA effects for days taken to first fruit picking ranged from -7.29 to 5.78 in 2020, -6.26 to 3.07 in 2021 and -6.49 to 4.33 in pooled over environments (Table 4.21). A total of 18 crosses in 2020, 15 crosses in 2021 and 17 crosses in pooled over environments exhibited significant negative SCA effects indicating good general combining ability. Among crosses, P_7 (average) \times P_8 (poor), P_2 (good) \times P_7 (average), P_4 (poor) \times P_6 (good), P_2 (good) \times P_4 (poor) and P_6 (good) \times P_7 (average) in 2020, P_4 (poor) \times P_6 (average), P_7 (average) \times P_8 (poor), P_2 (good)

Table 4.21: Estimates of specific combining ability effects for days to first female flower, nodal position of first female flower, number of female flowers/node and days to first fruit picking during 2020, 2021 and pooled over environments

Crosses	Days to first female flower			Nodal position of first female flower			Number of female flowers/node			Days to first fruit picking		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁ × P ₂	0.78 *	0.94 *	0.86 *	-0.82 *	-0.46 *	-0.66 *	0.18 *	0.24 *	0.21 *	3.14 *	1.57 *	2.36 *
P ₁ × P ₃	-3.22 *	-2.76 *	-2.99 *	0.69 *	0.25 *	0.45 *	0.35 *	0.08 *	0.22 *	-2.56 *	-0.96	-1.76 *
P ₁ × P ₄	1.61 *	1.47 *	1.54 *	0.61 *	0.40 *	0.49 *	0.42 *	0.41 *	0.41 *	-3.19 *	-0.53	-1.86 *
P ₁ × P ₅	1.18 *	-1.53 *	-0.17	-0.04	0.12 *	0.03	-0.31 *	-0.24 *	-0.28 *	-2.59 *	-2.23 *	-2.41 *
P ₁ × P ₆	-1.42 *	1.67 *	-0.62 *	-0.52 *	-0.61 *	-0.46 *	0.08 *	0.14 *	0.11 *	-3.32 *	-1.59 *	-2.46 *
P ₁ × P ₇	0.05	0.51	0.28	-1.30 *	-1.00 *	-1.16 *	0.18 *	0.16 *	0.17 *	3.71 *	2.81 *	3.26 *
P ₁ × P ₈	-0.22	-1.66 *	-0.19	0.34 *	0.06	0.18 *	-0.41 *	-0.34 *	-0.38 *	1.38 *	-0.69	0.34
P ₂ × P ₃	-3.39 *	3.16 *	-3.27 *	0.01	0.11 *	0.04	-0.36 *	-0.39 *	-0.37 *	-4.79 *	-1.86 *	-3.32 *
P ₂ × P ₄	-0.55	-0.93 *	-0.74 *	0.44 *	0.36 *	0.38 *	0.31 *	0.35 *	0.33 *	-5.09 *	-4.43 *	-4.76 *
P ₂ × P ₅	-2.32 *	-1.93 *	-2.12 *	-0.45 *	-0.68 *	-0.58 *	0.30 *	0.28 *	0.29 *	-4.16 *	-2.79 *	-3.47 *
P ₂ × P ₆	-1.92 *	-1.39 *	-1.57 *	0.04	-0.41 *	-0.08 *	-0.20 *	-0.23 *	-0.22 *	-1.56 *	-1.83 *	-1.69 *
P ₂ × P ₇	-0.79 *	-0.89 *	-0.84 *	1.22 *	1.27 *	1.23 *	0.36 *	0.34 *	0.35 *	-5.86 *	-2.43 *	-4.14 *
P ₂ × P ₈	-2.39 *	-1.06 *	-1.81 *	0.28 *	0.56 *	0.41 *	-0.03	-0.04	-0.03	-1.52 *	-1.59 *	-1.56 *
P ₃ × P ₄	1.45 *	0.37	0.91 *	-0.18 *	-0.17 *	-0.19 *	-0.10 *	-0.12 *	-0.11 *	-2.79 *	-2.63 *	-2.71 *
P ₃ × P ₅	1.35 *	6.37 *	3.86 *	-0.01	0.37 *	0.16 *	-0.06 *	-0.07 *	-0.07 *	-3.52 *	-2.33 *	-2.92 *
P ₃ × P ₆	-2.92 *	-1.76 *	-2.26 *	-1.16 *	-0.70 *	-0.82 *	0.28 *	0.47 *	0.38 *	-0.59	-0.36	-0.47
P ₃ × P ₇	0.55	-1.26 *	-0.36	0.18 *	-0.03	0.06	0.44 *	0.50 *	0.47 *	-1.22 *	0.71	-0.26
P ₃ × P ₈	3.61 *	1.91 *	2.68 *	0.51 *	0.62 *	0.56 *	-0.04 *	-0.00	-0.02	5.78 *	2.87 *	4.33 *
P ₄ × P ₅	1.18 *	-0.06	0.56 *	-0.19 *	-0.16 *	-0.19 *	0.03	0.05 *	0.04 *	4.18 *	1.44 *	2.81 *
P ₄ × P ₆	-2.09 *	-1.86 *	-1.89 *	0.68 *	0.78 *	0.84 *	-0.16 *	-0.22 *	-0.19 *	-5.56 *	-6.26 *	-5.91 *
P ₄ × P ₇	-3.29 *	-1.36 *	-2.32 *	0.14 *	0.12 *	0.11 *	-0.11 *	-0.11 *	-0.10 *	-4.52 *	-2.86 *	-3.69 *
P ₄ × P ₈	-0.89 *	-0.86 *	-0.96 *	-0.41 *	-0.23 *	-0.33 *	0.36 *	0.29 *	0.33 *	3.81 *	0.97	2.39 *
P ₅ × P ₆	4.15 *	2.47 *	3.39 *	0.41 *	0.84 *	0.74 *	-0.03	-0.16 *	-0.09 *	-3.29 *	-3.29 *	-3.29 *
P ₅ × P ₇	1.28 *	3.97 *	2.63 *	0.18 *	-0.15 *	-0.00	-0.23 *	-0.28 *	-0.25 *	1.41 *	-1.23	0.09
P ₅ × P ₈	-0.32	-1.86 *	-1.17 *	-0.14 *	-0.17 *	-0.16 *	0.22 *	0.24 *	0.23 *	2.41 *	-0.39	1.01 *
P ₆ × P ₇	0.35	-0.49	0.01	0.44 *	1.45 *	1.06 *	0.55 *	0.72 *	0.64 *	5.01 *	3.07 *	4.04 *
P ₆ × P ₈	-1.92 *	-0.66	-1.29 *	0.57 *	0.44 *	0.61 *	0.25 *	0.21 *	0.23 *	-3.99 *	-2.43 *	-3.21 *
P ₇ × P ₈	-3.12 *	-2.49 *	-2.89 *	-0.41 *	-0.56 *	-0.50 *	-0.42 *	-0.39 *	-0.41 *	-7.29 *	-5.69 *	-6.49 *
SE(Sij) ±	0.85	0.81	0.83	0.15	0.10	0.12	0.04	0.05	0.04	1.02	1.57	1.29
SE(Sij-Sik) ±	1.27	1.19	1.23	0.22	0.15	0.18	0.06	0.08	0.07	1.51	2.33	1.92
SE (Sij-Skl) ±	1.19	1.13	1.61	0.21	0.14	0.17	0.05	0.07	0.06	1.42	2.19	1.80
CD(Sij)	1.76	1.66	1.71	0.31	0.20	0.26	0.08	0.11	0.09	2.09	3.23	2.66
CD(Sij-Sik)	2.61	2.45	2.52	0.46	0.30	0.38	0.12	0.17	0.15	3.09	4.78	3.94
CD (Sij-Skl)	2.46	2.31	2.38	0.43	0.25	0.36	0.11	0.16	0.14	2.91	4.51	3.71

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kherra-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

× P₄ (poor), P₅ (poor) × P₆ (average) and P₄ (poor) × P₇ (average) in 2021 and P₇ (average) × P₈ (poor), P₄ (poor) × P₆ (average), P₂ (good) × P₄ (poor), P₂ (good) × P₇ (average) and P₄ (poor) × P₇ (average) in pooled over environments were the five promising good specific combiners. The significant positive SCA effects were recorded in 9 crosses in 2020, 5 crosses in 2021 and 7 crosses in pooled over environments indicating poor specific combiners. The results are supported by Kumar et al. (2013), Reddy et al. (2014), Jat et al. (2015), Singh et al. (2016), Thapliyal (2017), Thakur and Kumar (2020) and Kumar et al. (2021) who reported significant SCA effects for days taken to first fruit picking.

5. Fruit length (cm)

For fruit length, SCA effects ranged from -4.05 to 4.02 in 2020, -2.59 to 3.48 in 2021 and -3.32 to 3.75 in pooled over environments (Table 4.22). Among all cross combinations, 11 crosses in 2020, 13 crosses in 2021 and 14 crosses in pooled over environments exhibited significant positive SCA effects revealing good specific combiners. The top five combinations observed were P₁ (poor) × P₈ (average), P₃ (poor) × P₅ (good), P₆ (average) × P₇ (average), P₂ (good) × P₈ (average) and P₁ (poor) × P₃ (poor) in 2020, P₁ (poor) × P₈ (average), P₂ (good) × P₇ (poor), P₃ (poor) × P₆ (average), P₇ (poor) × P₈ (average) and P₂ (good) × P₃ (poor) in 2021 and P₁ (poor) × P₈ (average), P₂ (good) × P₇ (poor), P₃ (poor) × P₅ (good), P₂ (good) × P₈ (average) and P₄ (good) × P₈ (average) in pooled over environments. The significant negative SCA effects were exhibited by 8 crosses in 2020, 9 crosses in 2021 and 6 crosses in pooled over environments revealing poor specific combining ability for fruit length. These results are in line with the findings of Yadav et al. (2007), Sarkar and Sirohi (2010), Singh et al. (2010), Mule et al. (2012), Singh et al. (2012), Kumar et al. (2013), Thapliyal (2017), Malav et al. (2018), Thakur and Kumar (2020) and Manggoel et al. (2021) exhibiting significant SCA effects for this trait in their respective hybrid combinations.

6. Fruit diameter (cm)

The SCA effects for fruit diameter ranged from -0.50 to 0.47 in 2020, -0.35 to 0.37 in 2021 and -0.39 to 0.37 in pooled over environments (Table

4.22). The significant positive SCA effects were revealed by 11 crosses in 2020 and pooled over environments and 10 crosses in 2021 indicating good specific combiners. The best five combinations observed were P₁ (good) × P₇ (poor), P₄ (good) × P₇ (poor), P₃ (poor) × P₄ (good), P₂ (good) × P₆ (poor) and P₁ (good) × P₃ (poor) in 2020, P₄ (good) × P₇ (poor), P₁ (good) × P₇ (poor), P₂ (good) × P₆ (average), P₃ (poor) × P₄ (good) and P₁ (good) × P₄ (good) in 2021 and P₄ (good) × P₇ (poor), P₁ (good) × P₇ (poor), P₂ (good) × P₆ (poor), P₃ (poor) × P₄ (good) and P₁ (good) × P₄ (good) in pooled over environments. A total of 11 crosses in 2020, 6 crosses in 2021 and 9 crosses in pooled over environments exhibited significant negative SCA effects indicating poor specific combiners. The results are in conformity with respect to significant SCA effects for fruit diameter with previous studies of Singh et al. (2010), Bairagi et al. (2013), Kumar et al. (2013), Vidhya and Kumar (2014), Singh et al. (2016), Thapliyal (2017) and Thakur and Kumar (2020).

7. Fruit weight

The SCA effects for fruit weight varied from -30.97 to 23.66 in 2020, -32.07 to 23.48 in 2021 and -31.52 to 23.57 in pooled over environments (Table 4.22). A total of 14 crosses each in all environments exhibited significant positive SCA effects indicating good specific combining ability. Among crosses, P₁ (good) × P₈ (poor), P₃ (poor) × P₄ (poor), P₂ (good) × P₆ (average), P₂ (good) × P₇ (average) and P₁ (good) × P₆ (average) in 2020, P₁ (good) × P₈ (average), P₃ (poor) × P₄ (average), P₁ (good) × P₆ (average), P₂ (good) × P₄ (average) and P₃ (poor) × P₅ (average) in 2021 and P₁ (good) × P₈ (poor), P₃ (poor) × P₄ (poor), P₂ (good) × P₆ (average), P₁ (good) × P₆ (average) and P₂ (good) × P₇ (average) in pooled over environments were the best five combinations exhibiting good specific combining ability for fruit weight. The significant negative SCA effects were observed in 10 crosses each in all the three environments. The significant SCA effects for fruit weight are also reported by Singh et al. (2010), Singh et al. (2012), Bairagi et al. (2013), Reddy et al. (2014), Moradipour et al. (2016), Kaur and Dhall (2017), Malav et al. (2018) and Manggoel et al. (2021) in their respective lines.

Table 4.22: Estimates of specific combining ability effects for fruit length (cm), fruit diameter (cm), fruit weight (g) and number of fruits/plant during 2020, 2021 and pooled over environments

Crosses	Fruit length (cm)			Fruit diameter (cm)			Fruit weight (g)			Number of fruits/plant		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁ × P ₂	-4.05 *	-2.59 *	-3.32 *	-0.29 *	-0.16 *	-0.22 *	-30.97 *	-32.07 *	-31.52 *	-3.06 *	-3.62 *	-3.34 *
P ₁ × P ₃	1.93 *	-0.13	0.90 *	0.18 *	0.15 *	0.17 *	-7.96 *	-14.89 *	-11.43 *	3.89 *	0.26	2.08 *
P ₁ × P ₄	-3.03 *	-1.68 *	-2.35 *	0.14 *	0.21 *	0.18 *	1.22	0.71	0.97	4.01 *	0.47	2.24 *
P ₁ × P ₅	-0.05	-0.89 *	-0.47	-0.14 *	-0.03	-0.08 *	5.08 *	6.49 *	5.79 *	-1.10 *	1.36 *	0.13
P ₁ × P ₆	1.05 *	1.29 *	1.17 *	-0.42 *	-0.33 *	-0.37 *	15.42 *	16.85 *	16.14 *	1.22 *	0.72	0.97 *
P ₁ × P ₇	0.67	-0.26	0.20	0.47 *	0.26 *	0.36 *	12.63 *	13.24 *	12.93 *	-0.45	1.99 *	0.77 *
P ₁ × P ₈	4.02 *	3.48 *	3.75 *	0.11 *	0.05	0.08 *	23.66 *	23.48 *	23.57 *	1.90 *	1.13 *	1.52 *
P ₂ × P ₃	0.42	1.53 *	0.97 *	-0.11 *	0.10 *	-0.00	6.57 *	7.24 *	6.91 *	0.14	-0.20	-0.03
P ₂ × P ₄	1.56 *	0.81 *	1.18 *	-0.02	0.05	0.01	10.40 *	16.35 *	13.37 *	4.24 *	2.40 *	3.32 *
P ₂ × P ₅	-0.10	-0.63	-0.37	0.15 *	0.10 *	0.13 *	6.63 *	8.30 *	7.46 *	3.11 *	2.62 *	2.86 *
P ₂ × P ₆	-0.03	1.23 *	0.60 *	0.29 *	0.25 *	0.27 *	17.69 *	15.40 *	16.55 *	0.72	1.38 *	1.05 *
P ₂ × P ₇	1.91 *	3.09 *	2.50 *	0.16 *	0.10 *	0.13 *	16.19 *	15.73 *	15.96 *	0.19	2.85 *	1.52 *
P ₂ × P ₈	2.30 *	0.78 *	1.54 *	0.12 *	0.05	0.08 *	14.81 *	15.37 *	15.09 *	2.16 *	1.93 *	2.05 *
P ₃ × P ₄	-1.34 *	0.38	-0.49	0.31 *	0.22 *	0.27 *	17.91 *	18.49 *	18.20 *	0.77	2.41 *	1.59 *
P ₃ × P ₅	2.93 *	1.01 *	1.97 *	-0.11 *	0.05	-0.03	14.50 *	16.00 *	15.25 *	4.07 *	1.50 *	2.79 *
P ₃ × P ₆	0.41	1.65 *	1.03 *	0.03	-0.04	-0.01	-8.60 *	-7.73 *	-8.17 *	-0.86	0.67	-0.09
P ₃ × P ₇	-0.71 *	-0.84 *	-0.78 *	0.04	-0.02	0.01	-4.36 *	-5.99 *	-5.17 *	-0.12	-0.93 *	-0.53
P ₃ × P ₈	-1.23 *	-1.30 *	-1.26 *	0.02	-0.07	-0.02	-5.65 *	-5.06 *	-5.35 *	1.03 *	0.28	0.65 *
P ₄ × P ₅	0.18	-0.68 *	-0.25	0.06	0.03	0.04	6.61 *	4.86 *	5.74 *	-2.59 *	0.30	-1.15 *
P ₄ × P ₆	0.02	0.43	0.23	0.04	-0.02	0.01	-2.55	-2.94	-2.75	3.17 *	-0.19	1.49 *
P ₄ × P ₇	-1.69 *	-1.76 *	-1.73 *	0.37 *	0.37 *	0.37 *	0.57	-0.65	-0.04	0.31	0.54	0.43
P ₄ × P ₈	1.29 *	1.28 *	1.29 *	-0.50 *	-0.28 *	-0.39 *	-14.93 *	-15.59 *	-15.26 *	1.79 *	-1.45 *	0.17
P ₅ × P ₆	0.52	1.21 *	0.86 *	-0.20 *	-0.17 *	-0.18 *	-8.59 *	-9.72 *	-9.16 *	-4.99 *	-1.11 *	-3.05 *
P ₅ × P ₇	0.70 *	1.30 *	1.00 *	-0.19 *	-0.09 *	-0.15 *	-4.48 *	-3.77 *	-4.12 *	-2.07 *	-1.71 *	-1.89 *
P ₅ × P ₈	0.92 *	-0.41	0.26	-0.09 *	-0.07	-0.08 *	-4.24 *	-4.31 *	-4.27 *	0.92 *	-1.43 *	-0.25
P ₆ × P ₇	2.48 *	-0.97 *	0.75 *	-0.42 *	-0.35 *	-0.38 *	-22.04 *	-20.97 *	-21.51 *	1.42 *	0.26	0.84 *
P ₆ × P ₈	-2.28 *	-1.29 *	-1.79 *	0.12 *	0.12 *	0.13 *	8.80 *	8.75 *	8.78 *	2.33 *	1.61 *	1.97 *
P ₇ × P ₈	-1.24 *	1.57 *	0.17	-0.14 *	0.01	-0.06 *	1.51	1.97	1.74	0.51	0.74	0.62 *
SE(Sij) ±	0.81	0.78	0.79	0.07	0.10	0.09	4.4	4.29	4.37	1.06	0.93	0.99
SE(Sij-Sik) ±	1.19	1.17	1.18	0.10	0.15	0.13	6.59	6.35	6.47	1.57	1.38	1.48
SE (Sij-Skl) ±	1.13	1.10	1.12	0.09	0.14	0.12	6.21	5.99	6.10	1.48	1.30	1.39
CD(Sij)	1.66	1.62	1.64	0.14	0.21	0.17	9.14	8.81	8.97	2.18	1.91	2.04
CD(Sij-Sik)	2.46	2.39	2.42	0.21	0.32	0.26	13.52	13.03	13.28	3.22	2.83	3.03
CD (Sij-Skl)	2.32	2.25	2.29	0.19	0.29	0.25	12.75	12.29	12.52	3.04	2.67	2.86

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

8. Number of fruits per plant

For number of fruits per plant, SCA effects ranged from -4.99 to 4.24 in 2020, -3.62 to 2.85 in 2021 and -3.34 to 3.32 in pooled over environments (Table 4.22). The significant positive SCA effects were observed in 14 crosses in 2020, 11 crosses in 2021 and 17 crosses in pooled over environments indicating good specific combiners. Among crosses, P_2 (good) \times P_4 (poor), P_3 (poor) \times P_5 (average), P_1 (average) \times P_4 (poor), P_1 (average) \times P_3 (poor) and P_4 (poor) \times P_6 (poor) in 2020, P_2 (good) \times P_7 (good), P_2 (good) \times P_5 (average), P_3 (poor) \times P_4 (poor), P_2 (good) \times P_4 (poor) and P_1 (average) \times P_7 (good) in 2021 and P_2 (good) \times P_4 (poor), P_2 (good) \times P_5 (poor), P_3 (poor) \times P_5 (poor), P_1 (average) \times P_4 (poor) and P_1 (average) \times P_3 (poor) in pooled over environment were top five good specific combinations. Among 28 hybrid combinations, 5 crosses in 2020, 6 crosses in 2021 and 4 crosses in pooled over environments displayed significant negative SCA effects indicating poor specific combining ability for number of fruit per plant. Similar results are also reported by Mule et al. (2012), Bairagi et al. (2013), Kumar et al. (2013), Reddy et al. (2014), Pati et al. (2015), Tiwari et al. (2016), Thapliyal (2017), Thakur and Kumar (2020) and Manggoel et al. (2021) for significant SCA effects for number of fruits per plant in their respective hybrid combinations.

9. Marketable yield per plant (kg)

The SCA effects for marketable yield per plant (kg) ranged from -1.20 to 0.86, -1.28 to 0.83 and -1.24 to 0.81 in 2020, 2021 and pooled over environments, respectively (Table 4.23). Total of 15 crosses each in 2020 and 2021 and 16 crosses in pooled over environments showed significant positive SCA effects indicating good specific combining ability. The top five combinations for marketable yield per plant were P_1 (good) \times P_8 (average), P_3 (poor) \times P_5 (average), P_2 (good) \times P_4 (poor), P_2 (good) \times P_8 (average) and P_2 (good) \times P_5 (average) in 2020, P_2 (good) \times P_7 (average), P_1 (good) \times P_8 (average), P_2 (good) \times P_4 (poor), P_3 (poor) \times P_4 (poor) and P_2 (good) \times P_8 (average) in 2021, P_1 (good) \times P_8 (average), P_2 (good) \times P_4 (poor), P_2 (good) \times P_8 (average), P_3 (poor) \times P_5 (average) and P_2 (good) \times P_7 (average) in pooled over environments. The significant negative SCA effects were displayed by 9,

11 and 10 crosses in 2020, 2021 and pooled over environments, respectively indicating poor specific combiners. The present outcome is in congruous with the findings of Sarkar and Sirohi (2010), Mule et al. (2012), Kumar et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kumar et al. (2016), Kaur and Dhall (2017), Malav et al. (2018), Thakur and Kumar (2020) and Kumar et al. (2021).

10. Marketable yield per meter square area (kg)

The SCA effects for marketable yield per meter square area (kg) ranged from -7.18 to 5.18 in 2020, -7.10 to 9.08 in 2021 and -7.49 to 4.57 in pooled over environment (Table 4.23). The significant positive SCA effects were exhibited in 15 crosses in 2020, 13 crosses in 2021 and 17 crosses in pooled over environments. Out of 28 cross combinations, P₁ (good) × P₈ (average), P₃ (poor) × P₅ (average), P₂ (good) × P₄ (poor), P₂ (good) × P₈ (average) and P₂ (good) × P₅ (average) in 2020, P₃ (poor) × P₄ (average), P₂ (good) × P₇ (average), P₁ (good) × P₈ (poor), P₂ (good) × P₄ (average) and P₂ (good) × P₆ (poor) in 2021 and P₂ (good) × P₃ (poor), P₂ (good) × P₄ (poor), P₂ (good) × P₈ (poor), P₁ (good) × P₇ (average) and P₁ (good) × P₆ (poor) in pooled over environments were five promising combinations exhibiting good specific combining ability effects. The significant negative SCA effects were exhibited in 9 crosses each in 2020 and pooled over environments while, 12 crosses in 2021 revealing poor specific combining ability. The results are supported by the study of Sarkar and Sirohi (2010), Mule et al. (2012), Bairagi et al. (2013), Reddy et al. (2014), Jat et al. (2015), Kaur and Dhall (2017), Malav et al. (2018), Thakur and Kumar (2020) and Kumar et al. (2021).

11. Harvest duration (days)

The SCA effects for harvest duration ranged from -8.07 to 9.53 in 2020, -7.94 to 11.13 in 2021 and -8.00 to 10.30 in pooled over environments (Table 4.23). The significant positive GCA effects were recorded in 14 crosses in 2020, 17 crosses in 2021 and 19 crosses in pooled over environments. The top five combinations were P₃ (average) × P₆ (average), P₂ (good) × P₈ (poor), P₄ (good) × P₆ (average), P₂ (good) × P₅ (poor) and P₂ (good) × P₆ (average) in 2020, P₃ (average) × P₆ (average), P₂ (good) × P₈ (poor), P₂ (good) × P₅ (poor), P₄ (good)

× P₆ (average) and P₂ (good) × P₇ (average) in 2021 and P₃ (poor) × P₆ (average), P₂ (good) × P₈ (poor), P₂ (good) × P₅ (poor), P₄ (good) × P₆ (average) and P₂ (good) × P₇ (average) in pooled over environments for harvest duration. Out of 28 cross combinations, 5, 9 and 7 crosses in 2020, 2021 and pooled over environments, respectively exhibited significant negative SCA effects indicating poor specific combining ability. The results are in line with the study of Kumar et al. (2016), Kumari et al. (2018) and Thakur and Kumar (2020) who reported significant SCA effects for harvest duration in their respective hybrid combinations.

12 Internodal length (cm)

For internodal length, SCA effects ranged from -1.64 to 1.73 in 2020, -1.49 to 1.46 in 2021 and -1.32 to 1.68 in pooled over environments (Table 4.23). The significant negative SCA effects were observed in 12 crosses in each 2020 and 2021 and 13 crosses in pooled over environments revealing good specific combining ability. Among 28 cross combinations, P₄ (average) × P₈ (good), P₃ (good) × P₅ (poor), P₁ (average) × P₂ (average), P₅ (poor) × P₆ (poor) and P₃ (good) × P₆ (poor) in 2020, P₅ (poor) × P₆ (poor), P₆ (poor) × P₇ (average), P₃ (good) × P₆ (poor), P₂ (average) × P₅ (poor) and P₅ (poor) × P₈ (good) in 2021 and P₅ (poor) × P₆ (poor), P₃ (good) × P₅ (poor), P₁ (average) × P₂ (average), P₂ (average) × P₅ (poor) and P₄ (average) × P₈ (good) in pooled over environments were the top five good specific combiners for internodal length.

Out of 28 combinations, 9, 6 and 8 crosses in 2020, 2021 and pooled over environments, respectively expressed significant positive SCA effects indicating poor specific combining ability. The significant SCA effects for internodal length are also reported by Golabadi et al. (2015) and Kumar et al. (2021) in their respective hybrid combinations.

Table 4.23: Estimates of specific combining ability effects for marketable yield per plant (kg), marketable yield per meter square (kg), harvest duration (days) and internodal length (cm) during 2020, 2021 and pooled over environments

Crosses	Marketable yield per plant (kg)			Marketable yield per meter square (kg)			Harvest duration (days)			Internodal length (cm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁ × P ₂	-1.20 *	-1.28 *	-1.24 *	-7.18 *	-7.10 *	-7.49 *	-8.07 *	-7.94 *	-8.00 *	-1.26 *	-0.72 *	-1.16 *
P ₁ × P ₃	0.18 *	-0.36 *	-0.09 *	1.10 *	-2.73 *	1.56 *	-0.74	-2.27 *	-1.50 *	0.46 *	0.23	0.20
P ₁ × P ₄	0.47 *	0.04	0.26 *	2.85 *	-0.31	1.34 *	5.33 *	4.86 *	5.10 *	-0.10	-0.49 *	-0.25
P ₁ × P ₅	-0.03	0.33 *	0.15 *	-0.17	1.97 *	2.15 *	3.40 *	6.33 *	4.86 *	0.56 *	0.64 *	0.59 *
P ₁ × P ₆	0.57 *	0.53 *	0.55 *	3.39 *	3.15 *	3.59 *	0.96	4.33 *	2.61 *	-0.91 *	-0.70 *	-0.83 *
P ₁ × P ₇	0.28 *	0.60 *	0.44 *	1.71 *	3.61 *	3.72 *	2.53 *	-1.14 *	0.70 *	-0.09	0.01	-0.14
P ₁ × P ₈	0.86 *	0.76 *	0.81 *	5.18 *	5.13 *	2.11 *	4.53 *	3.33 *	3.93 *	0.90 *	0.48 *	0.74 *
P ₂ × P ₃	0.13 *	0.12 *	0.12 *	0.74 *	0.70 *	4.57 *	4.16 *	2.86 *	3.51 *	0.60 *	0.80 *	0.50 *
P ₂ × P ₄	0.78 *	0.76 *	0.77 *	4.71 *	4.53 *	4.26 *	1.23	4.99 *	3.11 *	-0.59 *	-0.52 *	-0.65 *
P ₂ × P ₅	0.58 *	0.55 *	0.57 *	3.47 *	3.90 *	2.86 *	7.63 *	8.46 *	8.05 *	-0.87 *	-0.87 *	-1.11 *
P ₂ × P ₆	0.57 *	0.59 *	0.58 *	3.39 *	4.12 *	3.04 *	5.53 *	4.46 *	4.96 *	1.73 *	1.29 *	1.48 *
P ₂ × P ₇	0.52 *	0.83 *	0.68 *	3.14 *	5.57 *	3.56 *	4.10 *	6.33 *	5.21 *	-0.83 *	-0.24	-0.46 *
P ₂ × P ₈	0.71 *	0.67 *	0.69 *	4.24 *	-0.61 *	4.05 *	9.10 *	9.13 *	9.11 *	0.18	-0.15	0.17
P ₃ × P ₄	0.48 *	0.74 *	0.61 *	2.89 *	9.08 *	3.06 *	0.23	3.33 *	1.78 *	0.05	0.21	-0.04
P ₃ × P ₅	0.81 *	0.57 *	0.69 *	4.85 *	2.83 *	3.37 *	-4.37 *	-4.87 *	-4.62 *	-1.31 *	-0.62 *	-1.20 *
P ₃ × P ₆	-0.30 *	-0.11 *	-0.20 *	-1.77 *	-1.24 *	-1.88 *	9.53 *	11.13 *	10.30 *	-0.95 *	-0.96 *	-0.87 *
P ₃ × P ₇	-0.13 *	-0.26 *	-0.20 *	-0.80 *	-2.16 *	-1.93 *	0.43	0.33	0.38	-0.60 *	-0.65 *	-0.59 *
P ₃ × P ₈	-0.09 *	-0.11 *	-0.10 *	-0.55 *	-0.68 *	-0.94 *	1.10	1.13 *	1.11 *	0.12	-0.07	-0.00
P ₄ × P ₅	-0.16 *	0.13 *	-0.02	-0.96 *	0.20	-0.04	-0.97	-3.07 *	-2.02 *	0.61 *	-0.02	0.30 *
P ₄ × P ₆	0.24 *	-0.10 *	0.07 *	1.46 *	-1.17 *	0.59 *	8.26 *	6.59 *	7.40 *	0.68 *	0.76 *	0.82 *
P ₄ × P ₇	0.03	0.01	0.03	0.20	-0.50	0.21	2.50 *	5.13 *	3.81 *	-0.27	0.09	-0.01
P ₄ × P ₈	-0.24 *	-0.56 *	-0.40 *	-1.47 *	-3.39 *	-1.93 *	0.16	-1.41 *	-0.62	-1.64 *	-0.77 *	-1.11 *
P ₅ × P ₆	-0.73 *	-0.37 *	-0.55 *	-4.38 *	-2.21 *	-3.30 *	-2.34 *	-3.94 *	-3.17 *	-1.00 *	-1.49 *	-1.32 *
P ₅ × P ₇	-0.34 *	-0.32 *	-0.33 *	-2.05 *	-1.94 *	-2.09 *	1.90 *	1.59 *	1.75 *	1.67 *	1.46 *	1.68 *
P ₅ × P ₈	-0.03	-0.29 *	-0.16 *	-0.22	-1.20 *	-0.66 *	-2.10 *	-1.27 *	-1.69 *	-0.87 *	-0.85 *	-1.10 *
P ₆ × P ₇	-0.46 *	-0.51 *	-0.49 *	-2.77 *	-3.07 *	-2.91 *	1.46 *	0.93	1.16 *	-0.70 *	-1.00 *	-1.11 *
P ₆ × P ₈	0.46 *	0.41 *	0.43 *	2.74 *	3.01 *	3.02 *	-1.87 *	-2.94 *	-2.44 *	-0.20	-0.10	-0.32 *
P ₇ × P ₈	0.08	0.11 *	0.09 *	0.49	1.22 *	0.92 *	1.03	3.26 *	2.15 *	0.49 *	0.00	0.37 *
SE(Sij) ±	0.10	0.11	0.10	0.60	0.65	0.63	1.44	1.88	1.31	0.40	0.48	0.44
SE(Sij-Sik) ±	0.15	0.16	0.15	0.89	0.97	0.93	2.13	1.76	1.94	0.59	0.71	0.65
SE (Sij-Skl) ±	0.14	0.15	0.15	0.84	0.91	0.87	2.01	1.66	1.83	0.56	0.67	0.62
CD(Sij)	0.21	0.22	0.21	1.24	1.34	1.29	2.95	2.44	2.69	0.83	0.98	0.91
CD(Sij-Sik)	0.31	0.33	0.32	1.83	1.99	1.91	4.37	3.61	3.99	1.23	1.45	1.34
CD (Sij-Skl)	0.29	0.31	0.30	1.73	1.87	1.79	4.12	3.40	3.76	1.16	1.37	1.26

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

13. Vine length (m)

The SCA effects for vine length (m) ranged from -0.87 to 0.71 in 2020, -0.80 to 0.80 in 2021, -0.84 to 0.76 in pooled over environments (Table 4.24). The significant positive SCA effects were expressed in 14 crosses in 2020, 16 crosses each in 2021 and pooled over environments revealing good specific combinations. Out of 28 cross combinations, the best five combinations were P₆ (poor) × P₇ (average), P₅ (poor) × P₈ (good), P₂ (good) × P₇ (average), P₃ (poor) × P₇ (average) and P₃ (poor) × P₆ (poor) in 2020, P₆ (poor) × P₇ (average), P₅ (poor) × P₈ (good), P₃ (poor) × P₆ (poor), P₄ (good) × P₈ (good) and P₁ (average) × P₄ (good) in 2021 and P₆ (poor) × P₇ (average), P₅ (poor) × P₈ (good), P₃ (poor) × P₆ (poor), P₂ (good) × P₇ (average) and P₄ (good) × P₈ (good) in pooled over environments expressing good specific combining ability effects for vine length (m). The present findings are in agreement with studies of Sharma (2006), Singh et al. (2010), Mule et al. (2012), Jat et al. (2015), Singh et al. (2016b), Thapliyal (2017), Malav et al. (2018) and Manggoel et al. (2021) displaying significant SCA effects for vine length

14. Flesh to seed cavity ratio

For flesh to seed cavity ratio, SCA effects ranged from -0.35 to 0.32 in 2020, -0.23 to 0.35 in 2021 and -0.28 to 0.29 in pooled over environments (Table 4.24). The significant positive SCA effects were expressed in 12 crosses in 2020 and 11 crosses each in 2021 and pooled over environments indicating good specific combiners. Out of 28 cross combinations, P₁ (average) × P₄ (average), P₄ (average) × P₅ (average), P₂ (good) × P₆ (good), P₁ (average) × P₃ (average) and P₂ (good) × P₈ (poor) in 2020, P₁ (average) × P₃ (average), P₇ (poor) × P₈ (poor), P₂ (good) × P₆ (good), P₂ (good) × P₈ (poor) and P₆ (good) × P₇ (poor) and P₄ (average) × P₅ (average) in 2021 and P₁ (average) × P₃ (average), P₄ (average) × P₅ (average), P₂ (good) × P₈ (poor), P₂ (good) × P₆ (good) and P₁ (average) × P₄ (average) in pooled over environments were the five promising cross combinations exhibiting good specific combining ability. Among crosses, 11, 7 and 8 crosses in 2020, 2021 and pooled over environments respectively revealed significant negative SCA effects indicating poor specific combiners for flesh to seed cavity ratio.

Table 4.24: Estimates of specific combining ability effects for vine length (m), flesh to seed cavity ratio and flesh thickness (mm) during 2020, 2021 and pooled over environments

Crosses	Vine length (m)			Flesh to seed cavity ratio			Flesh thickness (mm)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁ × P ₂	0.02	0.15*	0.08*	-0.35 *	-0.18 *	-0.28 *	0.70	0.83*	0.77*
P ₁ × P ₃	0.41*	0.24*	0.33*	0.25 *	0.35 *	0.29 *	0.12	-0.21	-0.04
P ₁ × P ₄	0.46 *	0.53*	0.50*	0.32 *	0.09 *	0.19 *	0.19	-0.23	0.02
P ₁ × P ₅	-0.58*	-0.39*	-0.48*	-0.17 *	0.08 *	-0.06 *	-0.15	-0.19	-0.17
P ₁ × P ₆	0.45*	0.19*	0.32*	-0.08 *	-0.15 *	-0.01	0.67	1.02*	0.85*
P ₁ × P ₇	0.14*	0.20*	0.17*	-0.08 *	0.01	-0.04	0.09	-0.17	-0.04
P ₁ × P ₈	-0.31*	-0.46*	-0.38*	0.23 *	-0.08 *	0.08 *	0.69	1.13*	0.91*
P ₂ × P ₃	0.04	-0.15*	-0.05*	0.09 *	0.05	0.07 *	0.58	0.13	0.36
P ₂ × P ₄	0.31 *	0.26*	0.29*	-0.08 *	0.02	-0.03	0.63	0.81*	0.72*
P ₂ × P ₅	-0.15*	-0.03	-0.09*	-0.01	0.04	0.02	-0.18	-0.82*	-0.50
P ₂ × P ₆	-0.09*	-0.06 *	-0.07*	0.27 *	0.17 *	0.21 *	-0.69	1.06*	0.18
P ₂ × P ₇	0.63*	0.50*	0.56*	-0.21 *	-0.15 *	-0.17 *	0.01	-0.43	-0.21
P ₂ × P ₈	0.00	0.11*	0.06*	0.24 *	0.17 *	0.22 *	0.37	-0.05	0.16
P ₃ × P ₄	0.08*	0.19*	0.13*	0.07 *	0.03	0.05 *	1.47*	0.33	0.91*
P ₃ × P ₅	-0.02	-0.06 *	-0.04*	0.07 *	-0.01	0.03	0.97	0.83*	0.91*
P ₃ × P ₆	0.56*	0.65*	0.60*	0.16 *	-0.10 *	0.02	-0.49	0.08	-0.19
P ₃ × P ₇	0.60*	0.43*	0.52*	0.15 *	0.08 *	0.12 *	-0.71	1.32*	0.30
P ₃ × P ₈	0.42*	0.46*	0.44*	-0.16 *	0.02	-0.06 *	0.64	-0.29	0.17
P ₄ × P ₅	0.31 *	0.13*	0.22*	0.31 *	0.14 *	0.23 *	-0.32	-1.48*	-0.90*
P ₄ × P ₆	-0.51*	-0.48*	-0.50*	-0.06	0.11 *	0.02	0.84	0.50	0.67*
P ₄ × P ₇	-0.29*	-0.41*	-0.35*	0.06	0.06	0.07 *	0.52	0.81*	0.66*
P ₄ × P ₈	0.48*	0.58*	0.53*	-0.19 *	-0.01	-0.09 *	-0.90	-0.25	-0.57
P ₅ × P ₆	-0.37*	-0.40*	-0.39*	0.00	-0.15 *	-0.09 *	0.26	0.64	0.44
P ₅ × P ₇	-0.34*	-0.39*	-0.37*	-0.20 *	-0.23 *	-0.20 *	0.35	-0.16	0.09
P ₅ × P ₈	0.65*	0.67*	0.66*	-0.17 *	0.09 *	-0.03	0.26	-0.12	0.07
P ₆ × P ₇	0.71 *	0.80*	0.76*	0.13 *	0.14 *	0.14 *	0.01	-1.11*	-0.55
P ₆ × P ₈	-0.24*	-0.35*	-0.29*	-0.30 *	-0.03	-0.16 *	-0.08	-0.97*	-0.52
P ₇ × P ₈	-0.87*	-0.80*	-0.84*	0.00	0.22 *	0.01	0.52	1.24*	0.88*
SE(Sij) ±	0.05	0.06	0.06	0.07	0.07	0.072	0.54	0.35	0.45
SE(Sij-Sik) ±	0.08	0.09	0.08	0.10	0.11	0.11	0.80	0.52	0.66
SE (Sij-Skl) ±	0.07	0.08	0.08	0.09	0.10	0.10	0.75	0.49	0.63
CD(Sij)	0.12	0.12	0.12	0.14	0.15	0.15	1.11	0.72	0.92
CD(Sij-Sik)	0.17	0.18	0.17	0.21	0.23	0.22	1.64	1.07	1.36
CD (Sij-Skl)	0.16	0.17	0.16	0.19	0.21	0.21	1.55	1.01	1.28

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

The results are in agreement with research carried by Kaur et al. (2016) and Thapliyal (2017) who reported significant SCA effects for flesh to seed cavity ratio in their respective hybrid combinations

15. Flesh thickness (mm)

The SCA effects for flesh thickness ranged from -0.90 to 1.47 in 2020, -1.48 to 1.32 in 2021 and -0.90 to 0.91 in pooled over environments (Table 4.24). The significant positive SCA effect was observed in one cross in 2020 and 9 crosses each in 2021 and pooled over environments revealing good specific combiners. Out of 28 crosses, best five combinations were P₃ (average) × P₇ (poor), P₇ (poor) × P₈ (average), P₁ (average) × P₈ (average), P₂ (poor) × P₆ (average) and P₁ (average) × P₆ (average) in 2021 and P₁ (average) × P₈ (good), P₃ (poor) × P₄ (good), P₃ (poor) × P₅ (average), P₇ (poor) × P₈ (good) and P₁ (average) × P₆ (average) in pooled over environments while only single cross viz., P₃ (poor) × P₄ (good) in 2020 exhibited significant positive effects. The significant negative SCA effects were observed in 4 crosses in 2021 and single cross in pooled over environments. The results are in consonance with the reports of Pandey et al. (2005), Munshi et al. (2006), Yoshioka et al. (2010) and Arab et al. (2020).

16. Total soluble solids (°Brix)

The SCA effects for total soluble solids (TSS) ranged from -1.10 to 1.27 in 2020, -0.93 to 1.37 in 2021 and -1.00 to 1.32 in pooled over environments (Table 4.25). The significant positive SCA effects were observed in 15 crosses each in 2020 and pooled over environments and 14 crosses in 2021. Out of 28 cross combinations, P₂ (poor) × P₇ (average), P₁ (poor) × P₄ (good), P₄ (good) × P₈ (good), P₆ (good) × P₇ (average) and P₄ (good) × P₇ (average) in 2020, P₂ (poor) × P₇ (good), P₆ (good) × P₇ (good), P₄ (good) × P₈ (average), P₁ (poor) × P₄ (good) and P₁ (poor) × P₃ (good) in 2021 and P₂ (poor) × P₇ (good), P₄ (good) × P₈ (good), P₆ (good) × P₇ (good), P₁ (poor) × P₄ (good) and P₄ (good) × P₈ (good) in pooled over environments were the top five good specific combinations for TSS. The significant negative SCA effects were recorded in 12 crosses in 2020 and 13 crosses each in 2021

and pooled over environments. The results are in line with previous studies of Sharma (2006), Vidhya and Kumar (2014), Kaur et al. (2016) and Thapliyal (2017) who reported significant GCA effects for TSS ($^{\circ}$ Brix).

17. Ascorbic acid (mg/100g)

The SCA effects for ascorbic acid ranged from -1.04 to 1.04 in 2020, -0.84 to 0.91 in 2021 and -0.90 to 0.98 in pooled over environments (Table 4.25). The significant positive SCA effects were recorded in 13 crosses in 2020 and 11 crosses each in 2021 and pooled over environments. Among crosses, P_4 (poor) \times P_5 (good), P_1 (good) \times P_7 (poor), P_7 (poor) \times P_8 (good), P_2 (poor) \times P_4 (poor) and P_6 (poor) \times P_8 (good) in 2020, P_2 (poor) \times P_4 (poor), P_4 (poor) \times P_5 (good), P_2 (poor) \times P_6 (poor), P_6 (poor) \times P_8 (good) and P_1 (good) \times P_3 (poor) in 2021 and P_4 (poor) \times P_5 (average), P_2 (good) \times P_4 (poor), P_7 (average) \times P_8 (good), P_2 (good) \times P_6 (poor) and P_6 (poor) \times P_8 (good) in pooled over environments were the five promising good specific combinations for ascorbic acid. Out of 28 crosses, 14 crosses in 2020 and 17 crosses each in 2021 and pooled over environments exhibited significant negative SCA effects indicating poor specific combiners. The results of present study are in agreement with the findings of Kaur et al. (2016) who reported significant SCA effects for ascorbic acid in their respective hybrid combinations.

18. Total sugar (%)

The SCA effects for total sugar (%) ranged from -0.47 to 0.56, -0.60 to 0.63 and -0.48 to 0.54 in 2020, 2021 and pooled over environments, respectively (Table 4.25). The significant positive SCA effects were recorded in 10 crosses each in 2020 and pooled over environments and 12 crosses in 2021. Among crosses, top five good specific combiners were P_2 (good) \times P_3 (poor), P_2 (good) \times P_6 (poor), P_1 (good) \times P_3 (poor), P_1 (good) \times P_4 (poor) and P_4 (poor) \times P_8 (good) in 2020, P_2 (good) \times P_6 (poor), P_1 (good) \times P_3 (average), P_4 (poor) \times P_6 (poor), P_5 (poor) \times P_6 (poor) and P_1 (good) \times P_5 (poor) in 2021 and P_2 (good) \times P_6 (poor), P_1 (good) \times P_3 (average), P_4 (poor) \times P_6 (poor), P_5 (poor) \times P_6 (poor) and P_1 (good) \times P_5 (poor) in pooled over environments. Out of 28 cross combinations, 12 crosses in 2020, 9 crosses in 2021 and 13 crosses in pooled over environments exhibited significant negative SCA effects revealing poor specific combiners.

Table 4.25: Estimates of specific combining ability effects for quality traits during 2020, 2021 and pooled over environments

Crosses	Total Soluble Solids (°B)			Ascorbic acid (mg/100g)			Total sugars (%)			Reducing sugar (%)		
	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled	2020	2021	Pooled
P ₁ × P ₂	-0.25 *	-0.40 *	-0.32 *	0.44 *	0.18 *	0.31 *	-0.47 **	-0.19*	-0.33*	-0.48*	-0.34*	-0.42*
P ₁ × P ₃	0.65 *	0.79 *	0.72 *	0.42 *	0.69 *	0.55 *	0.38 **	0.42*	0.40*	-0.21*	-0.24*	-0.23*
P ₁ × P ₄	1.06 *	0.87 *	0.97 *	0.01	-0.22 *	-0.11 *	0.33 **	0.14*	0.24*	0.482*	0.40*	0.44*
P ₁ × P ₅	0.15 *	0.28 *	0.21 *	-0.83 *	-0.84 *	-0.84 *	-0.19 **	0.24*	0.02	0.748*	0.58*	0.66*
P ₁ × P ₆	-0.69 *	-0.73 *	-0.71 *	0.35 *	0.28 *	0.32 *	-0.35 **	0.02	-0.16*	-0.043*	-0.33*	-0.19*
P ₁ × P ₇	-0.31 *	-0.24 *	-0.28 *	0.84 *	0.57 *	0.70 *	0.43 **	0.04	0.23*	-0.53*	-0.32*	-0.43*
P ₁ × P ₈	-0.79 *	-0.84 *	-0.82 *	-0.79 *	-0.56 *	-0.67 *	-0.29 **	-0.01	-0.15*	0.45*	0.33*	0.39*
P ₂ × P ₃	0.79 *	0.71 *	0.75 *	-0.11 *	-0.20 *	-0.15 *	0.56 **	0.24*	0.39*	-0.04*	0.22*	0.08*
P ₂ × P ₄	-0.43 *	-0.30 *	-0.36 *	0.57 *	0.91 *	0.74 *	-0.07	0.24*	-0.23*	0.35*	0.083*	0.22*
P ₂ × P ₅	-0.04	-0.12 *	-0.08 *	-0.19 *	0.07 *	-0.06 *	0.21 **	0.12*	0.16*	0.48*	0.37*	0.43*
P ₂ × P ₆	-0.55 *	-0.66 *	-0.61 *	0.51 *	0.83 *	0.67 *	0.45 **	0.63*	0.54*	0.09*	0.048*	0.07*
P ₂ × P ₇	1.27 *	1.37 *	1.32 *	-0.44 *	-0.61 *	-0.53 *	0.11 *	-0.11*	-0.004	0.09*	-0.10*	-0.121*
P ₂ × P ₈	-0.82 *	-0.66 *	-0.74 *	-0.85 *	-0.67 *	-0.76 *	-0.04	-0.32*	-0.18*	-0.28*	-0.16*	-0.23*
P ₃ × P ₄	-0.91 *	-0.76 *	-0.84 *	-0.14 *	-0.19 *	-0.16 *	-0.10 *	-0.003	-0.19*	-0.05	0.41*	0.29*
P ₃ × P ₅	0.19 *	0.17 *	0.18 *	-0.34 *	-0.25 *	-0.29 *	0.04	-0.28*	-0.12*	-0.04*	-0.01	-0.02*
P ₃ × P ₆	0.75 *	0.70 *	0.73 *	-0.39 *	-0.27 *	-0.33 *	-0.27 **	-0.52*	-0.39*	0.57*	0.44*	0.50*
P ₃ × P ₇	0.13 *	0.21 *	0.17 *	0.22 *	-0.07 *	0.07 *	-0.31 **	-0.07	-0.19*	0.06*	0.048*	0.05*
P ₃ × P ₈	0.10 *	-0.02	0.04 *	-1.04 *	-0.76 *	-0.90 *	-0.24 **	0.06	-0.08*	0.15*	0.18*	0.17*
P ₄ × P ₅	-0.86 *	-0.93 *	-0.90 *	1.04 *	0.90 *	0.98 *	-0.15 **	-0.41*	-0.28*	0.42*	0.32*	0.37*
P ₄ × P ₆	0.17 *	0.44 *	0.31 *	0.14 *	-0.34 *	-0.10 *	0.09 *	0.25*	0.17*	0.32*	0.59*	0.45*
P ₄ × P ₇	0.89 *	0.77 *	0.83 *	-0.64 *	-0.51 *	-0.58 *	-0.06	0.11*	0.03	-0.09*	-0.14*	-0.11*
P ₄ × P ₈	1.05 *	0.98 *	1.01 *	0.04 *	-0.16 *	-0.06 *	0.24 **	0.04	0.14*	-0.46*	-0.34*	-0.41*
P ₅ × P ₆	0.43 *	0.41 *	0.42 *	-0.65 *	-0.42 *	-0.53 *	-0.05	0.25*	0.10*	-0.72*	-0.62*	-0.67*
P ₅ × P ₇	-0.18 *	-0.28 *	-0.23 *	0.34 *	0.64 *	0.49 *	-0.05	0.12*	0.04	0.65*	0.59*	0.62*
P ₅ × P ₈	0.28 *	0.45 *	0.37 *	-0.30 *	-0.28 *	-0.29 *	-0.31 *	-0.39*	-0.35*	-0.26*	0.16*	0.21*
P ₆ × P ₇	1.02 *	1.01 *	1.01 *	-0.51 *	-0.61 *	-0.56 *	-0.36*	-0.60*	-0.48*	0.07*	0.07*	0.07*
P ₆ × P ₈	-1.10 *	-0.91 *	-1.00 *	0.55 *	0.79 *	0.67 *	0.20*	0.18*	0.19*	0.55*	0.55*	0.56*
P ₇ × P ₈	-0.42 *	-0.52 *	-0.47 *	0.83 *	0.60 *	0.72 *	-0.21 *	-0.41*	-0.31*	0.24*	0.15*	0.19*
SE(Sij) ±	0.04	0.04	0.04	0.03	0.09	0.02	0.04	0.03	0.04	0.010	0.01	0.01
SE(Sij-Sik) ±	0.06	0.06	0.06	0.04	0.01	0.03	0.06	0.05	0.06	0.02	0.01	0.02
SE (Sij-Skl) ±	0.05	0.05	0.06	0.04	0.01	0.03	0.05	0.05	0.05	0.02	0.01	0.01
CD(Sij)	0.08	0.08	0.08	0.06	0.01	0.04	0.08	0.07	0.08	0.02	0.02	0.02
CD(Sij-Sik)	0.13	0.12	0.13	0.09	0.03	0.06	0.12	0.11	0.11	0.03	0.03	0.03
CD (Sij-Skl)	0.12	0.11	0.12	0.08	0.03	0.05	0.11	0.10	0.11	0.03	0.03	0.03

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

19. Reducing sugars (%)

The SCA effects for reducing sugar ranged from -0.72 to 0.74 in 2020, -0.62 to 0.59 in 2021 and -0.67 to 0.66 in pooled over environments (Table 4.25). The significant positive SCA effects were recorded in 18 crosses each in 2020, 2021 and pooled over environments. Out of 28 crosses, P₁ (good) × P₅ (good), P₅ (good) × P₇ (poor), P₃ (poor) × P₆ (poor), P₆ (poor) × P₈ (poor) and P₁ (good) × P₄ (good) in 2020, P₄ (good) × P₆ (poor), P₅ (good) × P₇ (poor), P₁ (good) × P₅ (good), P₆ (poor) × P₈ (poor) and P₃ (poor) × P₆ (poor) in 2021 and P₁ (good) × P₅ (good), P₅ (good) × P₇ (poor), P₆ (poor) × P₈ (poor), P₃ (poor) × P₆ (good) and P₄ (good) × P₆ (poor) in pooled over environments were the five promising good specific combinations. Among crosses, 10 crosses in 2020 and 9 crosses each in 2021 and pooled over environments exhibited significant negative SCA effects indicating poor specific combiners.

The trait wise good specific hybrid combinations during 2020, 2021 and pooled over environments have been summarized in Table 4.26. It was noticed that no single cross combination could exhibit significant SCA effects for all the traits. Majority of the cross combinations revealed desirable SCA effects which had atleast one of the parents as good or average general combiner. These findings corroborate the observations of Sharma et al. (2006), Singh and Sharma (2006), Munshi et al. (2006), Yadav et al. (2007), Bairagi et al. (2013), Singh et al. (2016), Kumari et al. (2018) and Thakur and Kumar (2020). However, good SCA effects were also observed in certain combinations which had poor × poor or average × poor GCA effects. Cross combination poor × poor could perform better than good × good and good × poor due to complimentary gene action. It has been also reported that the superior hybrids need not necessarily have parents showing high GCA effects only.

The best specific combinations for fruit and its related traits in all the environments were P₁ (good) × P₈ (average), P₂ (good) × P₄ (poor), P₂ (good) × P₈ (average), P₃ (poor) × P₅ (average) and P₂ (good) × P₇ (average). The cross combination P₂ × P₇ displayed significant desirable SCA effects for 7 traits *viz.*, number of female flowers per node, days taken to first fruit picking,

Table 4.26: Best five hybrid combinations exhibiting significant desirable SCA effects during 2020, 2021 and pooled over environments

Trait	2020	2021	Pooled
Days to first female flower	P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)
Nodal position of first female flower	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₇ (DDPCG2) × P ₈ (DDPCG5)
Number of female flowers per node	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₈ (DDPCG5)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Days taken to first picking (days)	P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₆ (DDPCW1) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)
Fruit length (cm)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Fruit diameter (cm)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₄ (PPC-2)
Fruit weight (g)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₃ (PK-1) × P ₅ (PPC-3)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Number of fruits per plant	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₃ (PK-1)
Marketable yield per plant (kg)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Marketable yield per meter square area (kg)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)
Harvest duration (days)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)

Internodal length (cm)	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₅ (PPC-3) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₅ (PPC-3) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Vine length (m)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Flesh to seed cavity ratio	P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₅ (PPC-3)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₄ (PPC-2)
Flesh thickness (mm)	P ₃ (PK-1) × P ₄ (PPC-2)	P ₃ (PK-1) × P ₇ (DDPCG2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₆ (DDPCW1)
Total soluble solids (°B)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Ascorbic acid (mg/100g)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₆ (DDPCW1) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₆ (DDPCW1) × P ₈ (DDPCG5)
Total sugars (%)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₅ (PPC-3)
Reducing sugars (%)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₆ (DDPCW1)

fruit weight, marketable yield per plant, harvest duration, vine length and total soluble solids while, $P_2 \times P_8$ for fruit length, marketable yield per plant, marketable yield per meter square area, harvest duration and flesh to seed cavity ratio. The cross combinations $P_2 \times P_4$ exhibited significant desirable SCA effects for days taken to first fruit picking, number of fruits per plant, marketable yield per plant, marketable yield per meter square area and ascorbic acid while, $P_1 \times P_8$ for fruit length, fruit weight, marketable yield per plant, flesh thickness. Cross combination $P_3 \times P_5$ revealed significant desirable SCA effects for fruit length, number of fruits per plant, marketable yield per plant, internodal length and flesh thickness.

4.5 Heterosis

Heterosis breeding in cucumber is of commercial significance due to higher yield as well as better quality exhibited by hybrids. The term heterosis was first coined in 1914 by Shull and Hayes who lead to the development of heterosis breeding. It is the effective tool for improvement of yield and its component traits in various crop species including self and cross pollinated species. Irrespective of their breeding system, use of heterosis was suggested in self (Rick 1945 and Bishop 1954) and cross (Hutchins 1939) pollinated crops due to their similarity in heterotic response and therefore commercially exploited in various crop species. Hayes and Jones in 1916 first reported heterosis in cucumber and commercial F_1 hybrid Pusa Sanyog bred by IARI, Katrain by crossing gynococious line (Japanese variety i.e, Kaga Aomaga Fushinavi) and Green Long of Naples (an Italian variety) at national level enhanced 128.78 per cent yield over recommended variety (Gill et al. 1973). Heterosis breeding is one of most important tool for exploitation of genetic diversity in cucumber (Mohanty and Mishra 1999). Therefore, the present investigation was undertaken to identify superior heterotic cross combinations over better parent and standard check. The magnitude of heterosis of 28 cross combinations are presented trait wise below:

1. Days to first female flower

Earliness is the most desirable trait to get higher returns. The magnitude of heterosis for days to first female flower ranged from -28.00 ($P_2 \times P_3$) to 10.96 per cent ($P_5 \times P_6$) and -15.63 ($P_2 \times P_3$) to 28.13 per cent ($P_3 \times P_8$) in 2020, -22.89 ($P_2 \times P_8$) to 26.32 per cent ($P_3 \times P_5$) and -14.71 ($P_2 \times P_4$ and $P_4 \times P_6$) to

41.18 per cent ($P_3 \times P_5$) in 2021 and -25.31 ($P_2 \times P_8$) to 13.91 per cent ($P_3 \times P_5$) and -14.39 ($P_2 \times P_3$) to 30.30 per cent ($P_3 \times P_5$) in pooled over environments over better parent and standard check, respectively (Table 4.27). As many as, 19 crosses in 2020, 15 crosses in 2021 and 18 crosses in pooled over environments showed significantly negative heterosis over better parent. Similarly, 3 crosses in 2020, 4 crosses in 2021 and 5 crosses in pooled over environment exhibited negative heterosis over standard check. The cross combinations displaying high negative heterosis in pooled analysis were found to be $P_2 \times P_8$ (-25.31%), $P_2 \times P_3$ (-25.17%), $P_7 \times P_8$ (-22.84%), $P_4 \times P_7$ (-22.00%) and $P_2 \times P_6$ (-21.77%) over better parent and $P_2 \times P_3$ (-14.39%), $P_2 \times P_6$ (-12.88%), $P_4 \times P_6$ (-12.88%), $P_2 \times P_4$ (-12.12%) and $P_4 \times P_7$ (-11.36%) over standard check. The present findings related to negative significant heterosis for days to first female flower are in agreement with Bairagi et al. (2005), Hanchinamani and Patil (2009), Kumar et al. (2010), Tiwari and Singh (2016), Punetha et al. (2017b), Arab et al. (2020) and Umeh et al. (2021).

2. Nodal position of first female flower

For this trait, extent of heterosis over better parent and standard check ranged from -49.89 ($P_1 \times P_7$) to 46.29 per cent ($P_2 \times P_7$) and -16.18 ($P_1 \times P_7$) to 144.36 per cent ($P_4 \times P_6$) in 2020, -45.70 ($P_1 \times P_7$) to 74.88 per cent ($P_6 \times P_7$) and -4.04 ($P_1 \times P_7$) to 179.89 per cent ($P_6 \times P_7$) in 2021 and -47.78 ($P_1 \times P_7$) to 65.82 per cent ($P_6 \times P_7$) and -10.46 ($P_1 \times P_7$) to 148.10 per cent ($P_6 \times P_7$) in pooled over environment, respectively (Table 4.27). Among 28 cross combinations, 7 crosses in 2020, 10 crosses in 2021 and 11 crosses in pooled over environments showed significantly negative heterosis over their respective better parents while, none of the hybrids in all environments displayed significant negative heterosis over standard check. In pooled over environments, hybrid combinations namely, $P_1 \times P_7$ (-47.78%), $P_1 \times P_2$ (-29.27%), $P_2 \times P_5$ (-22.43%), $P_5 \times P_8$ (-20.37%) and $P_3 \times P_6$ (-16.30%) exhibited high negative heterosis over better parent. The results are in line with those of Bairagi et al. (2005), Kushwaha et al. (2011), Mule et al. (2012), Tiwari and Singh (2016), Malav et al. (2018) and Thakur and Kumar (2020)

who have reported desirable heterosis in their respective studies for nodal position of first female flower.

3. Number of female flowers per node

A total of 14 crosses in 2020 and pooled over environments and 11 crosses in 2021 expressed significantly positive heterosis over better parent while, 13 crosses in 2020, 10 crosses in 2021 and 11 crosses in pooled over environment exhibited significantly positive heterosis over standard check (Table 4.27). The extent of heterosis ranged from -32.43 ($P_7 \times P_8$) to 75.78 per cent ($P_6 \times P_7$) and -33.07 ($P_5 \times P_7$) to 40.27 per cent ($P_1 \times P_3$) in 2020, -29.60 ($P_7 \times P_8$) to 100.00 per cent ($P_6 \times P_7$) and -36.64 ($P_5 \times P_7$) to 36.07 per cent ($P_3 \times P_7$) in 2021 and -31.06 ($P_7 \times P_8$) to 87.86 per cent ($P_6 \times P_7$) and -34.98 ($P_5 \times P_7$) to 37.45 per cent ($P_3 \times P_7$) in pooled over environments over better parent and standard check, respectively. The most promising cross combinations in pooled analysis were $P_6 \times P_7$ (87.86%), $P_1 \times P_4$ (38.89%), $P_2 \times P_7$ (34.88%), $P_2 \times P_4$ (34.00%) and $P_1 \times P_2$ (30.24%) over better parent and $P_3 \times P_7$ (37.45%), $P_3 \times P_6$ (28.71%), $P_1 \times P_3$ (27.91%), $P_6 \times P_7$ (23.57%) and $P_4 \times P_8$ (19.20%) over standard check. The present findings are in close proximity to those of Manggoel et al. (2021) who observed heterosis in various hybrid combinations in their respective study.

4. Days taken to first fruit picking (days)

The respective magnitude of heterosis for days taken to first fruit picking ranged from -30.34 ($P_2 \times P_3$) to 5.11 per cent ($P_3 \times P_8$) and -22.90 ($P_2 \times P_3$) to 11.45 per cent ($P_4 \times P_8$) in 2020, -30.13 ($P_4 \times P_6$) to -0.76 per cent ($P_1 \times P_7$) and -13.49 ($P_4 \times P_6$) to 11.11 per cent ($P_4 \times P_5$) in 2021 and -29.97 ($P_4 \times P_6$) to -1.48 per cent ($P_1 \times P_7$) and -17.90 ($P_2 \times P_3$) to 10.89 per cent ($P_4 \times P_5$, $P_4 \times P_8$) in pooled over environments over better parent (BP) and standard check (SC), respectively (Table 4.28). As many as, 20 crosses in 2020, 22 crosses in 2021 and 24 crosses in pooled over environments exhibited positive heterosis over their respective better parent while, 18 crosses in 2020, 5 crosses in 2021 and 16 crosses in pooled over environments revealed positive

Table 4.27: Estimates of heterosis (%) for days to first female flower, nodal position of first female flower and number of female flowers per node over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Days to first female flower						Nodal position of first female flower						Number of female flowers per node					
	2020		2021		pooled		2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-10.96*	1.56	-8.11	0.00	-9.52*	0.76	-37.28*	4.91	-20.81*	39.94*	-29.27*	21.29*	26.64*	12.84*	27.99*	11.96*	30.24*	12.17*
P ₁ × P ₃	-20.00*	-6.25	-15.79*	-5.88	-17.88*	-6.06	12.77	92.73*	1.35	79.87*	7.22	86.31*	16.10*	40.27*	1.99	15.14*	9.14*	27.19*
P ₁ × P ₄	0.00	9.38	-2.82	1.47	-1.42	5.30	19.57*	100.00*	1.81	79.89*	10.86*	90.11*	37.55*	22.57*	40.23*	15.33*	38.89*	18.82*
P ₁ × P ₅	5.71	15.62*	-2.82	1.47	1.42	8.33	-19.30*	67.27*	-10.09*	79.93*	-15.05*	72.81*	-23.14*	-31.52*	-17.95*	-32.52*	-20.67*	-32.13*
P ₁ × P ₆	-15.07*	-3.13	2.82	7.35	-9.09*	-1.52	-27.19*	50.91*	-20.81*	39.94*	-15.30*	45.25*	10.70*	-1.36	17.73*	-3.18	14.00*	-2.47
P ₁ × P ₇	-10.39*	7.81	-2.74	4.41	-6.67	6.06	-49.89*	-16.18	-45.70*	-4.04	-47.78*	-10.46	21.18*	7.98*	22.95*	1.12	21.78*	4.18
P ₁ × P ₈	-12.66*	7.81	-20.48*	-2.94	-13.58*	6.06	-4.67	59.45*	-20.70*	39.94*	-12.64*	49.81*	-26.32*	-15.56*	-24.78*	-18.32*	-25.60*	-17.11*
P ₂ × P ₃	-28.00*	-15.63*	-22.37*	-13.24*	-25.17*	-14.39*	-2.13	67.27*	12.73*	99.92*	4.92	82.32*	-19.32*	-2.53	-17.72*	-7.10	-18.60*	-5.13
P ₂ × P ₄	-20.55*	-9.38	-21.62*	-14.71*	-21.09*	-12.12*	21.98*	101.82*	18.80*	105.92*	30.01*	103.42*	35.47*	15.18*	32.69*	16.07*	34.00*	15.40*
P ₂ × P ₅	-20.55*	-9.38	-13.51*	-5.88	-17.01*	-7.58	-24.56*	56.36*	-20.08*	59.94*	-22.43*	57.79*	20.82*	2.72	15.60*	1.12	18.10*	1.71
P ₂ × P ₆	-24.66*	-14.06*	-18.92*	-11.76*	-21.77*	-12.88*	-7.02	92.73*	3.81	79.93*	19.08*	86.31*	-5.03	-19.26*	-8.33	-19.81*	-6.84	-19.77*
P ₂ × P ₇	-20.78*	-4.69	-14.86*	-7.35	-17.33*	-6.06	46.29*	132.73*	50.06*	159.90*	56.74*	145.25*	37.99*	17.32*	32.05*	15.51*	34.88*	16.16*
P ₂ × P ₈	-27.85*	-10.94	-22.89*	-5.88	-25.31*	-8.33	18.40*	67.27*	14.65*	98.79*	16.40*	82.13*	-7.98*	5.45	-5.51	2.62	-6.83*	3.80
P ₃ × P ₄	-5.33	10.94	-9.21	1.47	-7.28	6.06	1.38	73.27*	-3.15	71.93*	-0.77	72.43*	-10.14*	8.56*	-10.10*	1.50	-10.11*	4.75
P ₃ × P ₅	1.33	18.75*	26.32*	41.18*	13.91*	30.30*	-10.53	85.45*	9.99*	120.11*	-0.84	101.71*	-18.20*	-1.17	-17.55*	-6.92	-17.94*	-4.37
P ₃ × P ₆	-21.33*	-7.81	-13.16*	-2.94	-17.22*	-5.30	-35.96*	32.73*	-9.91	59.94*	-16.30*	45.44*	4.51	26.26*	16.56*	31.59*	10.44*	28.71*
P ₃ × P ₇	-6.49	12.50*	-9.21	1.47	-6.62	6.82	6.06	81.27*	1.35	79.93*	3.83	80.42*	15.46*	39.49*	20.53*	36.07*	17.94*	37.45*
P ₃ × P ₈	3.80	28.13*	-3.61	17.65*	0.00	22.73*	8.51	85.45*	12.50*	99.92*	10.61*	92.21*	0.81	21.79*	3.31	16.64*	2.12	19.01*
P ₄ × P ₅	7.58	10.94	2.99	1.47	6.87	6.06	-9.74	87.09*	-10.09*	79.93*	-9.81*	83.46*	15.57*	-17.70*	12.31	-18.13*	13.72*	-18.06*
P ₄ × P ₆	-21.92*	-10.94	-17.14*	-14.71*	-19.58*	-12.88*	17.89*	144.36*	50.00*	139.90*	58.14*	142.02*	12.12*	-20.82*	2.84	-25.42*	7.45	-23.19*
P ₄ × P ₇	-27.27*	-12.50*	-16.44*	-10.29	-22.00*	-11.36*	15.05	90.36*	28.57*	79.93*	20.99*	85.17*	21.49*	-14.20*	15.98*	-15.89*	18.88*	-15.02*
P ₄ × P ₈	-18.99*	0.00	-22.89*	-5.88	-20.99*	-3.03	-11.32	46.73*	0.00	39.94*	-6.46	43.16*	7.81*	23.54*	6.20	15.33*	7.00*	19.20*
P ₅ × P ₆	10.96*	26.56*	14.29*	17.65*	12.59*	21.97*	12.28	132.73*	29.87*	159.90*	20.56*	145.25*	5.19	-25.10*	-7.95	-32.90*	-1.58	-29.09*
P ₅ × P ₇	-2.60	17.19*	17.81*	26.47*	7.33	21.97*	-5.61	95.64*	-10.09*	79.93*	-7.66*	87.83*	-6.01	-33.07*	-13.08	-36.64*	-9.76	-34.98*
P ₅ × P ₈	-10.13*	10.94	-15.66*	2.94	-12.96*	6.82	-20.79*	64.18*	-20.08*	59.94*	-20.37*	61.98*	-9.51*	3.70	-7.23	0.75	-8.36*	2.09
P ₆ × P ₇	-11.69*	6.25	-8.22	-1.47	-10.00*	2.27	6.05	119.82*	74.88*	179.89*	65.82*	148.10*	75.78*	20.04*	100.88*	27.29*	87.86*	23.57*
P ₆ × P ₈	-21.52*	-3.13	-18.07*	0.00	-19.75*	-1.52	2.63	112.73*	25.00*	99.92*	38.22*	106.27*	-1.70	12.65*	-1.38	7.10	-1.54	9.70*
P ₇ × P ₈	-22.78*	-4.69	-22.89*	-5.88	-22.84*	-5.30	-15.43	34.55*	-14.29*	19.95*	-14.74*	27.57*	-32.43*	-22.57*	-29.60*	-23.55*	-31.06*	-23.19*

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

heterosis over standard check. In pooled over environments, high positive heterosis was exhibited by cross combinations $P_4 \times P_6$ (-29.97%), $P_2 \times P_4$ (-28.66%), $P_2 \times P_3$ (-24.37%), $P_3 \times P_4$ (-24.10%) and $P_4 \times P_7$ (-23.45%) over better parent and $P_2 \times P_3$ (-17.90%), $P_2 \times P_7$ (-16.73%), $P_4 \times P_6$ (-16.34%), $P_2 \times P_4$ (-14.79%) and $P_2 \times P_6$ (-13.62%) over standard check. Similarly, Singh et al. (2010), Airina et al. (2013), Singh et al. (2016), Punetha et al. (2017b) and Umeh et al. (2021) have also revealed significant heterosis for days taken to first fruit picking for different cross combinations.

5. Fruit length (cm)

The perusal of data (Table 4.28) revealed that the extent of heterosis for fruit length over better parent and standard check ranged from -27.45 ($P_1 \times P_4$) to 29.82 per cent ($P_1 \times P_8$) and -8.64 ($P_1 \times P_2$) to 34.01 per cent ($P_2 \times P_8$) in 2020, -19.75 ($P_1 \times P_4$) to 22.43 per cent ($P_1 \times P_8$) and -5.06 ($P_3 \times P_7$) to 34.47 per cent ($P_2 \times P_7$) in 2021 and -23.72 ($P_1 \times P_4$) to 26.09 per cent ($P_1 \times P_8$) and -4.95 ($P_1 \times P_2$) to 32.35 per cent ($P_2 \times P_7$) in pooled over environments, respectively. Out of 28 cross combinations, 2 crosses each in 2020 and 2021 and 3 crosses in pooled over environments exhibited heterobeltiosis. The economic heterosis was observed in 15 crosses in 2020, 16 crosses in 2021 and 19 crosses in pooled over environments. The top heterotic combinations were $P_1 \times P_8$ (26.09%), $P_2 \times P_7$ (10.40%) and $P_2 \times P_8$ (9.62%) over better parent and $P_1 \times P_7$ (32.35%), $P_2 \times P_8$ (31.41%), $P_2 \times P_4$ (31.37%), $P_1 \times P_8$ (30.41%) and $P_5 \times P_6$ (27.48%) over standard check in pooled over environments. The present findings are in agreement with those of Pandey et al. (2005), Singh et al. (2010), Kushwaha et al. (2011), Mule et al. (2012), Airina et al. (2013), Kaur and Dhall (2017), Kumari et al. (2018) and Manggoel et al. (2021) who revealed desirable heterosis for fruit length in different hybrid combinations.

Table 4.28: Estimates of heterosis (%) for days taken to first fruit picking (days), fruit length (cm) and fruit diameter (cm) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Days taken to first fruit picking (days)						Fruit length (cm)						Fruit diameter (cm)					
	2020		2021		pooled		2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-11.03*	-1.53	-8.96	-3.17	-10.04*	-2.33	-25.03*	-8.64	-16.22*	-1.25	-20.71*	-4.95	-5.47*	2.58	-1.46	2.36	-3.45	2.47
P ₁ × P ₃	-13.85*	-14.50*	-6.45	-7.94	-10.24*	-11.28*	6.60	8.12	-2.84	-2.29	1.94	2.95	0.63	9.21*	0.16	4.05	0.48	6.64*
P ₁ × P ₄	-21.85*	-9.92*	-19.23*	0.00	-20.52*	-5.06	-27.45*	-6.65	-19.75*	-1.41	-23.72*	-4.05	5.87*	14.89*	7.47	11.64*	6.74 *	13.28*
P ₁ × P ₅	-14.79*	-7.63*	-20.26*	-3.17	-17.63*	-5.45	2.42	14.83	-13.63*	7.07	-5.95	10.97*	-6.90*	1.03	-1.95	1.85	-4.41	1.45
P ₁ × P ₆	-18.66*	-16.79*	-17.14*	-7.94	-17.88*	-12.45*	3.70	17.81*	9.45	14.50	6.41	16.15*	-13.88*	-6.54*	-11.60*	-4.89	-11.78*	-5.70*
P ₁ × P ₇	-2.16	3.82	-0.76	3.17	-1.48	3.50	6.55	10.44	-2.40	-1.85	3.32	4.35	8.49*	17.73*	4.38	8.43*	6.50*	13.02*
P ₁ × P ₈	-1.46	3.05	-14.19*	0.79	-8.07*	1.95	29.82*	31.85*	22.43*	28.97*	26.09*	30.41*	0.71	9.98*	0.48	5.23	0.56	7.49*
P ₂ × P ₃	-30.34*	-22.90*	-17.91*	-12.70*	-24.37*	-17.90*	-8.48	11.53	5.08	23.87*	-1.86	17.65*	-3.88	2.32	2.51	3.37	-0.82	2.81
P ₂ × P ₄	-28.48*	-17.56*	-28.85*	-11.90*	-28.66*	-14.79*	3.39	33.02*	5.59	29.73*	4.44	31.37*	3.03	11.27*	7.19	8.09	5.75*	9.62*
P ₂ × P ₅	-22.76*	-14.50*	-23.53*	-7.14	-22.37*	-10.89*	4.19	26.98*	0.66	24.79*	4.99	25.87*	2.34	9.12*	3.81	5.56	3.11	7.32*
P ₂ × P ₆	-24.14*	-16.03*	-20.00*	-11.11*	-20.43*	-13.62*	1.54	23.75*	10.53	30.29*	5.94	27.00*	5.50*	12.31*	2.35	10.12*	4.06	11.23*
P ₂ × P ₇	-28.97*	-21.37*	-17.16*	-11.90*	-23.30*	-16.73*	6.87	30.24*	14.08*	34.47*	10.40*	32.35*	3.56	10.24*	4.18	5.06	3.86	7.66*
P ₂ × P ₈	-15.86*	-6.87	-18.24*	-3.97	-14.74*	-5.45	9.96	34.01*	9.27	28.81*	9.62*	31.41*	1.42	10.76*	0.97	5.73	1.19	8.17*
P ₃ × P ₄	-23.84*	-12.21*	-24.36*	-6.35	-24.10*	-9.34*	-24.63*	-3.03	-9.45	11.25	-17.28*	4.05	5.82*	14.29*	7.13	6.41	6.40*	10.30*
P ₃ × P ₅	-19.72*	-12.98*	-21.57*	-4.76	-20.68*	-8.95*	12.54	26.18*	-4.16	18.80*	3.84	22.52*	-9.28*	-3.27	-3.32	-1.69	-6.30*	-2.47
P ₃ × P ₆	-15.67*	-13.74*	-15.71*	-6.35	-15.69*	-10.12*	-5.30	7.59	11.83	16.99*	2.83	12.25*	-5.83*	0.00	-9.87*	-3.04	-7.96*	-1.62
P ₃ × P ₇	-15.83*	-10.69*	-6.87	-3.17	-11.48*	-7.00*	-7.53	-4.16	0.13	-5.06	-3.92	-4.61	3.69	1.55	1.43	-4.05	2.56	-1.28
P ₃ × P ₈	5.11	9.92*	-8.11	7.94	-1.75	8.95*	-7.20	-5.74	-4.65	0.44	-5.90	-2.67	-6.07*	2.58	-7.57	-3.20	-6.77*	-0.34
P ₄ × P ₅	-3.97	10.69*	-10.26*	11.11*	-7.17*	10.89*	-3.22	24.52*	-4.16	18.80*	-3.27	21.68*	-0.08	7.92*	1.99	3.71	1.64	5.79*
P ₄ × P ₆	-29.80*	-19.08*	-30.13*	-13.49*	-29.97*	-16.34*	-6.74	19.98*	-2.45	19.85*	-4.66	19.92*	-0.80	7.14*	-3.92	3.37	-1.51	5.28*
P ₄ × P ₇	-23.84*	-12.21*	-23.08*	-4.76	-23.45*	-8.56*	-18.60*	4.73	-18.93*	-0.40	-18.77*	2.17	8.21*	16.87*	12.56*	11.80*	10.26*	14.30*
P ₄ × P ₈	-3.31	11.45*	-10.90*	10.32	-7.17*	10.89*	-3.69	23.91*	2.71	26.20*	-0.59	25.05*	-12.14*	-4.04	-6.92	-2.53	-9.55*	-3.32
P ₅ × P ₆	-19.72*	-12.98*	-22.22*	-5.56	-21.02*	-9.34*	11.58	26.76*	3.45	28.24*	8.05	27.48*	-11.54*	-5.68*	-10.97*	-4.22	-11.07*	-4.94
P ₅ × P ₇	-5.63	2.29	-17.65*	0.00	-11.86*	1.17	9.49	22.76*	-1.77	21.78*	3.62	22.26*	-10.17*	-4.22	-5.31	-3.71	-7.77*	-4.00
P ₅ × P ₈	0.70	9.16*	-11.11*	7.94	-5.42	8.56*	11.98	25.55*	-3.40	19.75*	3.96	22.66*	-8.51*	-0.09	-5.48	-1.01	-6.93*	-0.51
P ₆ × P ₇	-2.88	3.05	-6.43	3.97	-2.92	3.50	14.16*	29.69*	-2.15	2.37	6.40	16.13*	-15.64*	-10.41*	-15.67*	-9.27*	-15.61*	-9.79*
P ₆ × P ₈	-16.79*	-12.98*	-17.57*	-3.17	-17.19*	-8.17*	-9.41	2.91	3.20	8.72	-3.09	5.78	-3.78	5.08	-2.66	4.72	-1.83	4.94
P ₇ × P ₈	-20.86*	-16.03*	-23.65*	-10.32	-21.75*	-13.23*	0.34	4.00	12.89	18.92*	7.73	11.43*	-8.83*	-0.43	-4.19	0.34	-6.45*	0.00

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

6. Fruit diameter (cm)

The respective magnitude of heterosis ranged from -15.64 ($P_6 \times P_7$) to 8.49 per cent ($P_1 \times P_7$) and -10.41 ($P_6 \times P_7$) to 17.73 per cent ($P_1 \times P_7$) in 2020, -15.67 ($P_6 \times P_7$) to 12.56 per cent ($P_4 \times P_7$) and -9.27 ($P_6 \times P_7$) to 11.80 per cent ($P_4 \times P_7$) in 2021 and -15.61 ($P_6 \times P_7$) to 10.26 per cent ($P_4 \times P_7$) and -9.79 ($P_6 \times P_7$) to 14.30 per cent ($P_4 \times P_7$) in pooled over environments over better parent and standard check, respectively (Table 4.28). A total of 5 crosses each in 2020 and pooled over environments and single cross in 2021 showed heterobeltiosis while 13 crosses in 2020 and pooled over environment and 4 crosses in 2021 exhibited economic heterosis. Out of these, $P_4 \times P_7$ (10.26%), $P_1 \times P_4$ (6.74%), $P_1 \times P_7$ (6.50%), $P_3 \times P_4$ (6.40%) and $P_2 \times P_4$ (5.75%) were the top heterotic combinations over better parent in pooled over environments and $P_4 \times P_7$ (14.30%), $P_1 \times P_4$ (13.28%), $P_1 \times P_7$ (13.02%), $P_2 \times P_6$ (11.23%) and $P_3 \times P_4$ (10.30%) exhibited economic heterosis. The results are in close proximity with Pandey et al. (2005), Singh et al. (2010), Kushwaha et al. (2011), Mule et al. (2012), Airina et al. (2013), Kaur and Dhall (2017), Kumari et al. (2018) and Manggoel et al. (2021) who have reported hybrid vigour in various cross combinations for fruit diameter in their respective studies.

7. Fruit weight (g)

As many as, 9 crosses each in 2020 and pooled over environments and 10 crosses in 2021 exhibited significantly positive heterosis over better parent while, 8 crosses in 2020 and pooled over environments and 9 crosses in 2021 exhibited positive heterosis over standard check (Table 4.29). The extent of heterosis for this trait ranged from -20.89 ($P_6 \times P_7$) to 23.62 per cent ($P_3 \times P_4$) and -20.41 ($P_6 \times P_7$) to 25.23 per cent ($P_2 \times P_6$) in 2020, -18.47 ($P_6 \times P_7$) to 21.98 per cent ($P_2 \times P_7$) and -17.78 ($P_6 \times P_7$) to 24.62 per cent ($P_2 \times P_7$) in 2021 and -19.64 ($P_6 \times P_7$) to 22.59 per cent ($P_2 \times P_7$) and -19.06 ($P_6 \times P_7$) to 24.79 per cent ($P_2 \times P_7$) in pooled over environments over better parent and standard check, respectively. Cross combinations namely $P_2 \times P_7$ (22.59%), $P_3 \times P_4$ (22.29%), $P_2 \times P_6$ (22.26%), $P_1 \times P_8$ (21.73%) and $P_2 \times P_8$ (19.68%) revealed

heterobeltiosis whereas, $P_2 \times P_7$ (24.79%), $P_2 \times P_6$ (24.45%), $P_1 \times P_8$ (22.80%), $P_2 \times P_8$ (21.82%) and $P_2 \times P_4$ (20.07%) exhibited economic heterosis for this trait. The results are in agreement with those of Bairagi et al. (2005), Hanchinamani and Patil (2009), Kumar et al. (2010), Singh et al. (2010), Kushwaha et al. (2011), Mule et al. (2012), Jat et al. (2015), Sharma et al. (2016), Singh et al. (2016b), Kaur and Dhall (2017), Punetha et al. (2017b), Thapliyal (2017), Kumari et al. (2018) and Umeh et al. (2021) who have also revealed significant positive heterosis in hybrid combinations for fruit weight in their respective investigations.

8. Number of fruits per plant

The magnitude of heterosis for number of fruits per plant over better parent and standard check ranged from -25.84 ($P_5 \times P_6$) to 30.50 per cent ($P_3 \times P_4$) and -27.05 ($P_5 \times P_6$) to 21.49 per cent ($P_2 \times P_4$) in 2020, -7.72 ($P_1 \times P_2$) to 20.30 per cent ($P_3 \times P_4$) and -19.52 ($P_5 \times P_6$) to -10.12 per cent ($P_2 \times P_7$) in 2021 and -14.59 ($P_5 \times P_6$) to 24.93 per cent ($P_3 \times P_4$) and -23.18 ($P_5 \times P_6$) to 13.33 per cent ($P_2 \times P_4$) in pooled over analysis, respectively (Table 4.29). Only 10, 6 and 12 crosses expressed significant positive heterosis in 2020, 2021 and pooled over environments over better parent, respectively. On the other hand, 4 crosses each in 2020 and pooled over environments and none of the hybrid combination in 2021 exhibited economic heterosis for this trait. The top heterotic combinations for number of fruits per plant were $P_3 \times P_4$ (24.93%), $P_6 \times P_8$ (18.34%), $P_1 \times P_8$ (15.51%), $P_4 \times P_6$ (14.45%) and $P_1 \times P_4$ (14.34%) over better parent whereas, $P_2 \times P_4$ (13.33%), $P_2 \times P_7$ (12.41%), $P_2 \times P_8$ (12.36%) and $P_2 \times P_5$ (12.22%) expressed high economic heterosis. The results are in close proximity to those of Bairagi et al. (2005), Pandey et al. (2005), Kumar et al. (2010), Dogra and Kanwar (2011), Kushwaha et al. (2011), Mule et al. (2012), Airina et al. (2013), Jat et al. (2015), Singh et al. (2016b), Tiwari and Singh (2016), Punetha et al. (2017b), Thapliyal (2017), Preethi et al. (2019), Arab et al. (2020) and Umeh et al. (2021) who revealed hybrid vigour for number of fruits per plant in various cross combinations.

Table 4.29: Estimates of heterosis (%) for fruit weight (g), number of fruits per plant and marketable yield per plant (kg) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Fruit weight (g)						Number of fruits per plant						Marketable yield per plant (kg)					
	2020		2021		pooled		2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-14.68*	-13.49*	-14.53*	-12.68*	-14.60*	-13.07*	-9.00	-1.52	-7.72	-12.71*	-8.39*	-7.28	-22.30*	-14.67*	-20.95*	-23.32*	-21.63*	-19.21*
P ₁ × P ₃	-10.33	-10.05	-17.99*	-16.82*	-14.30*	-13.54*	24.23*	6.34	1.88	-9.88	12.55*	-2.01	10.64	-3.72	-16.54*	-24.72*	-4.07	-14.86*
P ₁ × P ₄	2.52	2.84	1.23	2.67	1.85	2.75	26.55*	8.32	3.22	-8.69	14.34*	-0.45	28.40*	11.74*	3.77	-6.41	15.19*	2.23
P ₁ × P ₅	10.42	10.76	9.69	11.26*	10.04	11.02	-7.10	-8.62	5.61	-6.58	2.76	-7.57*	5.43	0.79	15.65*	4.30	15.79*	2.76
P ₁ × P ₆	17.24*	17.60*	16.03*	17.69*	16.61*	17.65*	14.80*	-1.73	2.66	-9.19	8.46	-5.57	34.50*	17.04*	18.87*	7.21	26.08*	11.89*
P ₁ × P ₇	15.50*	16.19*	13.60*	15.22*	14.67*	15.69*	-5.95	0.11	12.53*	-0.46	4.12	-0.18	8.67	16.03*	27.41*	14.91*	19.82*	15.50*
P ₁ × P ₈	23.14*	23.52*	20.41*	22.12*	21.73*	22.80*	23.76*	5.94	7.99	-4.47	15.51*	0.57	50.19*	30.70*	29.74*	17.02*	39.23*	23.57*
P ₂ × P ₃	7.15	8.65	6.96	9.27	7.05	8.97	-3.30	4.65	1.48	-4.00	-0.99	0.21	3.49	13.66*	8.26	5.01	5.87	9.13*
P ₂ × P ₄	15.10*	16.70*	20.64*	23.24*	17.96*	20.07*	12.26*	21.49*	11.68*	5.65	11.98*	13.33*	28.98*	41.65*	34.57*	30.53*	31.72*	35.77*
P ₂ × P ₅	16.11*	17.72*	17.53*	20.07*	16.84*	18.93*	10.39	19.47*	11.43*	5.41	10.88*	12.22*	28.06*	40.63*	30.44*	26.53*	29.35*	33.33*
P ₂ × P ₆	23.50*	25.23*	21.11*	23.72*	22.26*	24.45*	0.48	8.75	6.44	0.69	3.34	4.59	24.15*	36.34*	28.59*	24.72*	26.36*	30.25*
P ₂ × P ₇	23.25*	24.97*	21.98*	24.62*	22.59*	24.79*	6.11	14.84*	16.40*	10.12	11.07*	12.41*	30.63*	43.45*	41.59*	37.34*	36.05*	40.23*
P ₂ × P ₈	19.43*	21.10*	19.91*	22.51*	19.68*	21.82*	10.17	19.23*	11.93*	5.88	11.02*	12.36*	31.96*	44.92*	33.95*	29.93*	32.96*	37.05*
P ₃ × P ₄	23.62*	6.13	21.07*	6.33	22.29*	6.23	30.50*	-9.61	20.30*	-5.19	24.93*	-7.34	65.63*	-4.29	44.83*	0.90	53.90*	-1.49
P ₃ × P ₅	11.50	7.48	11.67*	7.88	11.59	7.69	6.67	4.93	10.44	-9.41	8.45	-2.45	17.83*	12.64*	21.79*	-2.10	19.88*	4.99
P ₃ × P ₆	-14.49*	-15.90*	-14.31*	-14.67*	-14.40*	-15.26*	0.62	-15.31*	10.79	-12.69*	6.16	-13.96*	-14.36*	-28.67*	-2.99	-25.43*	-8.51	-26.96*
P ₃ × P ₇	-11.48	-10.96	-13.30*	-12.57*	-12.42*	-11.79*	-10.23	-4.44	-0.01	-14.12*	-5.52	-9.42*	-19.87*	-14.45*	-13.65*	-24.62*	-16.74*	-19.75*
P ₃ × P ₈	0.86	-14.75*	-0.20	-13.59*	0.31	-14.15*	20.87*	-3.14	4.25	-10.82*	12.03*	-7.11	21.81*	-18.06*	4.04	-22.72*	11.96*	-20.49*
P ₄ × P ₅	8.87	4.95	8.33	4.65	8.59	4.79	-17.15*	-18.51*	5.84	-13.19*	-6.37	-15.78*	-10.51	-14.45*	13.33*	-8.91	1.09	-11.46*
P ₄ × P ₆	-4.26	-5.84	-3.96	-4.36	-4.10	-5.07	20.36*	1.30	7.49	-15.28*	14.45*	-7.24	14.50*	-4.63	5.60	-18.82*	9.97*	-12.21*
P ₄ × P ₇	-2.50	-1.92	-2.62	-1.80	-2.56	-1.86	-7.29	-1.31	6.55	-8.48	-0.91	-5.00	-9.30	-3.16	3.10	-10.01	-3.19	-6.69
P ₄ × P ₈	-5.12	-18.55*	-4.71	-16.31*	-4.91	-17.39*	26.33*	1.24	-2.35	-16.47*	11.10*	-7.88*	22.82*	-17.38*	-5.66	-29.93*	6.88	-24.10*
P ₅ × P ₆	-5.30	-6.86	-6.06	-6.45	-5.70	-6.65	-25.84*	-27.05*	-1.88	-19.52*	-14.59*	-23.18*	-28.45*	-31.60*	-6.48	-24.82*	-17.70*	-27.92*
P ₅ × P ₇	-2.62	-2.04	-1.62	-0.78	-2.10	-1.39	-13.61*	-8.04	-3.85	-17.41*	-9.11*	-12.86*	-15.54*	-9.82*	-5.96	-17.92*	-10.90*	-14.12*
P ₅ × P ₈	-0.87	-4.45	0.35	-3.05	-0.24	-3.73	1.84	0.17	-3.45	-17.41*	1.31	-8.88*	0.12	-4.29	-0.12	-19.72*	0.00	12.42*
P ₆ × P ₇	-20.89*	-20.41*	-18.47*	-17.78*	-19.64*	-19.06*	-3.02	3.23	3.82	-10.82*	0.13	-4.01	-23.15*	-17.95*	-15.94*	-26.63*	-19.60*	-22.51*
P ₆ × P ₈	6.58	4.83	6.12	5.67	6.34	5.26	23.13*	3.63	8.66	-7.05	18.34*	-1.88	30.08*	8.35	27.86*	-1.70	29.12*	3.08
P ₇ × P ₈	-1.24	-0.65	-0.32	0.52	-0.77	-0.05	-1.43	4.93	9.56	-5.89	3.64	-0.64	-2.33	4.29	8.49	-5.31	2.97	-0.74

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

9. Marketable yield per plant (kg)

The perusal of data (Table 4.29) revealed that the extent of heterosis ranged from -28.45 ($P_5 \times P_6$) to 65.63 per cent ($P_3 \times P_4$) and -31.60 ($P_5 \times P_6$) to 44.92 per cent ($P_2 \times P_8$) in 2020, -20.95 ($P_1 \times P_2$) to 44.83 per cent ($P_3 \times P_4$) and -29.93 ($P_4 \times P_8$) to 37.34 per cent ($P_2 \times P_7$) in 2021 and -21.63 ($P_1 \times P_2$) to 53.90 per cent ($P_3 \times P_4$) and -27.92 ($P_5 \times P_6$) to 40.23 per cent ($P_2 \times P_7$) in pooled over environments over better parent and standard check, respectively. A total of 14 crosses in 2020, 13 crosses in 2021 and 15 crosses in pooled over environments expressed significant positive heterosis over better parent. Significant positive heterosis for this trait over standard check was observed for 11, 7 and 10 cross combinations in 2020, 2021 and pooled over environments, respectively. The high heterobeltiosis for marketable yield per plant was observed in $P_3 \times P_4$ (53.90%), $P_1 \times P_8$ (39.23%), $P_2 \times P_7$ (36.05%), $P_2 \times P_8$ (32.93%) and $P_2 \times P_6$ (30.25%) while economic heterosis in cross combinations viz., $P_2 \times P_7$ (40.23%), $P_2 \times P_8$ (37.05%), $P_2 \times P_4$ (35.77%), $P_2 \times P_5$ (33.33%) and $P_2 \times P_6$ (30.25%) in pooled over environments. Similarly, Bairagi et al. (2005), Pandey et al. (2005), Hanchinamani and Patil (2009), Kumar et al. (2010), Singh et al. (2010), Dogra and Kanwar (2011), Kushwaha et al. (2011), Mule et al. (2012), Airina et al. (2013), Jat et al. (2015), Arya and Singh (2016), Sharma et al. (2016), Singh et al. (2016b), Tiwari and Singh (2016), Kaur and Dhall (2017), Punetha et al. (2017b), Thapliyal (2017), Kumari et al. (2018); Malav et al. (2018), Preethi et al. (2019), Arab et al. (2020) and Umeh et al. (2021) have also observed desirable heterosis for marketable yield per plant.

10. Marketable yield per metre square (kg)

A total of 11 crosses in 2020, 7 crosses in 2021 and 10 crosses in pooled over environments displayed significant economic heterosis for marketable yield per metre square (Table 4.30). The significant heterobeltiosis was observed for 4, 12 and 17 crosses in 2020, 2021 and pooled over environments, respectively. For marketable yield per metre square, heterosis ranged from -28.45 ($P_5 \times P_6$) to 65.64 per cent ($P_3 \times P_4$) and -31.59 ($P_5 \times P_6$) to 44.92 per

cent ($P_2 \times P_8$) in 2020, -20.95 ($P_1 \times P_2$) to 86.58 per cent ($P_3 \times P_4$) and -30.05 ($P_4 \times P_8$) to 37.32 per cent ($P_2 \times P_7$) in 2021 and -19.59 ($P_6 \times P_7$) to 53.71 per cent ($P_3 \times P_4$) and -27.96 ($P_5 \times P_6$) to 40.25 per cent ($P_2 \times P_7$) in pooled over environments over better parent and standard check, respectively. The most desirable combinations expressing high heterosis were $P_3 \times P_4$ (65.64%), $P_1 \times P_8$ (50.24%), $P_1 \times P_6$ (34.33%), $P_2 \times P_8$ (31.82%) and $P_2 \times P_7$ (30.62%) over better parent and $P_2 \times P_7$ (40.25%), $P_2 \times P_8$ (36.92%), $P_2 \times P_3$ (35.74%), $P_2 \times P_4$ (35.74%) and $P_2 \times P_5$ (33.17%) over standard check for this trait in pooled over environments. The present findings are in close proximity with those of Hanchinamani and Patil (2009), Kumar et al. (2010), Kushwaha et al. (2011), Mule et al. (2012), Airina et al. (2013), Jat et al. (2015), Arya and Singh (2016), Sharma et al. (2016), Singh et al. (2016b), Punetha et al. (2017b), Kumari et al. (2018), Malav et al. (2018), Preethi et al. (2019), Arab et al. (2020) and Umeh et al. (2021) who observed desirable heterosis for marketable yield per metre square for various hybrids.

11. Harvest duration (days)

The magnitude of heterosis over better parent and standard check ranged from -8.06 ($P_3 \times P_5$) to 36.29 per cent ($P_3 \times P_6$) and -12.98 ($P_3 \times P_5$) to 32.06 per cent ($P_2 \times P_8$) in 2020, -5.31 ($P_3 \times P_5$) to 46.90 per cent ($P_3 \times P_6$) and -10.08 ($P_3 \times P_5$) to 39.50 per cent ($P_3 \times P_6$) in 2021 and -6.75 ($P_3 \times P_5$) to 41.35 per cent ($P_3 \times P_6$) and -11.60 ($P_3 \times P_5$) to 34.80 per cent ($P_2 \times P_8$) in pooled over environments, respectively (Table 4.30). The significant positive heterosis over better parent was observed in 15 crosses in 2020, 20 crosses in 2021 and 23 crosses in pooled over environments. A total of 16 crosses in 2020, 18 crosses in 2021 and 20 crosses in pooled over environments exhibited economic heterosis for this trait. Out of these, $P_3 \times P_6$ (41.35%), $P_4 \times P_6$ (39.57%), $P_2 \times P_8$ (38.11%), $P_2 \times P_7$ (36.89%) and $P_2 \times P_6$ (34.84%) in pooled over environments were top heterotic combinations over better parent while, $P_2 \times P_8$ (34.80%), $P_3 \times P_6$ (34.00%), $P_2 \times P_7$ (33.60%), $P_2 \times P_6$ (31.60%) and $P_4 \times P_6$ (31.20%) expressed high economic heterosis for harvest duration. The

present findings are in agreement with those of Kumar et al. (2016) who revealed hybrid vigour in different cross combinations for harvest duration.

12. Internodal length (cm)

The perusal of data (Table 4.30) revealed that magnitude of heterosis over better parent and standard check ranged from -26.38 ($P_4 \times P_8$) to 3.58 per cent ($P_2 \times P_6$) and -12.47 ($P_4 \times P_8$) to 33.31 per cent ($P_5 \times P_7$) in 2020, -25.17 ($P_3 \times P_6$) to 0.71 per cent ($P_2 \times P_3$) and -2.96 ($P_3 \times P_7$) to 32.91 per cent ($P_5 \times P_7$) in 2021 and -27.49 ($P_5 \times P_8$) to -1.44 per cent ($P_5 \times P_7$) and -9.14 ($P_4 \times P_8$) to 31.26 per cent ($P_5 \times P_7$) in pooled over environments, respectively. As many as, 12, 9 and 17 crosses in 2020, 2021 and pooled over environments expressed significant negative heterosis over better parent, respectively while, none of cross combination in all the environments exhibited economic heterosis. Hybrid $P_5 \times P_8$ (-27.49%), $P_3 \times P_5$ (-26.27%), $P_3 \times P_6$ (-23.46%), $P_2 \times P_5$ (-22.44%) and $P_4 \times P_8$ (-21.58%) revealed heteobeltiosis while, none of hybrid combination showed economic heterosis for internodal length in pooled over environments. The results are in line with those of Golabadi et al. (2015) and Punetha et al. (2017b) who have also reported significant heterosis for internodal length in their respective studies.

13. Vine length (m)

Among 28 cross combinations, 16 crosses showed both heteobeltiosis and economic heterosis for vine length in pooled over environments (Table 4.31). The perusal of data revealed that extent of heterosis varied from -22.41 ($P_7 \times P_8$) to 25.01 per cent ($P_2 \times P_7$) and -17.90 ($P_7 \times P_8$) to 23.35 per cent ($P_2 \times P_7$) in 2020, -19.77 ($P_7 \times P_8$) to 24.50 per cent ($P_6 \times P_7$) and -19.65 ($P_7 \times P_8$) to 21.19 per cent ($P_4 \times P_8$) in 2021 and -21.10 ($P_7 \times P_8$) to 24.68 per cent ($P_6 \times P_7$) and -18.79 ($P_7 \times P_8$) to 21.58 per cent ($P_4 \times P_8$) in pooled over environments over better parent and standard check, respectively. Out of 28 hybrids, $P_6 \times P_7$ (24.68%), $P_2 \times P_7$ (22.79%), $P_3 \times P_6$ (22.48%), $P_1 \times P_4$ (19.62%) and $P_2 \times P_4$ (18.57%) were the top heterotic combinations revealing heteobeltiosis. Hybrid combinations namely, $P_4 \times P_8$ (21.58%), $P_2 \times P_7$

Table 4.30: Estimates of heterosis (%) for marketable yield per meter square (kg), harvest duration (days) and internodal length (cm) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Marketable yield per meter square (kg)						Harvest duration (days)						Internodal length (cm)					
	2020		2021		pooled		2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-22.38*	-14.66*	-20.95*	-23.37*	-17.39*	-14.89*	-4.26	3.05	-3.13	4.20	-3.72	3.60	-14.64*	-1.89	-9.73	2.87	-15.89*	-2.32
P ₁ × P ₃	10.57	-3.67	-16.61*	-24.82*	15.15*	2.16	2.13	9.92	0.00	7.56	1.12	8.80*	-2.64	11.90	-5.78	7.37	-7.76	7.13
P ₁ × P ₄	28.44*	11.90*	3.79	-6.42	15.71*	2.65	19.15*	28.24*	20.31*	29.41*	19.70*	28.80*	-6.10	11.63	-7.73	5.15	-6.11	9.04
P ₁ × P ₅	5.47	0.85	15.65*	4.27	26.01*	11.79*	2.13	9.92	13.28*	21.85*	7.43*	15.60*	-4.55	23.70*	-7.44	25.53*	-7.57	23.09*
P ₁ × P ₆	34.33*	17.04*	18.89*	7.19	30.16*	15.47*	6.38	14.50*	17.19*	26.05*	11.52*	20.00*	-15.82*	7.82	-18.66*	10.55	-17.95*	8.13
P ₁ × P ₇	8.84	16.15*	27.43*	14.89*	28.10*	23.48*	12.06*	20.61*	4.69	12.61*	8.55*	16.80*	-4.17	10.15	-3.41	10.07	-7.24	7.73
P ₁ × P ₈	50.24*	30.89*	29.71*	16.94*	22.88*	9.02*	8.51	16.79*	7.81	15.97*	8.18*	16.40*	-1.44	13.28*	-1.64	12.08	-5.35	9.92
P ₂ × P ₃	3.37	13.65*	8.27	4.97	31.75*	35.74*	26.92*	25.95*	33.33*	27.73*	29.92*	26.80*	-2.45	11.53	0.71	12.43	-4.79	7.53
P ₂ × P ₄	28.97*	41.79*	34.54*	30.44*	31.75*	35.74*	24.62*	23.66*	42.98*	36.97*	33.20*	30.00*	-11.83*	4.82	-8.17	4.01	-11.66*	2.35
P ₂ × P ₅	28.05*	40.78*	30.50*	26.52*	29.27*	33.17*	25.38*	24.43*	40.35*	34.45*	32.38*	29.20*	-17.14*	7.38	-19.65*	8.96	-22.44*	3.29
P ₂ × P ₆	24.06*	36.39*	28.56*	24.63*	26.31*	30.13*	30.77*	29.77*	39.47*	33.61*	34.84*	31.60*	3.58	32.67*	-4.03	30.45*	-2.27	28.81*
P ₂ × P ₇	30.62*	43.60*	41.65*	37.32*	36.13*	40.25*	30.00*	29.01*	44.74*	38.66*	36.89*	33.60*	-11.77*	0.88	-4.47	6.64	-9.82*	1.85
P ₂ × P ₈	31.82*	44.92*	4.04	0.87	32.90*	36.92*	33.08*	32.06*	43.86*	37.82*	38.11*	34.80*	-8.94	4.11	-6.18	4.74	-10.06*	1.58
P ₃ × P ₄	65.64*	-4.27	86.58*	29.89*	53.71*	-1.57	15.87*	11.45*	28.32*	21.85*	22.78*	16.40*	-9.42	7.69	-6.15	6.30	-10.01*	4.27
P ₃ × P ₅	18.00*	12.82*	21.88*	-2.08	19.91*	4.90	-8.06	-12.98*	-5.31	-10.08*	-6.75*	-11.60*	-23.36*	-0.67	-21.67*	6.23	-26.27*	-1.82
P ₃ × P ₆	-14.34*	-28.58*	-2.93	-25.43*	-8.52	-26.93*	36.29*	29.01*	46.90*	39.50*	41.35*	34.00*	-20.43*	1.92	-25.17*	1.72	-23.46*	0.87
P ₃ × P ₇	-19.79*	-14.40*	-13.63*	-24.62*	-16.82*	-19.82*	14.17*	10.69*	18.58*	12.61*	17.23*	11.60*	-10.43	-0.44	-12.23	-2.96	-11.02*	-3.66
P ₃ × P ₈	21.91*	-17.88*	3.93	-22.80*	11.95*	-20.50*	9.68	3.82	12.39*	6.72	10.97*	5.20	-9.25	-0.07	-9.40	0.16	-11.70*	-4.40
P ₄ × P ₅	-10.38	-14.31*	13.29*	-8.99	1.17	-11.49*	3.17	-0.76	7.34	-1.68	5.11	-1.20	-4.24	24.11*	-13.14*	17.80*	-10.12*	19.70*
P ₄ × P ₆	14.45*	-4.57	5.64	-18.85*	9.98*	-12.15*	35.71*	30.53*	44.04*	31.93*	39.57*	31.20*	-3.37	23.77*	-8.11	24.91*	-5.66	24.34*
P ₄ × P ₇	-9.16	-3.05	3.06	-10.06	-3.30	-6.79	23.62*	19.85*	37.84*	28.57*	30.25*	24.00*	-8.96	8.23	-2.82	10.07	-6.24	8.64
P ₄ × P ₈	22.67*	-17.38*	-5.84	-30.05*	6.87	-24.10*	10.32	6.11	13.76*	4.20	11.91*	5.20	-26.38*	-12.47	-13.31	-1.81	-21.58*	-9.14
P ₅ × P ₆	-28.45*	-31.59*	-6.33	-24.75*	-17.65*	-27.96*	10.00	-7.63	3.70	-5.88	6.88*	-6.80*	-13.45*	12.17	-19.00*	10.10	-18.63*	8.37
P ₅ × P ₇	-15.45*	-9.77*	-6.02	-17.98*	-10.93*	-14.15*	7.87	4.58	16.22*	8.40	11.76*	6.40*	2.86	33.31*	-1.99	32.91*	-1.44	31.26*
P ₅ × P ₈	0.08	-4.31	-0.21	-19.83*	-0.02	-12.54*	3.64	-12.98*	2.78	-6.72	3.21	-10.00*	-22.29*	0.71	-21.85*	5.98	-27.49*	-3.43
P ₆ × P ₇	-22.97*	-17.79*	-15.96*	-26.65*	-19.59*	-22.49*	17.32*	13.74*	24.32*	15.97*	20.59*	14.80*	-15.48*	8.26	-21.83*	6.26	-22.21*	2.52
P ₆ × P ₈	30.05*	8.43	27.90*	-1.75	28.98*	3.02	17.43*	-2.29	12.50*	-1.68	14.49*	-2.00	-16.95*	6.37	-17.03*	12.79	-21.27*	3.76
P ₇ × P ₈	-2.20	4.37	8.50	-5.30	2.94	-0.78	10.24	6.87	22.52*	14.29*	15.97*	10.40*	-3.31	7.48	-4.17	5.95	-3.81	3.46

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

(19.84%), $P_6 \times P_7$ (18.94%), $P_1 \times P_4$ (17.38%) and $P_6 \times P_7$ (18.94%) were the top ranking hybrids showing economic heterosis. Significant heterosis for vine length reported by Bairagi et al. (2005), Singh et al. (2010), Mule et al. (2012), Tiwari and Singh (2016), Manggoel et al. (2021) and Umeh et al. (2021).

14. Flesh to seed cavity ratio

For flesh to seed cavity ratio, heterosis over better parent and standard check ranged from -19.76 ($P_6 \times P_8$) to 18.08 per cent ($P_3 \times P_4$) and -9.71 ($P_4 \times P_8$ and $P_5 \times P_7$) to 29.81 per cent ($P_2 \times P_6$) in 2020, -15.15 ($P_5 \times P_7$) to 22.22 per cent ($P_1 \times P_3$) and -13.81 ($P_5 \times P_7$) to 12.24 per cent ($P_1 \times P_3$) in 2021 and -16.90 ($P_5 \times P_7$) to 17.61 per cent ($P_1 \times P_3$) and -11.70 ($P_5 \times P_7$) to 19.93 per cent ($P_2 \times P_6$) in pooled over environments, respectively (Table 4.31). As many as, 4 crosses in 2020, 3 crosses in 2021 and 5 crosses in pooled over environments exhibited significant heterosis over better parent. Out of 28 hybrid combinations, 10, 1 and 7 crosses revealed economic heterosis for this trait in 2020, 2021 and pooled over environments, respectively. The top heterotic combinations over better parent were $P_1 \times P_3$ (17.61%), $P_3 \times P_4$ (15.96%), $P_1 \times P_4$ (11.79%) and $P_2 \times P_6$ (9.80%) for flesh to seed cavity ratio. Hybrid $P_2 \times P_6$ (19.93%), $P_1 \times P_3$ (16.64%), $P_4 \times P_5$ (12.85%), $P_2 \times P_8$ (11.70%) and $P_1 \times P_4$ (10.87%) revealed high economic heterosis. The results are in consonance with earlier studies of Dogra and Kanwar (2011), Kaur et al. (2016) and Thapliyal (2017) who revealed significant heterosis for flesh to seed cavity ratio in their respective studies.

15. Flesh thickness (mm)

A total of 1 cross, 5 crosses and 3 crosses exhibited higher heterosis over better parent in 2020, 2021 and pooled over environments, respectively (Table 4.31). The magnitude of heterosis ranged from -8.86 ($P_3 \times P_6$) to 17.22 per cent ($P_3 \times P_4$) and 2.29 ($P_3 \times P_7$) to 36.26 per cent ($P_4 \times P_6$) in 2020, -19.10 ($P_4 \times P_5$) to 27.46 per cent ($P_3 \times P_7$) and -17.45 ($P_6 \times P_7$) to 11.74 per cent ($P_4 \times P_6$) in 2021 and -7.79 ($P_2 \times P_5$) to 17.34 per cent ($P_1 \times P_2$) and -0.71 ($P_6 \times P_7$)

Table 4.31: Estimates of heterosis (%) for vine length (m), flesh to seed cavity ratio and flesh thickness (mm) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Vine length (m)						Flesh to seed cavity ratio						Flesh thickness (mm)					
	2020		2021		pooled		2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	6.52*	5.10*	10.05*	6.26*	8.30*	5.69*	-18.22*	-7.45	-10.02	-9.73	-13.93*	-8.40*	15.81	28.63*	20.80*	1.34	17.34*	13.17*
P ₁ × P ₃	18.46*	8.55*	10.66*	1.22	14.49*	4.82*	13.31*	20.97*	22.22*	12.24*	17.61*	16.64*	7.42	16.03	9.64	-8.39	7.87	2.49
P ₁ × P ₄	19.60*	17.48*	19.64*	17.28*	19.62*	17.38*	14.94*	22.70*	8.72	-0.16	11.79*	10.87*	10.26	27.10*	-8.96	2.35	0.31	13.88*
P ₁ × P ₅	-20.57*	-17.51*	-13.27*	-15.82*	-16.98*	-16.65*	-10.44*	-0.35	0.15	1.73	-5.12	0.82	3.26	20.99*	-9.42	-6.38	-3.25	6.05
P ₁ × P ₆	20.49*	10.42*	11.01*	1.55	15.67*	5.90*	-5.09	9.88	-10.96*	-8.16	-2.11	6.92	7.91	30.15*	15.64*	6.71	11.49*	17.44*
P ₁ × P ₇	10.52*	5.68*	9.35*	4.07	9.93*	4.86*	-8.77	-2.60	2.91	-5.49	-3.16	-3.95	9.09	19.08	7.63	-10.07	8.24	2.85
P ₁ × P ₈	-9.86*	-4.61	-11.85*	-11.72*	-10.84*	-8.23*	8.28	15.60*	-1.20	-9.26	3.65	2.80	10.06	33.59*	11.64*	9.40	10.49*	19.93*
P ₂ × P ₃	4.54	3.15	-1.09	-4.49	1.70	-0.74	0.92	14.21*	1.72	2.04	1.39	7.91*	7.90	19.85*	11.60	-6.38	9.23	5.34
P ₂ × P ₄	19.50*	17.90*	17.16*	14.85*	18.57*	16.35*	-8.73	3.29	0.31	0.63	-4.02	2.14	14.24	31.68*	-0.90	11.41*	6.27	20.64*
P ₂ × P ₅	-4.84*	-1.17	1.07	-1.90	-1.93	-1.54	-3.37	9.36	2.01	3.61	0.00	6.43	2.28	19.85*	-16.88*	-14.09*	-7.79	1.07
P ₂ × P ₆	1.67	0.31	3.04	-0.51	2.36	-0.10	12.13*	29.81*	7.61	10.99	9.80*	19.93*	-5.70	13.74	14.55*	5.70	3.72	9.25
P ₂ × P ₇	25.01*	23.35*	20.61*	16.46*	22.79*	19.84*	-18.68*	-7.97	-9.08	-8.79	-13.78*	-8.24*	5.50	17.18	2.40	-14.09*	3.32	-0.36
P ₂ × P ₈	2.58	8.54*	7.93*	8.09*	5.23*	8.31*	3.83	17.50*	5.95	6.28	4.95	11.70*	6.29	29.01*	-2.05	-4.03	2.30	11.03*
P ₃ × P ₄	6.29*	4.41	7.53*	5.42	6.92*	4.92*	18.08*	8.67	12.91*	-2.51	15.96*	2.97	17.22*	35.11*	-4.48	7.38	5.33	19.57*
P ₃ × P ₅	-8.36*	-4.82*	-7.58*	-10.29*	-7.97*	-7.61*	-0.31	10.92	-3.40	-1.88	-1.86	4.28	8.47	27.10*	-0.00	3.36	3.90	13.88*
P ₃ × P ₆	23.19*	10.79*	21.81*	10.64*	22.48*	10.72*	4.64	21.14*	-8.22	-5.34	-1.66	7.41	-8.86	9.92	4.73	-3.36	-2.70	2.49
P ₃ × P ₇	20.75*	15.47*	12.47*	7.04*	16.55*	11.18*	10.44	8.15	8.48	-1.57	9.44*	3.13	-6.29	2.29	27.46*	4.36	9.43	3.20
P ₃ × P ₈	6.37*	12.55*	9.50*	9.66*	7.92*	11.08*	-12.03*	-6.24	11.27	-3.92	-0.35	-4.94	3.77	25.95*	-3.77	-5.70	0.00	8.54
P ₄ × P ₅	7.65*	11.80*	5.45*	3.38	7.08*	7.51*	9.19	21.49*	3.09	4.71	6.20	12.85*	4.89	22.90*	-19.10*	-9.06	-7.21	5.34
P ₄ × P ₆	-9.11*	-10.72*	-8.82*	-10.61*	-8.96*	-10.66*	-6.59	8.15	1.52	4.71	-2.41	6.59	12.97	36.26*	-0.60	11.74*	7.84	22.42*
P ₄ × P ₇	0.45	-1.33	-4.57	-6.44*	-2.10	-3.93*	3.54	1.39	7.27	-2.67	5.42	-0.66	10.93	27.86*	-2.09	10.07	3.76	17.79*
P ₄ × P ₈	15.29*	21.99*	21.01*	21.19*	18.12*	21.58*	-15.28*	-9.71	10.09	-5.81	-3.11	-7.58	-1.89	19.08	-5.97	5.70	-1.88	11.39*
P ₅ × P ₆	-16.69*	-13.48*	-14.91*	-17.40*	-15.81*	-15.48*	-2.25	13.17*	-8.22	-5.34	-5.28	3.46	5.38	27.10*	0.65	4.03	3.90	13.88*
P ₅ × P ₇	-12.53*	-9.15*	-12.40*	-14.96*	-12.46*	-12.11*	-18.85*	-9.71	-15.15*	-13.81*	-16.90*	-11.70*	5.21	23.28*	-11.69*	-8.72	-3.25	6.05
P ₅ × P ₈	13.46*	20.06*	14.42*	14.59*	13.94*	17.28*	-15.89*	-6.41	-0.15	1.41	-7.91*	-2.14	7.23	30.15*	-5.19	-2.01	2.60	12.46*
P ₆ × P ₇	24.86*	19.40*	24.50*	18.49*	24.68*	18.94*	-2.10	13.34*	1.52	4.71	-0.30	8.90*	-1.27	19.08	-10.55	-17.45*	-5.74	-0.71
P ₆ × P ₈	-9.64*	-4.39	-10.04*	-9.90*	-9.84*	-7.20*	-19.76*	-7.11	-6.09	-3.14	-12.97*	-4.94	3.77	25.95*	-7.88	-9.73	-1.97	6.41
P ₇ × P ₈	-22.41*	-17.90*	-19.77*	-19.65*	-21.10*	-18.79*	-10.08	-4.16	14.53*	3.92	-1.73	-6.26	5.35	27.86*	9.93	7.72	7.54	16.73*

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

to 22.42 per cent ($P_4 \times P_6$) in pooled over environments over better parent and standard check, respectively. Hybrid combinations $P_1 \times P_2$ (17.34%) and $P_1 \times P_6$ (11.49%) revealed maximum heterobeltiosis for flesh thickness in pooled over environments. The top most economic heterotic combinations were $P_4 \times P_6$ (22.42%), $P_2 \times P_4$ (20.64%), $P_1 \times P_8$ (19.93%), $P_3 \times P_4$ (19.57%) and $P_4 \times P_7$ (17.79%). Munshi et al. (2006), Simi et al. (2017) and Arab et al. (2020) reported hybrid vigour for flesh thickness in their respective studies.

16. Total soluble sugars ($^{\circ}$ Brix)

The magnitude of heterosis varied from -49.72 ($P_2 \times P_8$) to 63.39 per cent ($P_2 \times P_7$) and -10.92 ($P_2 \times P_8$) to 89.50 per cent ($P_4 \times P_8$) in 2020, -46.08 ($P_1 \times P_8$) to 70.47 per cent ($P_2 \times P_7$) and -6.30 ($P_1 \times P_8$) to 89.00 per cent ($P_4 \times P_8$) in 2021 and -47.54 ($P_2 \times P_8$) to 66.98 per cent ($P_2 \times P_7$) and -7.86 ($P_2 \times P_8$) to 89.33 per cent ($P_4 \times P_8$) in pooled over environments over better parent and standard check, respectively (Table 4.32). As many as, 11 crosses each in 2020 and 2021 and 12 crosses in pooled over environments revealed heterobeltiosis while, 22 crosses expressed economic heterosis in all environments. Hybrid combination $P_2 \times P_7$ (66.98%), $P_2 \times P_3$ (46.42%), $P_4 \times P_7$ (41.24%), $P_3 \times P_7$ (39.81%) and $P_1 \times P_4$ (37.19%) were the promising combinations exhibiting heterobeltiosis for total soluble sugars in pooled over environments. The top ranking economic heterotic combinations were $P_4 \times P_8$ (89.33%), $P_6 \times P_7$ (86.30%), $P_2 \times P_7$ (81.54%) and $P_4 \times P_7$ (81.25%) in pooled analysis. These results are in conformity to the earlier findings of Dogra and Kanwar (2011), Kaur et al. (2016), Sharma et al. (2016), Malav et al. (2018) and Kumar et al. (2021) who observed positive heterosis for total soluble sugars.

Table 4.32: Estimates of heterosis (%) for total soluble solids (⁰B) and ascorbic acid (mg/100g) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Total Soluble Solids (⁰ B)						Ascorbic acid (mg/100g)					
	2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-15.21 *	0.43	-23.73 *	-2.93	-19.58 *	-1.08	4.48 *	12.17 *	-3.52 *	5.60 *	0.43	8.89 *
P ₁ × P ₃	32.34 *	56.74 *	32.83 *	69.06 *	32.47 *	62.94 *	2.21 *	9.73 *	-3.52 *	12.26 *	2.39 *	11.01 *
P ₁ × P ₄	37.60 *	77.02 *	36.70 *	74.78 *	37.19 *	76.06 *	-5.14 *	1.84 *	-12.16 *	-3.85 *	-8.69 *	-1.00 *
P ₁ × P ₅	-7.61 *	37.73 *	-1.85	48.09 *	-4.71 *	43.04 *	-17.92 *	-6.23 *	-14.88 *	-6.83 *	-15.48 *	-6.47 *
P ₁ × P ₆	-30.47 *	0.00	-26.97 *	0.44	-28.76 *	0.36	-0.44	6.88 *	-6.56 *	2.28 *	-3.53 *	4.59 *
P ₁ × P ₇	-4.67 *	12.91 *	-4.03	22.14 *	-4.45 *	17.52 *	11.28 *	19.47 *	2.93 *	12.67 *	7.06 *	16.07 *
P ₁ × P ₈	-46.84 *	-5.82 *	-46.08 *	-6.30 *	-46.47 *	-5.98 *	-20.20 *	-7.18 *	-13.00 *	-3.85 *	-16.66 *	-5.47 *
P ₂ × P ₃	47.11 *	59.01 *	45.64 *	59.09 *	46.42 *	59.19 *	-11.55 *	-6.82 *	-10.41 *	-11.03 *	-10.98 *	-8.89 *
P ₂ × P ₄	-14.66 *	9.79 *	-8.72 *	16.72 *	-11.69 *	13.34 *	6.96 *	4.93 *	20.00 *	8.23 *	13.25 *	6.65 *
P ₂ × P ₅	-15.22 *	26.38 *	-17.88 *	23.90 *	-16.52 *	25.31 *	-14.08 *	-1.84 *	-5.40 *	1.23 *	-9.84 *	-0.24
P ₂ × P ₆	-28.80 *	2.41	-29.74 *	-3.37	-29.27 *	-0.36	4.60 *	2.61 *	15.53 *	4.20 *	9.87 *	3.47 *
P ₂ × P ₇	63.39 *	76.60 *	70.47 *	86.22 *	66.98 *	81.54 *	-8.59 *	-10.33 *	-11.58 *	-15.76 *	-7.63 *	-13.01 *
P ₂ × P ₈	-49.72 *	-10.92 *	-45.15 *	-4.69	-47.54 *	-7.86 *	-27.19 *	-15.31 *	-21.87 *	-13.66 *	-24.55 *	-14.42 *
P ₃ × P ₄	-16.54 *	7.38 *	-9.52 *	15.69 *	-13.15 *	11.46 *	-14.42 *	-9.85 *	-12.70 *	-13.31 *	-13.57 *	-11.54 *
P ₃ × P ₅	3.24	53.90 *	3.50	56.16 *	3.27 *	55.01 *	-18.23 *	-6.59 *	-12.60 *	-6.48 *	-15.48 *	-6.47 *
P ₃ × P ₆	22.09 *	75.60 *	28.04 *	76.10 *	24.97 *	76.06 *	-19.77 *	-15.49 *	-16.75 *	-17.34 *	-18.34 *	-16.42 *
P ₃ × P ₇	36.06 *	46.10 *	43.40 *	54.55 *	39.81 *	50.40 *	-5.75 *	-0.71	-7.94 *	-8.58 *	-6.84 *	-4.65 *
P ₃ × P ₈	-17.29 *	46.52 *	-17.72 *	42.96 *	-17.57 *	44.77 *	-31.89 *	-20.77 *	-25.36 *	-17.51 *	-28.65 *	-19.07 *
P ₄ × P ₅	-24.83 *	12.06 *	-27.11 *	9.97 *	-25.94 *	11.18 *	2.96 *	17.63 *	6.06 *	13.49 *	4.47 *	15.60 *
P ₄ × P ₆	7.10 *	54.04 *	21.32 *	66.86 *	13.92 *	60.49 *	3.89 *	-6.59 *	-5.88 *	-18.74 *	1.37 *	-12.71 *
P ₄ × P ₇	40.90 *	81.28 *	41.74 *	81.23 *	41.24 *	81.25 *	-9.34 *	-16.44 *	-12.32 *	-16.46 *	-10.86 *	-16.42 *
P ₄ × P ₈	6.97 *	89.50 *	8.78 *	89.00 *	7.80 *	89.33 *	-15.82 *	-2.08 *	-16.01 *	-7.18 *	-15.88 *	-4.59 *
P ₅ × P ₆	10.47 *	64.68 *	9.43 *	65.10 *	9.99 *	65.10 *	-24.47 *	-13.71 *	-18.00 *	-12.26 *	-21.33 *	-12.95 *
P ₅ × P ₇	-9.04 *	35.60 *	-10.88 *	34.46 *	-9.99 *	35.11 *	-5.56 *	7.89 *	4.26 *	11.56 *	-0.80 *	9.77 *
P ₅ × P ₈	-11.53 *	56.74 *	-4.98 *	65.10 *	-8.37 *	60.92 *	-14.95 *	-1.07	-10.78 *	-1.40 *	-12.92 *	-1.24 *
P ₆ × P ₇	28.21 *	84.40 *	36.78 *	88.12 *	32.24 *	86.30 *	-7.98 *	-15.19 *	-16.91 *	-20.84 *	-12.55 *	-18.01 *
P ₆ × P ₈	-45.88 *	-4.11	-41.35 *	1.91	-43.68 *	-1.08	-8.88 *	5.99 *	-3.33 *	6.83 *	-6.18 *	6.42 *
P ₇ × P ₈	-31.47 *	21.42 *	-31.48 *	19.06 *	-31.44 *	20.40 *	-1.17	14.96 *	-1.43 *	8.93 *	-1.30 *	11.95 *

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

17. Ascorbic acid (mg/100g)

The magnitude of heterosis ranged from -31.89 ($P_3 \times P_8$) to 11.28 per cent ($P_1 \times P_7$) and -20.77 ($P_3 \times P_8$) to 19.47 per cent ($P_1 \times P_7$) in 2020, -25.36 ($P_3 \times P_8$) to 20.00 per cent ($P_2 \times P_4$) and -20.84 ($P_6 \times P_7$) to 13.49 per cent ($P_4 \times P_5$) in 2021 and -28.65 ($P_3 \times P_8$) to 13.25 per cent ($P_2 \times P_4$) and -19.07 ($P_3 \times P_8$) to 16.07 per cent ($P_1 \times P_7$) in pooled over environments, over better parent and standard check, respectively (Table 4.32). A total of 7, 5 and 6 crosses showed significant positive heterosis over better parent whereas, 11 crosses each in 2020 and 2021 and 10 crosses in pooled over environments expressed significant positive heterosis over standard check. Hybrid $P_2 \times P_3$ (13.25%), $P_2 \times P_6$ (9.87%), $P_1 \times P_7$ (7.06%), $P_4 \times P_5$ (4.47%) and $P_1 \times P_3$ (2.39%) were the top most economic heterotic combinations in pooled over environments. The best combinations revealing economic heterosis were $P_1 \times P_7$ (16.07%), $P_4 \times P_5$ (15.60%), $P_7 \times P_8$ (11.95%), $P_1 \times P_3$ (11.01%) and $P_5 \times P_7$ (9.77%) for ascorbic acid in pooled analysis. Similarly, Kaur et al. (2016) also revealed desirable heterosis for ascorbic acid

18. Total sugar (%)

For total sugar, heterosis ranged from -25.42 ($P_6 \times P_7$) to 26.00 per cent ($P_2 \times P_3$) and -21.88 ($P_6 \times P_7$) to 14.99 per cent ($P_1 \times P_7$, $P_2 \times P_3$) in 2020, -38.73 ($P_6 \times P_7$) to 17.58 per cent ($P_2 \times P_6$) and -23.84 ($P_4 \times P_5$) to 24.56 per cent ($P_2 \times P_6$) in 2021 and -32.40 ($P_6 \times P_7$) to 22.92 per cent ($P_2 \times P_6$) and -22.70 ($P_6 \times P_7$) to 17.45 per cent ($P_1 \times P_3$) in pooled over environments over better parent and standard check, respectively (Table 4.33). As many as, 4 crosses, 7 crosses and 3 crosses revealed significant positive heterotic effects on better parent in 2020, 2021 and pooled over environments. The economic heterosis was observed in 4 crosses in 2020, 7 crosses each in 2021 and pooled over environments. Hybrid $P_2 \times P_6$ (22.92%) and $P_2 \times P_3$ (16.48%) exhibited significant desirable heterosis over better parent while, $P_1 \times P_3$ (17.45%), $P_2 \times P_6$ (16.17%), $P_2 \times P_3$ (14.30%), $P_1 \times P_7$ (13.14%) and $P_6 \times P_8$ (5.12%) were the top economic heterotic combinations in pooled over environments.

Table 4.33: Estimates of heterosis (%) for total sugar (%) and reducing sugar (%) over better parent (BP) and standard check (SC) in cucumber during 2020, 2021 and pooled over environments

Crosses	Total sugar (%)						Reducing sugar (%)					
	2020		2021		pooled		2020		2021		pooled	
	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC	BP	SC
P ₁ × P ₂	-21.71 *	-17.13 *	-4.68 *	0.97	-10.78 *	-8.43 *	-52.58 *	-32.73 *	-48.16 *	-31.87 *	-50.34 *	-32.27 *
P ₁ × P ₃	5.17 *	11.33 *	17.55 *	24.08 *	14.44 *	17.45 *	-12.82 *	23.70 *	-33.40 *	-12.47 *	-23.29 *	4.61
P ₁ × P ₄	-2.76	2.93	7.32 *	6.40 *	1.92	4.60 *	80.69 *	156.36 *	51.55 *	99.19 *	65.86 *	126.18 *
P ₁ × P ₅	-12.76 *	-7.65 *	10.48 *	13.56 *	-1.77	2.54	124.31 *	218.24 *	72.04 *	126.12 *	97.71 *	169.61 *
P ₁ × P ₆	-22.75 *	-18.23 *	5.02 *	4.12	-9.86 *	-7.49 *	7.69 *	52.79 *	-48.54 *	-32.36 *	-20.92 *	7.84 *
P ₁ × P ₇	8.63 *	14.99 *	-10.87 *	11.14 *	-1.05	13.14 *	-52.58 *	-32.73 *	-45.86 *	-28.83 *	-49.16 *	-30.67 *
P ₁ × P ₈	-21.16 *	-6.18 *	-10.88 *	7.99 *	-16.18 *	0.63	73.00 *	145.45 *	36.74 *	79.73 *	54.55 *	110.76 *
P ₂ × P ₃	26.00 *	14.99 *	7.19 *	13.56 *	16.48 *	14.30 *	-3.96	30.97 *	46.61 *	48.83 *	19.02 *	40.40 *
P ₂ × P ₄	1.74	-14.59 *	-22.96 *	-18.39 *	-11.56 *	-16.41 *	53.33 *	109.09 *	31.82 *	33.82 *	43.56 *	69.36 *
P ₂ × P ₅	-1.38	4.39	-0.47	5.44 *	0.49	4.89 *	80.00 *	145.45 *	76.99 *	79.67 *	78.63 *	110.73 *
P ₂ × P ₆	18.81 *	8.42 *	17.58 *	24.56 *	22.92 *	16.17 *	13.33 *	54.55 *	14.74 *	16.48 *	13.97 *	34.45 *
P ₂ × P ₇	-3.84	0.73	-18.75 *	1.32	-11.65 *	1.01	-16.00 *	14.55 *	-6.41 *	-4.99	-11.64 *	4.23
P ₂ × P ₈	-15.63 *	0.39	-23.77 *	-7.62 *	-19.58 *	-3.46	-36.00 *	-12.73 *	-15.70 *	-14.42 *	-26.78 *	-13.62 *
P ₃ × P ₄	-10.00 *	-17.86 *	-9.39 *	-4.36	-9.68 *	-11.37 *	257.14 *	127.27 *	307.28 *	69.76 *	278.34 *	96.91 *
P ₃ × P ₅	-9.66 *	-4.37	-16.39 *	-11.74 *	-11.78 *	-7.91 *	148.57 *	58.18 *	186.61 *	19.46 *	164.65 *	37.74 *
P ₃ × P ₆	-12.81 *	-20.43 *	-26.47 *	-22.39 *	-19.87 *	-21.37 *	291.52 *	149.15 *	308.73 *	82.76 *	299.09 *	114.11 *
P ₃ × P ₇	-20.91 *	-17.14 *	-18.36 *	1.80	-19.57 *	-8.04 *	27.94 *	58.18 *	39.26 *	21.90 *	32.94 *	39.03 *
P ₃ × P ₈	-23.71 *	-9.22 *	-12.39 *	6.16 *	-18.22 *	-1.83	174.29 *	74.55 *	243.00 *	44.82 *	205.22 *	58.86 *
P ₄ × P ₅	-22.49 *	-17.96 *	-25.91 *	-23.84 *	-24.11 *	-20.78 *	813.11 *	149.03 *	470.65 *	81.25 *	619.40 *	113.25 *
P ₄ × P ₆	-5.60 *	-13.86 *	7.90 *	1.22	3.11	-20.78 *	228.67 *	109.15 *	378.91 *	114.15 *	294.77 *	113.25 *
P ₄ × P ₇	-18.46 *	-14.58 *	-18.06 *	2.17	-18.25 *	-6.53 *	10.29 *	36.36 *	11.46 *	-2.44	10.81 *	15.88 *
P ₄ × P ₈	-14.71 *	1.48	-18.68 *	-1.46	-16.64 *	0.07	8.92	-32.67 *	55.58 *	-34.31 *	29.13 *	-33.53 *
P ₅ × P ₆	-15.52 *	-10.57 *	2.22	5.07 *	-7.13 *	-3.06	-51.43 *	-69.09 *	-65.70 *	-84.66 *	-57.71 *	-77.31 *
P ₅ × P ₇	-10.68 *	-5.45 *	-14.96 *	6.04 *	-12.48 *	0.07	130.88 *	185.45 *	146.87 *	116.10 *	137.95 *	148.84 *
P ₅ × P ₈	-24.24 *	-9.86 *	-29.90 *	-15.06 *	-26.99 *	-12.35 *	244.02 *	112.67 *	247.75 *	46.83 *	245.64 *	77.91 *
P ₆ × P ₇	-25.42 *	-21.88 *	-38.73 *	-23.60 *	-32.40 *	-22.70 *	27.94 *	58.18 *	39.32 *	21.95 *	32.97 *	39.06 *
P ₆ × P ₈	-12.57 *	4.04	-12.30 *	6.28 *	-12.44 *	5.12 *	285.71 *	145.45 *	347.76 *	100.22 *	313.01 *	39.06 *
P ₇ × P ₈	-21.17 *	-6.19 *	-28.45 *	-10.78 *	-23.69 *	-8.40 *	54.41 *	90.91 *	56.41 *	36.91 *	55.29 *	39.06 *

*Significant at 5% level of significance

P₁: DDPCG4, P₂: DDPCG1, P₃: Punjab Kheera-1 (PK-1), P₄: Pant Parthenocarpic cucumber-2 (PPC-2), P₅: Pant Parthenocarpic cucumber-3 (PPC-3), P₆: DDPCW1, P₇: DDPCG2, P₈: DDPCG5

19. Reducing sugar (%)

A total of 20 crosses in 2020 and 21 crosses each in 2021 and pooled over environments exhibited significant positive heterosis over better parent (Table 4.33). The significant economic heterosis was observed in 23 crosses in 2020, 19 crosses in 2021 and 21 crosses in pooled over environments. The magnitude of heterosis for reducing sugar ranged from 52.58 ($P_1 \times P_2$ and $P_1 \times P_7$) to 813.11 per cent ($P_4 \times P_5$) and -69.09 ($P_5 \times P_6$) to 218.24 per cent ($P_1 \times P_5$) in 2020, -65.70 ($P_5 \times P_6$) to 470.65 per cent ($P_4 \times P_5$) and -84.66 ($P_5 \times P_6$) to 126.12 per cent ($P_1 \times P_5$) in 2021 and -57.71 ($P_5 \times P_6$) to 619.40 per cent ($P_4 \times P_5$) and -77.31 ($P_5 \times P_6$) to 169.61 per cent ($P_1 \times P_5$) in pooled over environments over better parent and standard check, respectively. Hybrid combinations *viz.*, $P_4 \times P_5$ (619.40%), $P_6 \times P_8$ (313.01%), $P_3 \times P_6$ (299.09%), $P_4 \times P_6$ (294.77%) and $P_5 \times P_8$ (245.64%) exhibited heterobeltiosis in pooled over environments. Out of these crosses, $P_1 \times P_5$ (169.61%), $P_5 \times P_7$ (148.84%), $P_1 \times P_4$ (126.18%) and $P_3 \times P_6$ (114.11%) were the top economic heterotic combinations in pooled over environments.

Fruit yield is complex trait due to the sum total of contributions provided by individual components. Grafius (1959) questioned the uniqueness of yield. To develop hybrids with higher yield, scientists must first simplify the complex trait and concurrently manage a number of linked features. The magnitude of these component traits is not completely known for effective application in selection for higher yield. In the present investigation, heterosis was seen practically for all the traits and in a few crosses it reached to the level obtained for yield. Based on the economic heterosis revealed over 'kian' a number of cross combinations showed significant desirable heterotic effects for various traits. Cross combinations, P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_4 (PPC-2) and P_2 (DDPCG1) \times P_5 (PPC-3) were top ranking hybrids for marketable fruit yield per plant (Table 4.34, Table 4.35, Table 4.36). The maximum heterosis was 40.23% for P_2 (DDPCG1) \times P_7 (DDPCG2) for marketable fruit yield/plant. The majority of the hybrid combination showing desirable heterotic effect also exhibited significant positive SCA effects with high GCA of female parent for marketable fruit yield/plant in pooled over environments. These combinations displayed heterotic effects for other component characters like fruit length, fruit weight, number of fruits per plant and harvest duration.

Table 4.34 Trait wise list of top crosses based on the heterobeltiosis, economic heterosis in cucumber during 2020, 2021 and pooled over environments

Trait	2020		2021		Pooled	
	BP	SC	BP	SC	BP	SC
Days to first female flower	P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_8 (DDPCG5), P_4 (PPC-2) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_6 (DDPCW1) and P_7 (DDPCG2) \times P_8 (DDPCG5)	P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_6 (DDPCW1) and P_4 (PPC-2) \times P_7 (DDPCG2)	P_2 (DDPCG1) \times P_8 (DDPCG5), P_4 (PPC-2) \times P_8 (DDPCG5), P_7 (DDPCG2) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_3 (PK-1) and P_2 (DDPCG1) \times P_4 (PPC-2)	P_2 (DDPCG1) \times P_4 (PPC-2), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_6 (DDPCW1)	P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_3 (PK-1), P_7 (DDPCG2) \times P_8 (DDPCG5), P_4 (PPC-2) \times P_7 (DDPCG2) and P_2 (DDPCG1) \times P_6 (DDPCW1)	P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_6 (DDPCW1), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2) and P_4 (PPC-2) \times P_7 (DDPCG2)
Nodal position of first female flower	P_1 (DDPCG4) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_2 (DDPCG1), P_3 (PK-1) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_6 (DDPCW1) and P_2 (DDPCG1) \times P_5 (PPC-3)	-	P_1 (DDPCG4) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_2 (DDPCG1), P_1 (DDPCG4) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_8 (DDPCG5) and P_2 (DDPCG1) \times P_5 (PPC-3)	-	P_1 (DDPCG4) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_2 (DDPCG1), P_2 (DDPCG1) \times P_5 (PPC-3), P_5 (PPC-3) \times P_8 (DDPCG5) and P_3 (PK-1) \times P_6 (DDPCW1)	-
Number of female flowers per node	P_6 (DDPCW1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_4 (PPC-2) and P_1 (DDPCG4) \times P_2 (DDPCG1)	P_1 (DDPCG4) \times P_3 (PK-1), P_3 (PK-1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_4 (PPC-2) \times P_8 (DDPCG5) and P_1 (DDPCG4) \times P_4 (PPC-2)	P_6 (DDPCW1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_7 (DDPCG2) and P_1 (DDPCG4) \times P_2 (DDPCG1)	P_3 (PK-1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_6 (DDPCW1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_8 (DDPCG5) and P_2 (DDPCG1) \times P_4 (PPC-2)	P_6 (DDPCW1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_4 (PPC-2) and P_1 (DDPCG4) \times P_2 (DDPCG1)	P_3 (PK-1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_3 (PK-1), P_6 (DDPCW1) \times P_7 (DDPCG2) and P_4 (PPC-2) \times P_8 (DDPCG5)
Days taken to first picking (days)	P_2 (DDPCG1) \times P_3 (PK-1), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_4 (PPC-2) and P_2 (DDPCG1) \times P_6 (DDPCW1)	P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2) and P_1 (DDPCG4) \times P_6 (DDPCW1)	P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2), P_3 (PK-1) \times P_4 (PPC-2), P_7 (DDPCG2) \times P_8 (DDPCG5) and P_4 (PPC-2) \times P_7 (DDPCG2)	P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_7 (DDPCG2) and P_2 (DDPCG1) \times P_6 (DDPCW1)	P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_3 (PK-1), P_3 (PK-1) \times P_4 (PPC-2) and P_4 (PPC-2) \times P_7 (DDPCG2)	P_2 (DDPCG1) \times P_3 (PK-1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2) and P_2 (DDPCG1) \times P_6 (DDPCW1)
Fruit length (cm)	P_1 (DDPCG4) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2)	P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_8	P_1 (DDPCG4) \times P_8 (DDPCG5) and P_2 (DDPCG1) \times P_7 (DDPCG2)	P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2), P_1	P_1 (DDPCG4) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_7 (DDPCG2) and P_2 (DDPCG1) \times P_8 (DDPCG5)	P_1 (DDPCG4) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_4 (PPC-2), P_1

		(DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₆ (DDPCW1) × P ₇ (DDPCG2)		(DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)		(DDPCG4) × P ₈ (DDPCG5) and P ₅ (PPC-3) × P ₆ (DDPCW1)
Fruit diameter (cm)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₄ (PPC-2)
Fruit weight (g)	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)
Number of fruits per plant	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	-	P ₃ (PK-1) × P ₄ (PPC-2), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3)
Marketable yield per plant (kg)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)
Marketable yield per meter square area (kg)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₅ (PPC-3)

Harvest duration (days)	$P_3 (PK-1) \times P_6 (DDPCW1), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_6 (DDPCW1)$ and $P_2 (DDPCG1) \times P_7 (DDPCG2)$	$P_2 (DDPCG1) \times P_8 (DDPCG5), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_7 (DDPCG2)$ and $P_3 (PK-1) \times P_6 (DDPCW1)$	$P_3 (PK-1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_8 (DDPCG5)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_3 (PK-1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_4 (PPC-2)$ and $P_2 (DDPCG1) \times P_5 (PPC-3)$	$P_3 (PK-1) \times P_6 (DDPCW1), P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_7 (DDPCG2)$ and $P_2 (DDPCG1) \times P_6 (DDPCW1)$	$P_2 (DDPCG1) \times P_8 (DDPCG5), P_3 (PK-1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_6 (DDPCW1)$ and $P_4 (PPC-2) \times P_6 (DDPCW1)$
Internodal length (cm)	$P_4 (PPC-2) \times P_8 (DDPCG5), P_3 (PK-1) \times P_5 (PPC-3), P_5 (PPC-3) \times P_8 (DDPCG5), P_3 (PK-1) \times P_6 (DDPCW1)$ and $P_2 (DDPCG1) \times P_5 (PPC-3)$	-	$P_4 (PPC-2) \times P_5 (PPC-3), P_6 (DDPCW1) \times P_8 (DDPCG5), P_1 (DDPCG4) \times P_6 (DDPCW1), P_3 (PPC-3) \times P_6 (DDPCW1)$ and $P_2 (DDPCG1) \times P_5 (PPC-3)$	-	$P_5 (PPC-3) \times P_8 (DDPCG5), P_3 (PK-1) \times P_5 (PPC-3), P_3 (PK-1) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_5 (PPC-3)$ and $P_4 (PPC-2) \times P_8 (DDPCG5)$	-
Vine length (m)	$P_2 (DDPCG1) \times P_7 (DDPCG2), P_6 (DDPCW1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_3 (PK-1) \times P_7 (DDPCG2)$ and $P_1 (DDPCG4) \times P_6 (DDPCW1)$	$P_2 (DDPCG1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_8 (DDPCG5), P_5 (PPC-3) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_6 (DDPCW1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_4 (PPC-2) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_7 (DDPCG2)$ and $P_1 (DDPCG4) \times P_4 (PPC-2)$	$P_4 (PPC-2) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_7 (DDPCG2)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_6 (DDPCW1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_7 (DDPCG2), P_3 (PK-1) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_4 (PPC-2)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_4 (PPC-2) \times P_8 (DDPCG5), P_2 (DDPCG1) \times P_7 (DDPCG2), P_6 (DDPCW1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2)$ and $P_6 (DDPCW1) \times P_7 (DDPCG2)$
Flesh to seed cavity ratio	$P_3 (PK-1) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_3 (PK-1)$ and $P_2 (DDPCG1) \times P_6 (DDPCW1)$	$P_2 (DDPCG1) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_4 (PPC-2), P_4 (PPC-2) \times P_5 (PPC-3), P_3 (PK-1) \times P_6 (DDPCW1)$ and $P_1 (DDPCG4) \times P_3 (PK-1)$	$P_1 (DDPCG4) \times P_3 (PK-1), P_7 (DDPCG2) \times P_8 (DDPCG5)$ and $P_3 (PK-1) \times P_4 (PPC-2)$	$P_1 (DDPCG4) \times P_3 (PK-1)$	$P_1 (DDPCG4) \times P_3 (PK-1), P_3 (PK-1) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_4 (PPC-2), P_2 (DDPCG1) \times P_6 (DDPCW1)$ and $P_3 (PK-1) \times P_7 (DDPCG2)$	$P_2 (DDPCG1) \times P_6 (DDPCW1), P_1 (DDPCG4) \times P_3 (PK-1), P_4 (PPC-2) \times P_5 (PPC-3), P_2 (DDPCG1) \times P_8 (DDPCG5)$ and $P_1 (DDPCG4) \times P_4 (PPC-2)$
Flesh thickness (mm)	$P_3 (PK-1) \times P_4 (PPC-2)$	$P_4 (PPC-2) \times P_6 (DDPCW1), P_3 (PK-1) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_8 (DDPCG5)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_3 (PK-1) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_2 (DDPCG1), P_1 (DDPCG4) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_6 (DDPCW1)$ and $P_1 (DDPCG4) \times P_8 (DDPCG5)$	$P_4 (PPC-2) \times P_6 (DDPCW1)$ and $P_2 (DDPCG1) \times P_4 (PPC-2)$	$P_1 (DDPCG4) \times P_2 (DDPCG1)$ and $P_1 (DDPCG4) \times P_6 (DDPCW1)$	$P_4 (PPC-2) \times P_6 (DDPCW1), P_2 (DDPCG1) \times P_4 (PPC-2), P_1 (DDPCG4) \times P_8 (DDPCG5), P_3 (PK-1) \times P_4 (PPC-2)$ and $P_4 (PPC-2) \times P_7 (DDPCG2)$
Total soluble solids (°B)	$P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_3 (PK-1), P_4 (PPC-2) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2)$ and $P_3 (PK-1) \times P_7 (DDPCG2)$	$P_4 (PPC-2) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_7 (DDPCG2), P_1 (DDPCG4) \times P_4 (PPC-2)$	$P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_3 (PK-1), P_3 (PK-1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_7 (DDPCG2)$ and $P_6 (DDPCW1) \times P_7 (DDPCG2)$	$P_4 (PPC-2) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_7 (DDPCG2), P_4 (PPC-2) \times P_7 (DDPCG2)$ and $P_3 (PK-1) \times P_7 (DDPCG2)$	$P_2 (DDPCG1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_3 (PK-1), P_4 (PPC-2) \times P_7 (DDPCG2), P_3 (PK-1) \times P_7 (DDPCG2)$ and $P_1 (DDPCG4) \times P_4 (PPC-2)$	$P_4 (PPC-2) \times P_8 (DDPCG5), P_6 (DDPCW1) \times P_7 (DDPCG2), P_2 (DDPCG1) \times P_7 (DDPCG2)$ and $P_4 (PPC-2) \times P_7 (DDPCG2)$

		and P ₂ (DDPCG1) × P ₇ (DDPCG2)	(DDPCW1) × P ₇ (DDPCG2)	× P ₆ (DDPCW1)	(DDPCG4) × P ₄ (PPC-2)	
Ascorbic acid (mg/100g)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₅ (PPC-3) × P ₇ (DDPCG2) and P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₅ (PPC-3) × P ₇ (DDPCG2)
Total sugars (%)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₃ (PK-1) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₆ (DDPCW1) × P ₈ (DDPCG5)
Reducing sugars (%)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₅ (PPC-3)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₃ (PK-1) × P ₆ (DDPCW1)

Table 4.35 Trait wise lists of top crosses on the basis of per se performance, heterobeltiosis, economic heterosis and SCA effects in cucumber during 2020, 2021 and pooled over environments

Character	Year	Per se performance	Heterobeltiosis	Economic heterosis	SCA effects
Days to first female flower	2020	P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₇ (DDPCG2) , P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₈ (DDPCG5) , P ₄ (PPC-2) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)
	2021	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₃ (PK-1)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₃ (PK-1) and P ₂ × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ , P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₅ (PPC-3) × P ₈ (DDPCG5)
	Pooled	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)
Nodal position of first female flower	2020	P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₁ (DDPCG4) × P ₇ (DDPCG2), check	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)	-	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)
	2021	P ₁ (DDPCG4) × P ₇ (DDPCG2), check, P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	-	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₇ (DDPCG2) × P ₈ (DDPCG5)
	Pooled	P ₁ (DDPCG4) × P ₇ (DDPCG2), check, P ₁ (DDPCG4) × P ₂ (DDPCG1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	-	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₇ (DDPCG2) × P ₈ (DDPCG5)
Number of female flowers per node	2020	P ₁ (DDPCG4) × P ₃ (PK-1), P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁	P ₁ (DDPCG4) × P ₃ (PK-1), P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₈ (DDPCG5) and P ₁	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄

			(DDPCG4) × P ₂ (DDPCG1)	(DDPCG4) × P ₄ (PPC-2)	(PPC-2) × P ₈ (DDPCG5)
	2021	P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₂ (DDPCG1)	P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₄ (PPC-2)
	Pooled	P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₈ (DDPCG5)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₂ (DDPCG1)	P ₃ (PK-1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₈ (DDPCG5)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Days taken to first picking (days)	2020	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₆ (DDPCW1) × P ₇ (DDPCG2)
	2021	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₇ (DDPCG2)
	Pooled	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₃ (PK-1) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)
Fruit length (cm)	2020	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₆ (DDPCW1) × P ₇ (DDPCG2)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₃ (PK-1)
	2021	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₃ (PK-1)
	Pooled	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₈	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₇ , P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ , P ₃ (PK-1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈

		(DDPCG5) and P ₅ (PPC-3) × P ₆ (DDPCW1)		(DDPCG4) × P ₈ (DDPCG5) and P ₅ (PPC-3) × P ₆ (DDPCW1)	(DDPCG5) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Fruit diameter (cm)	2020	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₃ (PK-1)
	2021	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₄ (PPC-2)
	Pooled	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₄ (PPC-2)
Fruit weight (g)	2020	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ and P ₁ (DDPCG4) × P ₆ (DDPCW1)
	2021	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₃ (PK-1) × P ₅ (PPC-3)
	Pooled	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Number of fruits per plant	2020	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₄ (PPC-2) × P ₆ (DDPCW1)
	2021	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂	P ₃ (PK-1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁	-	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₃ (PK-1)

		(DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	(PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)	(DDPCG1) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)
	2021	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
	Pooled	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₇ (DDPCG2)
Internodal length (cm)	2020	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)	-	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₆ (DDPCW1)
	2021	P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₁ × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)	-	P ₅ (PPC-3) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₅ (PPC-3) × P ₈ (DDPCG5)
	Pooled	P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₅ (PPC-3), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₄ (PPC-2) × P ₈ (DDPCG5)	-	P ₅ (PPC-3) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₂ (DDPCG1) × P ₅ (PPC-3) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Vine length (m)	2020	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)
	2021	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₅ (PPC-3)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2) and	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄

		× P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₄ (PPC-2)	(PPC-2)
	Pooled	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₅ (PPC-3) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Flesh to seed cavity ratio	2020	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₂ (DDPCG1) × P ₈ (DDPCG5)
	2021	P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₄ (PPC-2) × P ₅ (PPC-3) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₅ (PPC-3)
	Pooled	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₄ (PPC-2)
Flesh thickness (mm)	2020	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₃ (PK-1) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₃ (PK-1) × P ₄ (PPC-2)
	2021	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₃ (PK-1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₂ (DDPCG1), P ₁ (DDPCG4) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₈ (DDPCG5)	P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₄ (PPC-2)	P ₃ (PK-1) × P ₇ (DDPCG2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₆ (DDPCW1)
	Pooled	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₁ (DDPCG4) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₁ (DDPCG4) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2), P ₃ (PK-1) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₆ (DDPCW1)
Total soluble solids (°B)	2020	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₁	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1)

		(PPC-2) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	(DDPCG4) × P ₄ (PPC-2) and P ₃ (PK-1) × P ₇ (DDPCG2)	(DDPCG4) × P ₄ (PPC-2) and P ₂ (DDPCG1) × P ₇ (DDPCG2)	× P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)
	2021	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₃ (PK-1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₆ (DDPCW1) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₇ (DDPCG2) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₁ (DDPCG4) × P ₃ (PK-1)
	Pooled	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₄ (PPC-2) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₇ (DDPCG2) and P ₄ (PPC-2) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₈ (DDPCG5), P ₆ (DDPCW1) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₈ (DDPCG5)
Ascorbic acid (mg/100g)	2020	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₄ (PPC-2) × P ₆ (DDPCW1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₂ (DDPCG1) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₄ (PPC-2) and P ₆ (DDPCW1) × P ₈ (DDPCG5)
	2021	P ₄ (PPC-2) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₅ (PPC-3) × P ₇ (DDPCG2) and P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₃ (PK-1), P ₅ (PPC-3) × P ₇ (DDPCG2) and P ₇ (DDPCG2) × P ₈ (DDPCG5)	P ₂ (DDPCG1) × P ₄ (PPC-2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₃ (PK-1)
	Pooled	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₅ (PPC-3) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₅ (PPC-3), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₅ (PPC-3) × P ₇ (DDPCG2)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₄ (PPC-2), P ₇ (DDPCG2) × P ₈ (DDPCG5), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₆ (DDPCW1) × P ₈ (DDPCG5)
Total sugars (%)	2020	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₅ (PPC-3)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₁ (DDPCG4) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₇ (DDPCG2), P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₃ (PK-1) and P ₂ (DDPCG1) × P ₆ (DDPCW1)	P ₂ (DDPCG1) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₄ (PPC-2) and P ₄ (PPC-2) × P ₈ (DDPCG5)
	2021	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₅ (PPC-3) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₂ (DDPCG1) × P ₃ (PK-1) and P ₁ (DDPCG4) × P ₇ (DDPCG2)	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₅ (PPC-3)
	Pooled	P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂ (DDPCG1) × P ₃	P ₂ (DDPCG1) × P ₆ (DDPCW1) and P ₂ (DDPCG1) × P ₃ (PK-1)	P ₁ (DDPCG4) × P ₃ (PK-1), P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₂	P ₂ (DDPCG1) × P ₆ (DDPCW1), P ₁ (DDPCG4) × P ₃ (PK-1), P ₄ (PPC-2)

		(PK-1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₂ (DDPCG1) × P ₅ (PPC-3)		(DDPCG1) × P ₃ (PK-1), P ₁ (DDPCG4) × P ₇ (DDPCG2) and P ₆ (DDPCW1) × P ₈ (DDPCG5)	× P ₆ (DDPCW1), P ₅ (PPC-3) × P ₆ (DDPCW1) and P ₁ (DDPCG4) × P ₅ (PPC-3)
Reducing sugars (%)	2020	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₅ (PPC-3)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₄ (PPC-2) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ , P ₁ (DDPCG4) × P ₄ (PPC-2), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₅ (PPC-3)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₃ (PK-1) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)
	2021	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₁ (DDPCG4) × P ₄ (PPC-2)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₃ (PK-1) × P ₄ (PPC-2)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₄ (PPC-2) × P ₆ (DDPCW1), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₆ (DDPCW1), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)
	Pooled	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₁ (DDPCG4) × P ₄ (PPC-2), P ₆ (DDPCW1) × P ₈ (DDPCG5) and P ₃ (PK-1) × P ₆ (DDPCW1)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₄ (PPC-2) × P ₅ (PPC-3), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1), P ₄ (PPC-2) × P ₆ (DDPCW1) and P ₅ (PPC-3) × P ₈ (DDPCG5)	P ₁ (DDPCG4) × P ₅ (PPC-3), P ₅ (PPC-3) × P ₇ (DDPCG2), P ₆ (DDPCW1) × P ₈ (DDPCG5), P ₃ (PK-1) × P ₆ (DDPCW1) and P ₄ (PPC-2) × P ₆ (DDPCW1)

Table 4.36 Top four promising hybrids for yield and yield related traits under protected environment

Hybrid combinations	Characters		
	Per se performance	SCA	Economic heterosis
DDPCG1 × DDPCG2	Days taken to first fruit picking Fruit length Fruit weight Number of fruits per plant Marketable yield per plant Marketable yield per meter square area Harvest duration Internodal length Vine length Total soluble solids	Number of female flowers per node Days taken to first fruit picking Fruit weight Marketable yield per plant Harvest duration Vine length Total soluble solids	Days taken to first fruit picking Fruit length Fruit weight Number of fruits per plant Marketable yield per plant Harvest duration Vine length Total soluble solids
DDPCG1 × DDPCG5	Fruit length Fruit weight Marketable yield per plant Marketable yield per meter square area Harvest duration Internodal length Flesh to seed cavity ratio	Fruit length Marketable yield per plant Marketable yield per meter square area Harvest duration Flesh to seed cavity ratio	Fruit length Fruit weight Marketable yield per plant Marketable yield per meter square area Harvest duration Flesh to seed cavity ratio
DDPCG1 × PPC-2	Days taken to first fruit picking Fruit length Fruit weight Number of fruits per plant Marketable yield per plant Marketable yield per meter square area Harvest duration Flesh thickness	Days taken to first fruit picking Number of fruits per plant Marketable yield per plant Marketable yield per meter square area Ascorbic acid	Days to first female flower Days taken to first fruit picking Fruit length Fruit weight Number of fruits per plant Marketable yield per plant Marketable yield per meter square area Flesh thickness
DDPCG1 × PPC-3	Number of fruits per plant Marketable yield per plant Marketable yield per meter square area Harvest duration Total sugars	Nodal position of first female flower Number of fruits per plant Harvest duration Internodal length	Number of fruits per plant Marketable yield per plant Marketable yield per meter square area

1. BEST COMBINATION

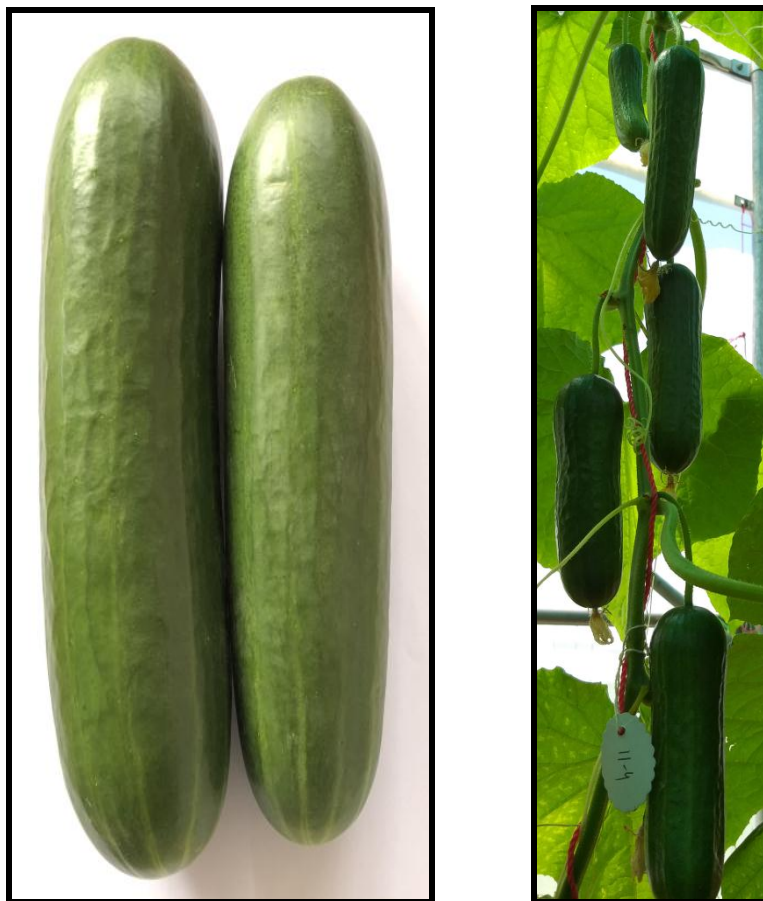


Plate 6: DDPCG1 × DDPCG2

2. BEST COMBINATION



Plate 7: DDPCG1 × DDPCG5

3. BEST COMBINATION



Plate 8: DDPCG1 × Pant Parthenocarpic Cucumber-2 (PPC-2)

4. BEST COMBINATION



Plate 9: DDPCG1 × Pant Parthenocarpic Cucumber-3 (PPC-3)

5. SUMMARY AND CONCLUSIONS

The present study entitled “Genetical studies in parthenocarpic cucumber (*Cucumis sativus* L.)” were carried out to estimate the gene action and to identify the potential parental lines and hybrid combinations based on combining ability and extent of heterosis for various characters viz., days to first female flower, nodal position of first female flower, number of female flowers per node, days taken to first fruit picking, fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square (kg), harvest duration, internodal length (cm), vine length (m), flesh to seed cavity ratio, flesh thickness (mm), colour of the fruit, incidence of downy mildew disease (%), total soluble solids (°B), ascorbic acid (mg/100g), total sugar (%) and reducing sugar (%). Eight parthenocarpic gynoecious parental lines viz., DDPCG4, DDPCG1, Punjab Kheera-1 (PK-1), Pant Parthenocarpic Cucumber-2 (PPC-2), Pant Parthenocarpic Cucumber-3 (PPC-3), DDPCW1, DDPCG2 and DDPCG5 along with 28 F₁ hybrid combinations developed by crossing these parental lines in half diallel mating system excluding reciprocals and standard check (Kian) were evaluated in randomized block design with three replications during spring summer seasons of 2020 and 2021. Genetic diversity of eight parental lines was assessed using SSR markers to identify the diverse parents.

In the present investigation, a total of 61 SSRs cucumber primers were used to assess the genetic diversity of eight parental lines using PCR amplification. Out of 61 primers, 56 showed high polymorphism. Based on molecular data, dendrogram grouped 8 eight cucumber genotypes into two major clusters. AMOVA revealed that variation within population was higher i.e., 92 per cent of total variation while, only 8 per cent among populations. PCoA grouped 8 genotypes into two populations and per cent variation was elucidated by the three axis which contributed 21.10 per cent, 17.66 per cent and 15.28 per cent variation, respectively. The populations were divided into three main groups by STRUCTURE analysis.

The significant differences were recorded for fruit yield and its component traits which revealed sufficient genetic variability among genotypes. Similarly, analysis of variance indicated significant genotype \times environment interaction for most of the traits which revealed the role of environment on genotypes or hybrids performance under protected conditions. The combined analysis of variance revealed significant differences due to parents, hybrids and parents vs. hybrids for majority of the traits demonstrating appreciable diversity in the experimental material.

Based on the *per-se* performance of cross combinations DDPCG1 \times DDPCG2 ($P_2 \times P_7$) gave maximum fruit yield to the tune of 4.41 kg per plant and three other hybrids viz., DDPCG1 \times PPC-2 ($P_2 \times P_4$), DDPCG1 \times PPC-3 ($P_2 \times P_5$) and DDPCG1 \times DDPCG5 ($P_2 \times P_8$) were also observed significantly superior due to higher fruit yield per plant. These crosses were significantly superior for yield and its components traits like days taken to first fruit picking, fruit length, fruit weight, number of fruits per plant, marketable yield per plant, marketable yield per meter square area, harvest duration, internodal length, vine length and total soluble solids. Cross combinations viz., PPC-2 \times DDPCG5 ($P_4 \times P_8$) and DDPCW1 \times DDPCG2 ($P_6 \times P_7$) for total soluble solids, DDPCG4 \times DDPCG2 ($P_1 \times P_7$), DDPCG4 \times PK-1 ($P_4 \times P_5$) for ascorbic acid, DDPCG4 \times DDPCG2 ($P_1 \times P_7$), DDPCG4 \times PK-1 ($P_1 \times P_3$) and DDPCG1 \times PK-1 ($P_2 \times P_3$) for total sugar and DDPCG4 \times PPC-3 ($P_1 \times P_5$) for reducing sugar were significantly superior for quality traits. Hybrid combinations namely, DDPCG1 \times PK-1 ($P_2 \times P_3$), DDPCG4 \times PK-1 ($P_1 \times P_3$), DDPCW1 \times DDPCG2 ($P_6 \times P_7$) and DDPCG1 \times DDPCW1 ($P_2 \times P_6$) recorded minimum incidence of downy mildew.

Mean squares due to general combining ability and specific combining ability were highly significant for all the traits. In GCA \times environment interaction, mean sum of squares were significant for nodal position of first female flower, total soluble solids ($^{\circ}$ brix), ascorbic acid (mg/100g), total sugar (%) and reducing sugar (%) while, mean squares due to SCA \times environment interaction were highly significant for days to first female flower, nodal position of first female flower, number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square (kg), vine length (m), flesh to seed cavity ratio, total soluble solids ($^{\circ}$ brix), ascorbic acid (mg/100 g), total sugar (%) and reducing sugar (%).

The estimates of GCA effects revealed that parents DDPCG1 (P₂), DDPCG4 (P₁), PPC-2 (P₄) and DDPCG5 (P₈) were best general combiners for earliness, fruit yield and its component traits. Among parents, DDPCG1 (P₂) was found to be the best general combiner for 12 traits out of 19 traits studied, namely, days to first female flower, number of female flowers per node, days taken to first fruit picking, fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, marketable yield per plant (kg), marketable yield per meter square area (kg), harvest duration (days), vine length (m) and flesh to seed cavity ratio in pooled over environments followed by DDPCG4 (P₁) which revealed significant desirable GCA effects for 9 traits viz., nodal position of first female flower, fruit diameter (cm), fruit weight (g), marketable yield per plant (kg), marketable yield per meter square area (kg), harvest duration (days), ascorbic acid (mg/100g), total sugar (%) and reducing sugar in pooled over environments. PPC-2 (P₄) and DDPCG5 (P₈) were also promising parents for 8 traits which could also be included in breeding programme due to good general combining ability estimates.

Based on estimates of SCA effects, it was noticed that no single cross combination could exhibit significant SCA effects for all the traits. Majority of the cross combinations revealed desirable SCA effects which had atleast one of the parents as good or average general combiner. However, DDPCG4 × DDPCG5 (P₁ × P₈), DDPCG1 × PPC-2 (P₂ × P₄), DDPCG1 × DDPCG5 (P₂ × P₈), PK-1 × PPC-3 (P₃ × P₅) and DDPCG1 × DDPCW1 (P₂ × P₇) exhibited significant desirable SCA effects for most of the traits including marketable yield per plant. These hybrid combinations were also included among top ten crosses for marketable yield per plant. Some crosses with 'Average × Poor' GCA effects also represented high SCA effects which might be due to complementary gene interactions.

The estimates of σ^2 SCA were higher for all the traits in all the environments indicating the predominance of non-additive gene action in controlling these traits. The magnitude of dominant component (σ^2 D) was higher than the additive component (σ^2 A) for the all traits studied in all the environments except for fruit length and internodal length in 2021 indicating the predominance of non-additive gene action in controlling all these traits. However, involvement of non-additive gene action in

governing most of the traits indicates the exploitation of hybrid vigour to develop superior hybrid combinations for crop improvement.

Among cross combinations, sufficient variation in magnitude of heterosis was recorded for all the traits. A considerable heterobeltiosis and economic heterosis was observed for most of the traits. A total of 14 crosses in 2020, 13 crosses in 2021 and 15 crosses in pooled over environments showed heterobeltiosis for marketable fruit yield/plant. On the other hand, 11 crosses in 2020, 7 crosses in 2021 and 10 crosses in pooled over environments exhibited significant positive economic heterosis for marketable fruit yield/plant. Hybrid combination DDPCG1 \times DDPCG2 ($P_2 \times P_7$) exhibited maximum magnitude of economic heterosis i.e., 40.23 per cent followed by DDPCG1 \times DDPCG5 ($P_2 \times P_8$) with 37.05 per cent heterosis. Hybrid combinations, DDPCG1 \times DDPCG2 ($P_2 \times P_7$), DDPCG1 \times DDPCG5 ($P_2 \times P_8$), DDPCG1 \times PPC-2 ($P_2 \times P_4$), DDPCG1 \times PK-1 ($P_2 \times P_5$) and DDPCG1 \times DDPCW1 ($P_2 \times P_6$) were the top heterotic combinations for marketable fruit yield per plant and also for days to first female flower, fruit length, fruit diameter, fruit weight, number of fruits per plant and harvest duration. These hybrid combinations were also found to be superior on the basis of per se performance for most of traits.

Conclusions:

The following inferences may be drawn from the present investigation:

- Diverse parental lines of cucumber revealed sufficient genetic variability for yield and its component traits using SSR molecular markers and diallel mating design method 2 (excluding reciprocals).
- PCA revealed 54.04 per cent variation as justified by first three principal components and maximum genetic variation (21.10%) was contributed by PC1.
- Eight cucumber genotypes were grouped into two clusters and both the clusters were divided into 2 sub clusters (NTSYS software) and DARwin software exhibited three clusters out of which cluster II was further divided into two sub clusters and was also confirmed by population structure.

- Based on *per se* performance, top combinations were DDPCG1 × DDPCG2, DDPCG1 × DDPCG5, DDPCG1 × PPC-2 and DDPCG1 × PPC-3 for fruit yield and its component traits under protected environment. Hybrid combinations namely, DDPCG1 × PK-1 ($P_2 \times P_3$), DDPCG4 × PK-1 ($P_1 \times P_3$), DDPCW1 × DDPCG2 ($P_6 \times P_7$) and DDPCG1 × DDPCW1 ($P_2 \times P_6$) recorded minimum incidence of downy mildew.
- The estimates of general combining ability revealed that parents DDPCG1 (P_2), DDPCG4 (P_1), PPC-2 (P_4) and DDPCG5 (P_8) were most promising general combiners for earliness, fruit yield and its component traits.
- Based on SCA effects, DDPCG4 × DDPCG5 ($P_1 \times P_8$), DDPCG1 × PPC-2 ($P_2 \times P_4$), DDPCG1 × DDPCG5 ($P_2 \times P_8$), PK-1 × PPC-3 ($P_3 \times P_5$) and DDPCG1 × DDPCW1 ($P_2 \times P_7$) were the promising hybrid combinations for most of the traits including marketable yield per plant.
- The magnitude of dominant component (σ^2D) was higher than the additive component (σ^2A) for the majority of the traits studied in all the environments indicating the predominance of non-additive gene action in controlling all these traits.
- Appreciable heterosis was exhibited by hybrid combinations viz., DDPCG1 × DDPCG2 ($P_2 \times P_7$), DDPCG1 × DDPCG5 ($P_2 \times P_8$), DDPCG1 × PPC-2 ($P_2 \times P_4$), DDPCG1 × PK-1 ($P_2 \times P_5$) and DDPCG1 × DDPCW1 ($P_2 \times P_6$) for marketable fruit yield/plant and were also heterotic for days to first female flower, fruit length, fruit diameter, fruit weight, number of fruits per plant and harvest duration. These hybrid combinations were top ranking combinations based on *per se* performance and heterosis for earliness and yield related traits under protected conditions.

LITERATURE CITED

Ahirwar CS, Singh DK and Kushwaha ML. 2018. Assessment of genetic variation in cucumber (*Cucumis sativus* L.) germplasm on correlation, path analysis and cluster analysis. *Chemical Science Review and Letters* 6: 1886-1893

Airina CK, Kumar TP, George TE, Sadhankumar PG and Krishnan S. 2013. Heterosis breeding exploiting gynoecey in cucumber (*Cucumis sativus* L.). *Journal of Tropical Agriculture* 51: 14-48

Allard RW. 1960. Principles of Plant Breeding. John Wiley and Sons, New York, London. pp. 485

Ammar MH, Alghamdi SS, Migdadi HM, Khan MA, El-Harty EH and Al-Faifi SA. 2015. Assessment of genetic diversity among faba bean genotypes using agromorphological and molecular markers. *Saudi Journal of Biological Sciences* 22: 340-350

Anderson JA, Churchill GA, Autrique JE, Tanksley SD and Sorrells ME. 1993. Optimizing parental selection for genetic linkage maps. *Genome* 36: 181-186

Anonymous. 2020. National Horticulture Board. <http://www.nhb.gov.in>.

Anonymous. 2021. Area and Production of vegetables in Himachal Pradesh. Directorate of Agriculture (H.P.), Shimla-5

AOAC. 1970. Official Methods of Analysis of the Association of Official Analytical Chemists. (Ed. William Horwitz). Benjamin Franklin Station, Washington, D.C., USA

Arab DEAA, Ebidob AI, Alyb MA, Wahb-Allahc MA and Bayoumya AM. 2020. General performance, heterosis and potence ratio for some important characters using complete diallel cross among five inbred lines of cucumber (*Cucumis sativus* L.) under greenhouse conditions. *Journal of Advanced Agricultural Research* 25: 364-387

Arya K and Singh DK. 2016. Exploitation of heterosis among and monoecious genotypes of cucumber (*Cucumis sativus* L.) under polyhouse. *International Journal of Basic and Applied Agricultural Research* 12: 68-71

Bairagi SK, Ram HH and Singh DK. 2013. Analysis of combining ability in cucumber (*Cucumis sativus* L.) through half diallel mating system. *Annual Horticulture* 6: 308-314

Bairagi SK, Ram HH, Singh DK and Maurya SK. 2005. Exploitation of hybrid vigour for yield and attributing traits in cucumber. *Indian Journal of Horticulture* 62: 41-45

Bishop CJ. 1954. A stamenless male-sterile tomato. *American Journal of Botany* 41: 540-542

Castilla L, Hernandez RG, Anguilar CC, Hernandez AM, Garcia MM and Noh RHA. 2019. Structure and genetic diversity of nine important landraces of *Capsicum* species cultivated in the Yucatan Peninsula, Mexico. *Agronomy* 9: 376

Clarke J. 2009. Cetyltrimethyl Ammonium Bromide (CTAB) DNA miniprep for plant DNA isolation. *Cold Spring Harbor Protocol* 10:1101.

Cockerham CC. 1961. Implication of genetic variances in hybrid breeding programme. *Crop Science* 1: 47-52

Dabholkar AR. 1992. Elements of biometrical genetics. Concept Publishing Company, New Delhi. pp 251-270

Dar AA, Mahajan R, Lay P and Sharma S. 2017. Genetic diversity and population structure of *Cucumis sativus* L. by using SSR markers. *3 Biotech* 7: 307

Das T, Saikia L and Kumar V. 2018. Comparative quality analysis of cucumber grown under polyhouse and in open condition. *International Journal of Biochemistry Research & Review* 22: 1-11

De Candolle A. 1882. Origin of cultivated plants. Hafnar Publishing Co, New York. pp. 264-267

Dogra BS and Kanwar MS. 2011. Exploiting for yield and horticultural traits in cucumber (*Cucumis sativus* L.). *Indian Journal of Plant Genetic Resources* 24: 332-339

Dogra LK. 2012. Genetic evaluation of some hybrids of cucumber under modified naturally ventilated greenhouse in mid hills of Western Himalayas. M.Sc. Thesis, p 92. Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India

Evanno G, Regnaut S and Goudet J. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14: 2611-2620

Falconer DS and Mackay TFC. 1996. Introduction to Quantitative Genetics. John Wiley and Sons, New York, London. pp 528

Falush D, Stephens M and Pritchard JK. 2003. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164: 1567-1587

Fisher RA. 1918. The correlation between relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edinburgh* 52: 399-433

Gaikwad AG, Sonawane HG, Dhumal SS and Musmade AM. 2011. Variability studies in cucumber (*Cucumis sativus* L.). *Asian Journal of Horticulture* 6: 148-150

Garzon-Martinez GA, Osorio-Guarin JA, Delgadillo-Duran P, Mayorga F, Enciso-Rodriguez FE, Landsman D, Marino-Ramirez L and Barrero LS. 2015. Genetic diversity and population structure in *Physalis peruviana* and related taxa based on InDels and SNPs derived from COSII and IRG markers. *Plant Gene* 4: 29-37

Gill HS, Singh JP and Pachauri DC. 1973. Pusa Sanyog out yields other cucumbers. *Indian Horticulture* 18: 11-13

Godoy AR, Higuti ARO and Cardoso AII. 2008. Yield and heterosis in cucumber inbred lines crosses. *Bragantia* 67: 839-844

- Golabadi M, Eghtedary AR and Golkar P. 2015. Determining relationships between different horticultural traits in (*Cucumis sativus* L.) genotypes with multivariate analysis. *SABRAO Journal of Breeding and Genetics* 45: 447-457
- Gomez KA and Gomez AA. 1983. Statistical procedures for agricultural research. John Wiley and Sons, New York, USA. pp. 357-427
- Grafius JE. 1959. Heterosis in barley. *Agronomy Journal* 51: 551-554
- Griffing B. 1956a. Concept of general and specific combining ability in relation to diallel crossing system. *Australian Journal of Biological Science* 9: 463-493
- Griffing B. 1956b. A generalised treatment of the use of diallel crosses in quantitative inheritance. *Heredity* 10:31-50
- Hanchinamani C N and Patil M G. 2009. Heterosis in cucumber (*Cucumis sativus* L.). *Asian Journal of Horticulure* 4: 21-24.
- Hayes HK and Jones DR. 1916. First generation crosses in cucumbers. *Connecticut Agricultural Experiment Station Research* 40: 319-22.
- Hayman BI. 1954. The theory and analysis of diallel crosses. *Genetics* 39: 789-809
- Hayman BI. 1960. The theory and analysis of diallel crosses-III. *Genetics* 45: 155-172
- Hu J, Wang L and Li J. 2011. Comparison of genomic SSR and ESTSSR markers for estimating genetic diversity in cucumber. *Biologia Plantarum* 55: 577-580
- Hu J, Zhou X and Li J. 2010. Development of novel EST-SSR markers for cucumber (*Cucumis sativus*) and their transferability to related species. *Scientia Horticulturae* 125: 534-538
- Hutchins AE. 1939. Some examples of heterosis in cucumber (*Cucumis sativus* L.). *Proceedings of American Society for Horticultural Science* 36: 660-664
- Jat GS, Munshi AD, Behera TK, Choudhary H and Dev B. 2015. Exploitation of heterosis in cucumber for earliness, yield and yield components utilizing gynococious lines. *Indian Journal of Horticulture* 72: 494-499

Jinks JL and Hayman BI. 1953. The analysis of diallel crosses. *Maize Genetics Crop Newsletter* 27: 43-54

Karakurt Y, Guvercin D, Onder S and Isler O. 2020. Assessment of genetic diversity in cucumber (*Cucumis sativus* L.) genotypes using morphological characters and AFLP Analysis. *KSU Journal of Agriculture and Nature* 23: 577-585

Kaur K and Dhall RK. 2017. Heterosis and combining ability for yield and yield attributes in cucumber (*Cucumis sativus* L.). *SABRAO Journal of Breeding and Genetics* 49: 94-103

Kaur K, Dhall RK and Chawala N. 2016. Heterosis and combining ability for quality attributing traits in cucumber (*Cucumis sativus* L.). *Agriculture Research Journal* 53: 475-477

Keopraparl K. 1997. Comparison of local cucumber varieties homudonthani with commercial varieties. Asian Regional center- AVRDC, Bangkok, Thailand. pp. 5

Kumar J, Munshi AD, Kumar R and Sureja AK. 2010. Studies on heterosis in slicing cucumber. *Indian Journal of Horticulture* 67: 197-201

Kumar J, Munshi AD, Kumar R, Sureja AK and Sharma RK. 2013. Combining ability and its relationship with gene action in slicing cucumber. *Indian Journal of Horticulture* 70: 135-138

Kumar P, Khapte PS, Saxena A and Kumar. 2019. Evaluation of gynoecious cucumber (*Cucumis sativus*) hybrids for early-summer greenhouse production in Western Indian arid plains. *Indian Journal of Agricultural Sciences* 89: 545-550

Kumar S, Kumar D, Kumar R, Thakur KS and Dogra BS. 2013. Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in North-Western Himalayas. *Universal Journal of Plant Science* 1: 27-36

Kumar S, Kumar R, Kumar D, Gautam N, Dogra RK, Mehta DK, Sharma HD and Kansal H. 2016. Parthenocarpic gynoecious parental lines of cucumber introduced from Netherlands for developing high-yielding, quality hybrids. *Journal of Crop Improvement* 30: 352-369

Kumar S, Shukla IN, Singh HC, Lal B, Yadav MK, Singh VP and Verma AK. 2021. To study the combining ability of different traits in cucumber (*Cucumis sativus* L.). *The Pharma Innovation Journal* 10: 1378-1384

Kumari R, Kumar R and Kumar S. 2018. Combining ability and heterosis for TSS and seed traits in cucumber (*Cucumis sativus* L.). *Vegetable Science* 44: 12-1

Kumbhar HC, Dumbre AD and Patil HE. 2005. Heterosis and Combining ability in cucumber. (*Cucumis sativus* L.) *Journal of Maharashtra agricultural University* 30: 272-275

Kushwaha ML, Yadav LB and Maurya RP. 2011. Heterobeltiosis and combining ability in cucumber (*Cucumis sativus* L.) under mid hilly area of Uttrakhand. *Progressive Agriculture* 11: 103-107

Lee PY, Costumbrado J, Hsu CY and Kim YH. 2012. Agarose gel electrophoresis for the separation of DNA fragments. *Journal of Visualized Experiments* 62: 3791-3923

Lopez-Sese AI and Staub J. 2002. Combining ability analysis of yield components in cucumber. *Journal of American Society of Horticultural Science* 127: 931-937

Lv J, Qi J, Shi Q, Shen D, Zhang S, Shao G, Li H, Sun Z, Weng Y, Shang Y, Gu X, Li X, Zhu X, Zhang J, Treuren R, Dooijeweert W, Zhang Z and Huang S. 2012. Genetic diversity and population structure of cucumber (*Cucumis sativus* L.). *PLoS One* 7: e46919

Mahajan R, Zargar SM, Singh R, Salgotra RK, Farhat S and Sonah H. 2016. Population structure analysis and selection of core set among common bean genotypes from Jammu and Kashmir India. *Applied Biochemistry* 182: 16-28

Malav N, Yadav ML and Maurya IB. 2018. Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies* 6: 457-460

Manggoel W, Uguru MI, Ogbonna PE and Dasbak MA. 2021. Exploiting combining ability in a diallel cross between native and elite cucumber (*Cucumis sativus* L.) varieties. *Journal of Plant Breeding and Crop Science* 13: 136-143

Matzinger DP and Kempthorne O. 1956. The modified diallel table with partial inbreeding and interactions with environment. *Genetics* 41: 822-83

Mehta P and Sharma P. 2020. Evaluation for fruit yield and related traits in parthenocarpic cucumber. *International Journal of Current Microbiology and Applied Sciences* 9: 1388-1404

Mehta P. 2019. Genetic evaluation for fruit yield and related traits in parthenocarpic cucumber. M.Sc. Thesis, p 121. Department of Vegetable Science and Floriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya Palampur, Himachal Pradesh, India

Mohanty BK and Mishra RS. 1999. Studies on heterosis for yield and yield attributes in pumpkin (*Cucurbita moschata* Duch. Ex, Poir.). *Indian Journal of Horticulture* 56: 171-178

Moradipour F, Olfati JA, Hamidoghli Y, Sabouri A and Zahedi B. 2016. General and specific combining ability and heterosis for yield in cucumber fresh market lines. *International Journal of Vegetable Science* 1: 1-21

Mule PN, Khandelwal V, Lodam VA, Shinde DA, Patil PP and Patil AB. 2012. Heterosis and combining ability in cucumber (*Cucumis sativus* L.). *Madras Agricultural Journal* 99: 420-423

Munshi AD, Kumar R and Panda B. 2006. Studies on genetic components of variation in cucumber (*Cucumis sativus* L.). *Indian Journal of Horticulture* 63: 213-217

Normohamadi S, Solouki M and Heidari F. 2017. Diversity in cucumber genotypes based on morphological traits and SSR molecular markers. *Biosciences Biotechnology Research Asia* 14: 775-782

Panday S, Singh B, Singh M and Rai M. 2005. Heterosis in cucumber (*Cucumis sativus* L.). *Vegetable Science* 32: 143-145

Pandey S, Ansari WA, Atri N, Singh B, Gupta S and Bhat KV. 2016. Standardization of screening technique and evaluation of muskmelon genotypes for drought tolerance. *Plant Genetic Resource* 16: 1-8

Pandey S, Ansari WA, Mishra VK, Singh AK and Singh M. 2013. Genetic diversity in Indian cucumber based on microsatellite and morphological markers. *Biochemical Systematic and Ecology* 51: 19-27

Pandey S, Ansari WA, Pandey M and Singh B. 2018. Genetic diversity of cucumber estimated by morpho-physiological and EST-SSR markers. *Physiology and Molecular Biology of Plants* 1: 1-12

Panse VG and Sukhatme PV. 1984. Statistical methods for agricultural workers. ICAR, New Delhi. pp 381

Park G, Choi Y, Jung JK, Shim EJ, Kang MY, Sim SC, Chung SM, Lee GP and Park Y. 2021. Genetic diversity assessment and cultivar identification of cucumber (*Cucumis sativus* L.) using the fluidigm single nucleotide polymorphism assay. *Plants* 10: 395

Pati K, Munshi DA and Behera KT. 2015. Inheritance of gynoecism in cucumber (*Cucumis sativus* L.) using genotype GBS-1 as gynoecious parent. *Genetika* 47: 349-356.

Peakall R and Smouse PE. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics* 28: 2537-2539

Perrier X and Jacquemoud-Collet J P. 2006. DARwin software. <http://darwin.cirad.fr/darwin>

Preethi GP, Anjanappa M, Pitchaimuthu M, Devappa V, Ramachandra RK and Venugopalan R. 2016. Heterosis study in cucumber (*Cucumis sativus* L.). *Indian Journal of Pure Applied Biosciences* 7: 395-400

Pritchard JK, Stephens M and Donnelly P. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155: 945-959

- Punetha S, Singh D and Singh N. 2017a. Genetic diversity assessment of cucumber (*Cucumis sativus* L.) genotypes using molecular markers. *Electronic Journal of Plant Breeding* 8: 986-991
- Punetha S, Singh DK, Makanur B, Singh NK and Panday DT. 2017b. Heterosis studies for yield and yield contributing traits in cucumber (*Cucumis sativus* L.). *Plant Archives* 17: 21-27
- Rai PS, Mulge R, Kulkarni MS, Allolli TB, Hegde NK and Prabhuling G. 2018. Gene effects for fruit yield and its component traits in cucumber (*Cucumis sativus* L.). *International Journal of Current Microbiology and Applied Sciences* 7: 193-198
- Ranganna S. 1979. Manual of analysis of fruits and vegetables products. Tata Mc Graw Hill Book Company, New Delhi
- Reddy ANK, Munshi AD, Behera TK, Sureja AK and Sharma RK. 2014. Studies on combining ability in cucumber. *Indian Journal of Horticulture* 71: 349-353
- Ren Y, Zhang ZH, Liu JH, Staub JE, Han YH, Cheng Z, Li X, Lu J, Miao H, Kang H, Xie B, Gu X, Wang X, Du Y, Jin W and Huang S. 2009. An integrated genetic and cytogenetic map of the cucumber genome. *PLoS One* 4: e5795
- Rick CM. 1945. Field identification of genetically male sterile tomato plants to use in producing F₁ hybrid seed. *Proceedings of American Society for Horticultural Science* 46: 277-283
- Robou AMA and Hamed AA. 2011. Heterosis and combining ability in cucumber. *Egypt Journal of Plant Breeding* 15: 181-191
- Rohlf FJ. 1993. Numerical Taxonomy and Multivariate Analysis System, Version 2.02. Exeter Software: Setauket, New York
- Sadasivam S and Manickam A. 1992. In: Biochemical methods for agricultural sciences, Willey Eastern Limited, New Delhi, pp 6-11

Sarkar M and Sirohi PS. 2006. Gene action of quantitative characters including yield in cucumber (*Cucumis sativus* L.). *Indian Journal of Horticulture* 63: 341-342

Sarkar M and Sirohi PS. 2010. Combining ability analysis for yield and its contributing characters in cucumber. *Indian Journal of Horticulture* 64: 525-530

Sen B and Kapoor IJ. 1974. Field trials of systemic and non-systemic fungicides against powdery mildew of cucurbits. *Pesticides* 8: 43-46

Sharma M, Singh Y, Singh SK and Dhangra VK. 2016. Exploitation of gynoecious lines in cucumber (*Cucumis sativus* L.) for heterosis breeding. *International Journal of Bio-resource and Stress Management* 7: 184-190

Sharma M. 2006. Gene action and heterosis studies involving gynoecious lines in cucumber (*Cucumis sativus* L.). Ph.D. Thesis, pp 208. Department of Vegetable Science and Floriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishwavidyalaya Palampur, Himachal Pradesh, India

Shull GH. 1914. The genotype of maize. *America Nature* 45: 234

Simi F, Ivy NA, Sai HB, Akter S and Anik MFA. 2017. Heterosis in cucumber (*Cucumis sativus* L.). *Bangladesh Journal of Agriculture Research* 42: 731-747.

Singh D. 1973. Diallel analysis for combining ability over several environments. *Indian Journal of Genetics* 33: 469-481

Singh DK, Rajani T, Singh NK and Shashank SS. 2016a. Genetic diversity cucumber using inter simple sequence repeats (ISSR). *Transcriptomics* 4: 1

Singh G, Brar PS and Dhall RK. 2016b. Exploiting yield potential in Cucumber (*Cucumis sativus* L.) through heterosis breeding. *Plant Gene Trait* 7: 1-5

Singh HK and Tiwari A. 2018. Exploitation of heterosis for yield and contributing traits in cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry* 7: 395-397

Singh HK, Pandey S, Tiwari A and Singh MC. 2010. Heterosis and combining ability for yield and contributing traits in cucumber (*Cucumis sativus* L.). *Vegetable Science* 37: 64-66

Singh R, Singh AK, Kumar S, Singh BK and Singh SP. 2012. Heterosis and inbreeding depression for fruit characters in cucumber. *Indian Journal of Horticulture* 69: 200-204

Singh RK and Chaudhary BD. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India. p 146

Someh M, Kiani G, Ranjbar GA and Alavi SM. 2016. Assessment of genetic diversity in cucumber varieties using RAPD markers. *Journal of Applied Horticulture* 18: 64-67

Sood S, K Naveen, Chandel KS and Sharma P. 2011. Determination of genetic variation for morphological and yield traits in bell pepper (*Capsicum annuum* var. *grossum*). *Indian journal of Agricultural Sciences* 81: 590-594.

Sprague GF and Tatum LA. 1942. General vs specific combining ability in single crosses of corn. *Journal of American Society of Agronomy* 34: 923-932

Sprague GF. 1966. Quantitative genetics in plant improvement. *Plant Breeding Abstracts* 38: 202, pp 315-354

Sun Z, Staub JE, Chung SM and Lower RL. 2006. Identification and comparative analysis of quantitative trait loci associated with parthenocarpy in processing cucumber. *Plant Breeding* 125: 281-287

Sushir KV, Dumbre AD, Patil HE, Kamdi SR and Saitwal VM. 2005. Combining ability studies in cucumber (*Cucumis sativus* L.). *Journal of Soils and Crops* 15: 72-75

Tamang B, Bhutia KD, Kumar R, Sharma L and Bamaniya BS. 2018. Genetic variation and character association study in local cucumber (*Cucumis sativus* L.) genotypes of Sikkim. *Current Journal of Applied Science and Technology* 31: 1-9

Tatlioglu T. 1993. Cucumber (*Cucumis sativus* L.). In: *Genetic Improvement in Vegetable Crops*. Pergamon Press, New York.

Thakur M and Kumar R. 2020. Combining ability and gene action studies for different yield contributing traits in cucumber. *Indian Journal of Horticulture* 77: 491-495

Thapliyal. 2017. Heterosis and combining ability for yield and yield attributing traits of parthenocarpic cucumber (*Cucumis sativus* L.) under poly-net house conditions. M.Sc. Thesis, p 54. Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India

Tiwari JK, Munshi AD, Kumar R, Sharma RK and Sureja AK. 2009. Combining ability for yield and related traits in cucumber (*Cucumis sativus* L.). *Vegetable Science* 36: 159-162

Tiwari R and Singh DK. 2016. Study of heterosis and combining ability for earliness and vegetative traits in cucumber (*Cucumis sativus* L.). *Journal of Applied and Natural Science* 8: 999-1005

Umeh OA, Ngwuta AA, Onyishi GC and Anyanwu CP. 2021. Heterosis for yield and its components in cucumber (*Cucumis sativus* L.) in Owerri Southeastern Nigeria. *International Journal of Agricultural and Rural Development* 24: 5704-5710

Valcarcel JV, Perez-de-Castro A, Diez MJ and Peiro R. 2018. Molecular characterization of the cucumber (*Cucumis sativus* L.) accessions held at the COMAV's genebank. *Spanish Journal of Agriculture Research* 16: 2171-9292

Verma S. 2003. Genetic variability and correlation studies in cucumber (*Cucumis sativus* L.). M.Sc. Thesis, p 44. Department of Vegetable Science, Dr. Y S Parmar University of Horticulture and Forestry, Nauni, Solan, India

Vidhya C and Kumar S. 2014. Studies on combining ability in cucumber. *Cucumis sativus* L. *Trends in Bioscience* 7: 1891-1892

- Yadav JR, Singh SP, Parihar NS, Yadav JK, Mishra G, Kumar S and Yadav A. 2007. Combining ability for yield and its contributing characters in cucumber (*Cucumis sativus* L.). *Progressive Agriculture* 7: 116-118
- Yang YT, Liu Y, Qi F, Xu LL and Li XZ. 2015. Assessment of genetic diversity of cucumber cultivars in China based on simple sequence repeats and fruit traits. *Genetics and Molecular Research* 14: 19028–19039
- Yoshioka Y, Sugiyama M and Sakata Y. 2010. Combining ability analysis of fruit texture traits in cucumber by mechanical measurement. *Breeding Science* 60: 65-70
- Yuan XJ, Pan JS, Cai R, Guan Y, Liu LZ, Zhang WW, Li Z, He HL, Zhang C, Si LT and Zhu LH. 2008. Genetic mapping and QTL analysis of fruit and flower related traits in cucumber (*Cucumis sativus* L.) using recombinant inbred lines. *Euphytica* 164: 473–491

APPENDICES

APPENDIX-I

Meteorological data during the cropping season (April to August, 2020) inside the polyhouse.

Standard Weeks	Temperature Maximum (°C)	Temperature Minimum (°C)	Relative Humidity (%)
14	30.70	17.36	71.53
15	34.14	21.20	71.95
16	32.71	20.14	72.36
17	32.86	21.21	72.76
18	33.21	22.64	73.28
19	34.13	21.69	73.06
20	35.07	22.31	73.64
21	39.57	26.60	74.54
22	35.24	22.86	74.97
23	34.93	23.89	74.72
24	36.71	26.36	74.69
25	36.75	26.36	74.26
26	36.21	25.86	73.52
27	36.91	26.31	72.62
28	36.14	26.36	71.91
29	35.71	26.21	71.26
30	35.14	26.43	70.60

APPENDIX-II

Meteorological data during the cropping season (March to August, 2021) inside the polyhouse.

Standard Weeks	Temperature Maximum (°C)	Temperature Minimum (°C)	Relative Humidity (%)
10	23.49	13.74	49.36
11	27.56	17.57	49.64
12	27.56	17.57	49.64
13	29.84	16.30	45.71
14	31.36	20.37	57.07
15	32.50	21.76	53.36
16	34.33	23.36	70.29
17	35.74	24.44	48.71
18	36.03	24.76	63.71
19	36.56	25.61	72.93
20	37.39	26.31	61.86
21	37.74	26.69	52.43
22	38.64	27.56	66.57
23	38.91	28.26	65.79
24	37.64	27.74	81.71
25	37.26	28.01	74.71
26	36.40	28.49	66.00
27	35.53	28.00	69.71
28	34.70	27.76	90.43
29	33.87	27.70	98.14
30	33.53	27.60	100.29

Brief Biodata of student

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Academic Qualification

Sr. No.	Degree obtained	Years of passing	Marks obtained (%age)	Institution/ Board/ University
1.	Matriculation	2010	86.0%	CBSE, New Delhi
2.	B.Sc. Agriculture (Hons.)	2016	79.00%	PAU, Ludhiana (Punjab)
3.	M. Sc. Agriculture (Vegetable Science)	2018	81.9%	PAU, Ludhiana (Punjab)
4.	Ph. D. Agriculture (Vegetable Science)	2022	83.0%	CSK HP KV, Palampur (Himachal Pradesh)