GENETIC STUDIES FOR YIELD AND RELATED TRAITS IN CUCUMBER (*Cucumis sativus* L.)

THESIS

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By

Manisha Kumari

Id. No. H-10586/18

DEPARTMENT OF VEGETABLE SCIENCE

ACHARYA NARENDRA DEVA UNIVERSITY OF AGRICULTURE & TECHNOLOGY,
NARENDRA NAGAR (KUMARGANJ), AYODHAYA-224 229 (U.P.)
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आचार्य नरेन्द्र देव कृषि एवं प्रौद्योगिक विश्वविद्यालय, कुमारगंज, अयोध्या
ACHARYA NARENDRA DEVA UNIVERSITY OF AGRICULTURE & TECHNOLOGY, KUMARGANJ
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U.P. INDIA
उत्तर प्रदेश भारत
अन्नं हि जीवानां ज्येष्ठम्

DEDICATED

To My
Beloved Parents

Manisha….

Dr. C.N. Ram

Associate Professor

Department of Vegetable Science

A.N.D. University of Agriculture &
Technology, Narendra Nagar,
(Kumarganj), Ayodhya- 224229 (U.P.)

CERTIFICATE-I

This is to certify that the thesis entitled **“Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)”** submitted for the degree of **Master of Science** (**Horticulture)** in the subject of **Vegetable Science** of the Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya, is a bonafide research work carried out by **Miss. Manisha Kumari, Id.No.H-10586/18** under my supervision and that no part of this thesis has been submitted for any other degree.

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

Narendra Nagar

June, 2020

(C.N. Ram)

Major Advisor and Chairman,

CERTIFICATE-II

This is to certify that the thesis entitled **“Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)”**submitted by **Miss. Manisha Kumari, Id. No. H-10586/18** to the Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya in partial fulfillment of the requirements for the degree of **Master of Science** (**Horticulture)** in the subject of **Vegetable Science** has been approved by the student’s Advisory Committee after an oral examination on the same in collaboration with an external examiner.

( )
External Examiner

ADVISORY COMMITTEE

Major Advisor & Chairman

(C.N. Ram)
Associate Professor
Department of Vegetable Science

Member (Major)

(V. B. Singh)
Associate Professor
Department of Vegetable Science

Member (Minor)

(A. K. Singh)
Associate Professor
Department of Horticulture

Member (Related Field)

(D.K. Dwivedi)
Professor
Department of PMB &GE

Dean’s Nominee

(Sanjay Pathak)
Professor
Department of Post-Harvest Technology

Dean
College of Horticulture & Forestry

Head of the Department

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Narendra Nagar (Kumarganj) ***(Manisha Kumari)***

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Chapter-I

INTRODUCTION

Vegetables are important nutritive component of the daily diet because their nutritive value as a vital source of micronutrients has been well recognized. Thus, vegetables are getting increasingly higher importance in India as well as in the world due to their relevance in achieving nutritional security from emerging nutritional problems in human beings. India is the world's second largest producer of vegetables next only to China. In India, total area under vegetable production 10.43 million hectares with the total production of 187.47 million tons and productivity 17.01 MT per hectare (Anon.,2018-19).In the country, vegetable crops are grown only in 2.8% of total cultivated land and share about 12% of the world vegetable production with a productivity of 13.6 tonnes per hectare that is quite less as compared to other advanced countries. The present status of production is not sufficient to meet the vegetables requirement of 285g per capita per day. Considering the present situation as well as the growing demand of vegetable consumption to fulfil the need of next coming generations of the country, there is an urgent need to increase the productivity per unit area and overall production of the vegetables in the country.

Among the vegetable crops, cucumber (*Cucumis sativus*L.; 2n=2x=14) is considered as one of the major vegetable crops in India as well as in the world. Cucumber is the second most widely cultivated cucurbit in the world after watermelon. It is grown primarily for processing (pickling) or for fresh market (slicing). The cucumber fruit is said to have cooling effect, prevents constipation and checks Jaundice and indigestion (Nandkarni, 1927). The fruits are eaten with salt and pepper or as ingredient of salad and pickles. Immature fruit are also used with curd for the preparation of “Rayata”. Mature fruit are also used as Vegetable in India. The fruits are used as an astringent and antipyretic, while pulp of fruits is used for making mash cakes. The seed oil is also used as antipyretic.

Cucumber are rich in vitamin 'B' and 'C' as well as minerals such as calcium, phosphorus, iron and potassium. Besides those, it contains about 2.5% carbohydrate, 0.4% protein, 0.1% fat and 0.4% fibre. It has Antioxidants which help to discard substances from the body known as free radicals. Some free radicals come from natural bodily processes, and some come from outside pressures, such as pollution. If more accumulation in the body, they can lead to cell damage and various types of disease.

Cucumber is a thermophilic, day-neutral, frost susceptible and annual plant having climbing or trailing habit through axillary un-branched tendrils. It is basically a monoecious plant. The fruit is a special type of berry, commonly known as ‘pepo’. Cucumber is said to be native of Northern India (Purglove, 1969) and belongs to family Cucurbitaceae. The cucumber belongs to the genus *Cucumis* of which there are 20 to 25 species found mostly in Asia and Africa. Only two *Cucumissativus* (cucumber) and *Cucumismelo* (melon, muskmelon and Persian melon) are of commercial importance in North America. It is an annual trailing or climbing vine usually with flowers of both sexes on the same plant (monoecious). Current market hybrids are produced on genetically gynoecious lines (all female blooms). Commercial seed lots have up to 10% of a monecious variety to provide sufficient pollen for fruit set. European greenhouse cucumbers set fruit without pollination (parthenocarpic).

The cucumber is native to the North-West of India and has been cultivated from at least 3000 years. The calyx and corolla of staminate, pistilate and hermaphroditic flower are five lobed. The staminate flower have three stamens (two have bilocular anthers and the third has one anther, pistilate flowers are epigynous. Cucumber is open-pollinated and self-compatible. Pollination is takes placed by insects mainly bees.

It is grown throughout the year in southern states the India, however, in plains of Northern India, it is grown during summer and rainy seasons. In spite of being native of India and endowed with enormous variability for various plant characters, cucumber remains underutilized in context of its economic potential and unexploited from breeding point of view. The objectives of cucumber improvement include the development of early fruiting and high yielding varieties, uniform size, cylindrical fruit shape, soft seeds at edible maturity, free from bitterness, attractive green colour with smooth surface etc. along with resistance to biotic and abiotic stresses. The ultimate goal of any plant breeding programme is to evolve improved genotypes which are better than the existing ones. The assessment of parents for their ability to donate desirable genes to their off-springs is an important pre-requisite for a systematic plant breeding programme aimed at development of superior strains or variety.

The importance of genetic variability was perceived for the first time by a Russian scientist, Vavilov (1951) who advocated that wide range of variability provides better scope of selecting a desirable genotype. Earlier, Fisher (1918) partitioned the continuous variation exhibited by quantitative traits into heritable and non-heritable components because only phenotypic variability may not prove effective in crop improvement as the phenotypic variability depends upon the genotype, the environment and their interaction.

Since many important traits are quantitative in nature and are highly influenced by the environment, study of such traits using genetic parameters like heritability and genetic gain/genetic advance enable the breeders to predict the extent of advancement of traits through selection for identifying most potential genotypes. Yield being a complex and polygenic trait; depends upon large number of contributing traits and their interactions. Therefore, while improving yield, one should take the improvement of such yield contributing characters into account, provided that the correlations of such characters with yield are available. Further, correlation coefficient only indicates the nature of association among traits whereas, path coefficient analysis splits the correlation coefficient into measures of direct and indirect effect of each yield contributing characters.

Now-a-days, commercial F_1 hybrids are becoming popular in cucumber owing to high yield. Generally, diverse plants are expected to give higher yield (Harrington, 1940). Hence, it is necessary to study genetic divergence among the available germplasms for identification of parents to be included in the hybridization programme. The information of genetic divergence of various traits, particularly of those that contribute to yield and quality would be most useful. D^2 statistics developed by Mahalanobis (1928) provides a measure of magnitude of divergence between two genotypes under comparison. Grouping of genotypes based on D^2 analysis will be useful in choosing suitable parental lines for heterosis breeding.

Such studies are also useful in selection of parents for hybridization to recover superior progenies which can further be released as an improved open pollinated variety.Till date, very few public sector varieties are accepted by farmers for commercial cultivation. So, in order to isolate desirable genotypes with higher yield and better quality, there is an urgent need to assess the existing variability under specific environment (Saikia *et al.,* 1995).

Keeping these facts in view, the present investigation entitled "Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)"has been planted with the following objectives:

1. To find out the phenotypic and genotypic coefficient of variation (PVC and GCV),
2. to assess the heritability (in broad sense) and genetic advance,

3. to find out correlation and path coefficient among yield and its contributing traits and
4. to work out the genetic divergence among the genotypes.

Chapter-II

REVIEW OF LITERATURE

The literature pertaining to the various aspects of the present study has been reviewed under the following heads:

2.1 Genetic variability

2.2 Heritability and genetic advance in per cent of mean

2.3 Correlation coefficients

2.4 Path coefficient analysis and

2.5 Genetic divergence (D^2)

2.1 Genetic variability

The nature and extent of variability provides the basis of improvement for any crops. Genetic variability is the raw material with respect to yield and yield contributing traits on which selection acts to obtain superior genotypes or varieties in crop improvement programme. Some of the findings related to variability revealed in cucumber are reviewed as follows:

Karuppaiah *et al.* (2002) observed high GCV for number of female flowers per plant, yield per plant, number of fruits per plant and flesh thickness in ridge gourd.

Shetty and Whener (2002) evaluated the USDA cucumber germplasm collections and reported wide range of phenotypic variability for fruit size which could be selected to develop high yielding cultivar.

Das *et al.* (2003) reported high genetic variability for vine length, fruit length, fruit diameter and fruit weight in eighteen genotypes of cucumber. The pooled analysis revealed that the highest variability for marketable fruit yield and the genotypic coefficient of variation was high for marketable fruit yield and fruit weight.

Verma (2003) studied variability in twenty five diverse cucumber genotypes and observed significant differences for traits namely, days to first female flower appearance, node at which first female flower appears, number of days to first picking, fruit length, fruit diameter, fruit weight, number of marketable fruits per plant, harvest duration and fruit yield per plant. The maximum phenotypic and genotypic coefficients of variability were recorded for fruit yield per plant followed by node at which first female flower appears, harvest duration, fruit weight, fruit length and vine length. Rest all the studied traits had moderate or low co-efficient of variability at both phenotypic and genotypic levels.

Das *et al*. (2005) reported eighteen diverse cucumber genotypes for stability in the summer and rainy season was considerable and significant variability in traits namely vine length, fruit number, fruit length, fruit diameter and fruit weight.

Kumar (2006) studied genetic variability study in thirty five cucumber genotypes carried out by indicated significant differences among all the genotypes for node number at which first female flower appears, days to first female flower appearance, fruit weight, fruit length, number of fruits per plant and yield per plant. Phenotypic co-efficient of variability were higher in magnitude than genotypic co-efficient of variability for all the characters studied.

Munshi *et al*. (2007) reported highly significant variation for first fruit picking, fruit weight, fruits per plant, fruit length : diameter (L : D ratio) and yield per plant in thirty one indigenous accessions of Indian wild cucumber (*Cucumis sativus* L. var. *hardwickii*). The highest genotypic co-efficient of variation was recorded for fruit weight followed by number of fruits per plant, indicating the high selection response in respect of these traits.

Hanchinamani *et al*. (2008) studied forty five genotypes of cucumber for mean variability of twenty characters. Among the all the genotypes, Bheemarayana Gudi Local (BGDL) recorded the maximum mean value for number of primary branches and average fruit weight.

Kumar *et al*. (2008) evaluated twenty five diverse cucumber genotypes and recorded wide range of variability along with high estimates of phenotypic co-efficient of variation and genotypic coefficients of variation for days taken to first female flower anthesis, number of primary branches per plant, number of fruits per plant, fruit length, fruit weight and fruit yield per plant. The magnitude of phenotypic co-efficient of variation was higher than genotypic coefficients of variation for all the characters under study.

Mohd and Khan (2009) found wide range of phenotypic variation for the characters *viz*. fruit diameter, fruit length, fruit weight, number of fruit per plant and fruit yield per plant and also noted high genotypic coefficient of variation for these characters.

Yogesh *et al.* (2009) studied genetic variability, heritability and genetic advance for different characters in 20 diverse cucumber genotypes. The study indicated existence of considerable amount of genetic variability for all the traits except cavity of fruit at edible stage. The magnitude of phenotypic coefficients of variation (PCV) was higher than genotypic coefficients of variation (GCV) for all the traits under study and the maximum value of phenotypic and genotypic co-efficient was observed for number of days to first female flower anthesis followed by number of primary branches at maturity, number of nodes bearing female flower per plant and cavity of fruit at edible stage.

Yadav *et al.* (2009) revealed existence of considerable amount of genetic variability in twenty diverse genotypes of cucumber for all the traits namely, days to fifty per cent germination, days taken to first male and female flower anthesis, node number bearing first male flower, node number bearing first female flower, vine length, number of primary branches per plant, number of fruits per plant, fruit length, fruit diameter, fruit weight, days to first fruit harvest and edible fruit yield per plant except seed cavity of fruit at edible stage.

Hossain *et al.* (2010) evaluated fifty four cucumber genotypes and recorded wide variability for the traits like days to first male and female flower anthesis, number of fruits per plant, average fruit weight, fruit length, fruit diameter, days taken to seed germination and vine length. Highest genotypic coefficient of variation was recorded for yield per plant followed by number of fruits per plant, fruit length and node number bearing first male and female flowers.

Shukla *et al.* (2010) carried out an experiment with twenty morphologically diverse cucumber genotypes to assess genetic variability. Results recorded high estimates of genotypic coefficient variation for fruit yield per plant, fruit length, vine length, number of fruits per plant, node number bearing first female flower, internodal length, diameter of fruit and number of nodes per vine, indicating their reliability for effective selections.

Arunkumar *et al.* (2011) observed variability for number of female flowers per vine, number of male flowers per vine, number of branches per vine, average fruit weight, number of good fruits per vine, total number of fruits per vine and total fruit yield per vine. High PCV and GCV were recorded for number of misshaped fruits per vine whereas, moderate PCV and GCV were observed for number of good fruits per vine, total number of fruits per vine, fruit diameter and total fruit yield per vine.

Gaikwad *et al*. (2011) evaluatedeighteen genotypes of cucumber for genetic variability. A high degree of variation was observed in respect of all the characters studied. The estimates of genotypic coefficient of variation were slightly low as compared to estimates of phenotypic coefficient of variation indicating the substantial modifying effect of environment in the expression of the traits studied. The high genotypic as well as phenotypic coefficient of variation was observed for characters such as PDI followed by length of fruit, number of fruits per vine, weight of fruit and node number of first female flower.

Kumar *et al.* (2011) recorded wide variability for number of female flowers, male flowers and primary branches per vine, average fruit weight, number of marketable fruits, total fruits and yield per vine. Further, high phenotypic as well as genotypic coefficient of variation was recorded for number of unmarketable fruits whereas, it was moderate for number of marketable and total fruits per vine, fruit diameter and yield.

Yadav *et al.* (2012) assessed twenty diverse genotypes of cucumber and revealed variability for fruit weight, germination percentage, days to first fruit harvest, days to anthesis of first male and female flowers, node number bearing first male and female flowers, vine length, number of branches per vine, hundred seed weight, seed cavity of fruits at edible stage and fruit yield per vine.

Ullah *et al.* (2012) grown twelve exotic cultivars of cucumber (*Cucumissativus*) to assess the presence of variability for desired traits and amount of variation for different parameters. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for yield per plant, fruits per plant, fruit weight and fruit length.

Veena *et al*. (2012) evaluated 38 advanced lines of cucumber for variability for yield and contributing traits. Highest variability for node at first female flower appearance followed by node at first male flower appearance, yield per plant, seed cavity breadth, average fruit weight and number of fruits per plant.

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

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

Khan *et al.* (2015) evaluated twenty four genotypes of cucumber to find out their similarities and differences based on quantitative traits. The experiment was laid out in Randomized Complete Block Design (RBCD) with replicated twice. Quantitative traits of the genotypes were measured according to the coding criteria specified by European Cooperative Programmed for Plant Genetics Resources (ECPGR) 2008. Data showed much variation for almost all the traits. Maximum germination (67.5%) was observed in genotype Mardan local while minimum germination (17.5%) was recorded in genotype 28295. The genotypes Haripur local and 28293 showed early flowering. Similarly highest yield was observed in USA Poinsett, Dargai local and Mardan local. These genotypes could be chosen for crossing with other genotypes like 28295 and Sialkot selection having low germination rate and low yield to get a better genotype of cucumber with high germination and maximum yield. Correlation analysis represent that yield was positively correlated with fruit length (0.523** $P \leq 0.01$) and fruit width (0.439* $P \leq 0.01$). While fruit per plant showed positive significant correlation with vine length.

Pal *et al.* (2016) revealed that magnitude of PCV was higher than the corresponding GCV for all the characters studied. High GCV was recorded for node number bearing first female flower (33.68%), number of marketable fruits per plant (41.41%), number of primary branches per plant (31.22%), seed vigour index II (37.38%), yield per plant (43.76%) and disease severity of angular leaf spot (41.09%), anthracnose (43.91%), downy mildew (38.72%) and powdery mildew (40.12%).

Pushpalatha *et al*. (2016) carried out an experiment to assess variability existing in twenty four diverse cucumber genotypes. Results revealed high phenotypic and genotypic coefficient of variation for yield per plant, fruit flesh thickness, number of fruits per plant, number of nodes per plant, number of branches per plant, average fruit weight, internode length and vine length.

Ene *et al*.(2016)evaluated sixteen cucumber (*Cucumissativus* L.) genotypes in the early and late planting seasons to estimate the magnitude of their genetic variability. A high coefficient of variation was recorded for most traits in both seasons and high variability was found among genotypes. High broad-sense heritability was associated with all the traits in both seasons, except for mean fruit weight in the early planting season and fruit girth, mean fruit weight, and total fruit yield in late planting season. Principal component analysis involved vine length as the most discriminating trait that accounted for greater variability in cucumber in both the early and late planting seasons, and it should be considered in cucumber improvement programs.

Rajawat and Collis(2017) clearlyindicated existence of considerable amount of genetic variability for all the traits in all the genotypes of cucumber used in the experiment. The maximum phenotypic and genotypic coefficient (PCV and GCV) was observed for number of female flowers per vine (19.28 and 21.54), number of male flowers per vine (19.62 and 20.79), fruit yield per vine (19.86 and 19.88), number of branches per vine (13.79 and 16.29), number of fruits per vine (14.20 and 15.51), node number at which first male flowers appear (10.11 and 15.22), node number at which first female flowers appear (12.7 8 and 15.14) and fruit length (11.66 and 11.92).

Kandasamy(2017)evaluated twenty diverse genotypes of cucumber collected from Tamil Nadu and Kerala regions for morphological characters like days to first female flowering, node number of first female flower, vine length, number of secondary branches, days to fruit harvest, fruit length, fruit girth, fruit diameter, average fruit weight, number of fruits per plant, 1000 seed weight and yield per plant to estimate the variability, heritability, genetic advance. In variability studies, yield per vine was obtained highest mean value CS 6 genotype. Maximum phenotypic and genotypic co-efficient of variation (PCV and GCV) was for yield per plant followed by average fruit weight, fruit diameter and number of fruits per plant.

Deepa *et al*. (2018) studied research involving thirty cucumber genotypes in Randomized Block Design with three replications. Estimates of phenotypic co-efficient of variation (PCV) were higher than the corresponding values of genotypic coefficient of variation (GCV), High phenotypic and genotypic co-efficient of variation were observed for vine length, average fruit weight, fruit length.

Shah *et al.* (2018) reported that the phenotypic coefficient of variations (PCV) was higher than the genotypic coefficients of variations (GCV) for all traits studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the characters. The genotypic coefficients of variation and phenotypic coefficients of variation were moderate to low for all the characters except number of nodes bearing first male flower (33.02%, 33.66%) showed high GCV and PCV.

2.2 Heritability and genetic advance in per cent of mean

The concept of heritability is important to determining whether phenotypic differences observed among various individuals are due to genetic changes or influence of environmental factors. The genetic gain is the product of heritability and selection differential expressed in terms of phenotypic standard deviation of that character, heritability and genetic advance both are the components of direct selection parameters. It is necessary to utilize heritability estimates in conjunction with selection differential which indicates the expected genetic gain.

Verma (2003) observed high heritability along with high genetic gain for fruit yield per plant, indicating that this character is under additive gene effects whereas, high heritability estimates coupled with low genetic gain were observed for number of marketable fruits per plant and node number bearing first female flower, indicating non-additive gene effects for these characters.

Das *et al*. (2003) studied heritability in broad sense and genetic advance for fruit yield per vine and six other characters (vine length, number of primary branches per vine, number of fruits per vine, fruit length, fruit diameter and fruit weight) in 18 genotypes of cucumber. They reported that all the characters were highly heritable in nature. High heritability coupled with high genetic advance as percentage of mean was observed for fruit yield per vine and fruit weight, which indicated that these characters are more reliable for effective selection.

Kumar (2006) recorded highest heritability and genetic gain for node number bearing first female flower while, **Gulamuddin *et al*. (2006)**studying twenty five diverse cucumber genotypes, recorded high heritability and genetic gain for all the characters studied whereas, fruit width showed moderate heritability.

Afangideh and Uyoh (2007) imported eleven exotic cucumber cultivars from Nigeria and evaluated in USA along with six indigenous cultivars. They recorded highest genetic gain for vine length whereas, high heritability estimates were obtained for days to flower anthesis and days to fifty per cent flowering.

Kumar *et al*. (2008) recorded high heritability and high genetic gain for days to first female flower anthesis, number of fruits per plant, fruit length, fruit diameter, at edible stage and fruit yield per plant. The results indicated that these characters had additive gene effect and therefore, these are more reliable for effective selection.

Mohd and Khan (2009) recorded high heritability along with high genetic advance for the characters namely, fruit length, fruit weight, number of fruits per plant and fruit yield per plant, revealing that these characters are governed by additive genes.

Yadav *et al*. (2009)noted high estimates of heritability for node number bearing first female flower, fruit length, fruit diameter, fruit weight, days to first fruit harvest, number of fruits per plant and fruit yield per plant. Further, maximum genetic advance was recorded for number of days to first female flower anthesis followed by fruit weight, days to first fruit harvest, number of days to first male flower anthesis, fruit length and number of fruits per plant.

Gaikwad *et al*. (2011) found high heritability estimates (Broad sense) for all characters. The high estimates of heritability and genetic advance were recorded for final vine length and weight of fruit.

Veena *et al.* (2012) estimated high heritability and high genetic advance over mean for nodes per vine (83.43), node at first female flower appearance (82.17), days to first female flower opening (83.72), days to first male flower opening (92.63), days to first harvest (83.04), number of fruits per plant (85.78), fruit length (88.92), fruit breadth (86.91), seed cavity length (85.97), seed cavity breadth (85.09), number of seeds per fruit (95.17) and 100 seed weight (93.10) thus indicating that these characters had additive gene effect and therefore, they are more reliable for effective selection.

Jat *et al.* (2014) observed high estimates of heritability (broad sense) for days to anthesis of first female flower (96.66 per cent), weight of fruit (92.67 per cent) and diameter of fruit (92.51 per cent) with high genetic advance. The maximum genetic advance in per cent of mean were observed for acidity of fruit (54.06), weight of fruit (47.71) and total yield per vine (47.49). Hence, it can be concluded that selection would be rewarding for acidity of fruit, total yield per vine, weight of fruit, number of fruits per vine, total soluble solids and diameter of fruit in bringing out the improvement in the Valan Kakri.

Basavarajeshwari *et al*. (2014) recorded high heritability coupled with high genetic advance for the characters *viz*. vine length and node number of first female flower. Hence these traits can be improved by selection. Similarly, high heritability with low genetic advance over mean was observed for days to first male flower anthesis, indicating the predominance of non-additive gene action for these characters. Hence, these traits can be improved by hybridization with divergent genotypes to produce transgressive segregants.

Ranjan *et al*. (2015) recorded high heritability for characters namely, number of fruits per plant, number of primary branches per plant and fruit length showed moderate heritability. Further, low heritability was recorded for vine length, fruit diameter, fruit weight.

Pushpalatha *et al.* (2016) revealed high heritability, coupled with high genetic advance as per cent mean for all the characters studied except days to first female flower opening, days to 50% flowering and days to first fruit harvest, indicating a scope for improvement through selection.

Rajawat and Collis (2017) found high genetic advance over mean coupled with high heritability in characters like number of male flowers per vine, vine length and fruit weight (g). However, the estimates were moderate for number of female flowers per vine. Higher heritability estimates were accompanied by lower genetic advance over the mean for vitamin C, TSS, fruit yield per vine and days to first fruit harvest. The maximum genetic gain in per cent was recorded for fruit yield per vine (kg), number of male flowers per vine, number of female flowers per vine, number of fruit per vine, number of branches per vine, fruit length and node number at which first appears of female flower.

Shah *et al.* (2018) estimated high heritability coupled with high genetic advance for most of the traits *viz.*, fruit length (100%, 58.40%), fruit weight (99%, 39.92%), vine length (98%, 36.12%), number of seeds per fruit (98%, 50.16%), number of nodes per vine (97%, 53.57%), number of fruits per vine (97%, 44.33%), number of nodes bearing first male flower (96%, 66.74%), total soluble solids (96%, 44.25%), calcium content (95%, 21.75%), number of nodes bearing first female flower (94%, 58.36%), duration of harvesting (93%, 36.04%), total fruit yield per vine (92%, 35.93%) and diameter of fruit (92%, 35.80%) thus indicating that these traits had additive gene effect so that, they are more reliable for effective selection.

Kumar *et al.* (2018) revealed that the characters like primary branches per plant, days to first male flowering, days to first female flowering, days to 50% male flowering, days to 50% female flowering, days to first fruit harvest, days to last harvest, number of seeds per fruit, TSS, carotenoids, acidity, ascorbic acid and fruit yield per vine recorded high heritability in conjunction with high genetic advance as percent of mean, suggests the predominant role of additive genetic component in governing of these traits and improvement of these traits through simple selection can be employed in cucumber.

Pradhan *et al*. (2018) were observed high heritability and high expected genetic gain for days to 1st male and female flower bloom, days to first fruit harvest, fruit yield per hectare, fruit length, fruit girth, fruit weight, vine length, no of branches per vine, internodal length, sex ratio indicating that these characters had additive gene effect and therefore are more reliable for effective selection.

Setyaningastuti (2019) revealed that the days to first harvest, fruit length, fruit weight, fruit diameter, and flesh thickness give high heritability while, the number of fruits and potential yield per hectare gives moderate heritability, and seed rendement gives low heritability.

Bartaula *et al.*(2019) estimated heritability in broad sense ranged from 0.74 for fruit diameter to 0.98 for days to germination. Traits namely weight per fruit, days of germination, number of flower and days to flowering can be used effectively in selection process of crop improvement program as they had heritability along with high genetic advance as percentage of mean.

Deepa *et al.*(2018) studied research involving thirty cucumber genotypes and found high heritability coupled with high to moderate genetic advance were observed for all the characters except for days to first male and female flowering and fruit set percentage.

2.3Correlation coefficient analysis

Correlation measures the degree and direction of relationship between two or more variable. Study of character association helps to breeder in fixing a selection criteria for seed yield in parental lines showed that selection will be effective in isolation than the correlation of phenotypic values and subjected to change in the environment. A brief review of several workers on the association of characters in garden pea is presented below:

Ram *et al*. (2001) recorded that biological yield per plant had positive and significant correlation with fruit yield and number of fruits per plant whereas it was negatively and significantly correlated with fruit length and diameter.

Singh *et al*. (2002) studied ninety eight hybrids of cucumber. Highly positive and significant correlation of fruit weight, fruit length and fruit diameter with fruit yield. The genotypic correlation co-efficient were higher than the phenotypic correlation co-efficient for all the traits, which indicated strong inherent association among these traits.

Qian *et al*. (2002) observed eight selected inbred lines of gynoecious parthenocarpic cucumber (*Cucumis sativus*) as experimental materials, the genetic correlation of six agronomic characters of cucumber were studied by the second method of Griffin's complete diallel cross. The fruit yield showed positive genetic correlation with single fruit weight, fruit number per plant, leaf area and plant height. No significant genetic correlation was found between fruit yield and stem number per plant.

Verma *et al.* (2003) carried out the correlation studies among different horticultural traits in twenty five genotypes of cucumber and reported that fruit weight had positive and significant correlation with days to first picking, fruit length and fruit yield per plant. Further, first female flower anthesis had positive and significant correlations with number of days to first picking at both phenotypic and genotypic levels.

Rao *et al*. (2004) recorded that fruit yield was positively correlated with fruit weight and fruit length, that was negatively correlated with days to first female flower anthesis at both genotypic and phenotypic levels.

Ying *et al*. (2004) studies carried out correlation in eight selected lines of gynoecious parthenocarpic cucumber for six agronomic characters. They observed positive genotypic correlation of yield with single fruit weight, number of fruits per plant vine length but no significant genetic correlation was found between yield and number of primary branches per plant.

Dhiman and Chander (2005) reported that the genotypic correlations were higher than the phenotypic correlations for the characters *viz*. fruit length, fruit diameter, days to first male flower anthesis, days to first female flower anthesis, fruit yield.

Kumar (2006) studied character association in thirty five diverse genotypes of cucumber was carried results revealed that number of fruits per plant, fruit length, fruit diameter and fruit weight had positive and significant correlation with fruit yield per plant, at both genotypic and phenotypic levels whereas, days to first female flower anthesis. In all the traits studied, the genotypic correlation co-efficient were slightly higher in magnitude than phenotypic correlation co-efficient.

Afangideh and Uyoh (2007) studied genetic correlation in USA in eleven exotic genotypes from Nigeria and six indigenous cucumber cultivars. Linear correlation analysis showed that number of fruits per plant and length of vine were significantly and positively associated with yield, while days to first female flower anthesis and fruit yield.

Parihar *et al*. (2007) evaluated forty five F_1's along with fifteen lines and three testers of cucumber and estimated the phenotypic and genotypic correlation co-efficient among the characters observed. Highly significant and positive association was found between fruit yield per plant with number of fruits per plant, average fruit weight, fruit length, vine length. Further, association of vine length with fruit length was positive and significant whereas, fruit length showed significant negative association with days taken to first female flower anthesis.

Kumar *et al*. (2008) studied character association in twenty five diverse cucumber genotypes. The fruit yield per plant was found to be significantly and positively associated with number of primary branches, whereas, significant and negative correlation was recorded for fruit yield, days to first fruit harvest with fruit length and fruit length.

Hanchinamani and Patil (2009) evaluated forty five cucumber genotypes and recorded positive and significant association of fruit yield with vine length, number of primary branches, fruit length, fruit diameter, average fruit weight. Strong association of these traits revealed that selection based on these traits could ultimately improve fruit yield.

Mohd and Khan (2009) recorded significant positive correlation of fruit yield per plant with fruit weight and number of fruits per plant at both genotypic and phenotypic levels. Further, average fruit weight exhibited significant positive correlation with fruit length whereas fruit length had negative correlation with number of fruits per plant.

Singh *et al*. (2009) assessed fifteen diverse cucumber genotypes and recorded positive and significant correlation of number of fruits per plant with number of primary branches per plant and fruit weight.

Yadav *et al*. (2010) evaluated twenty diverse genotypes of cucumber and recorded correlation of number of days taken for fifty per cent germination with number of days to first female flower anthesis whereas, correlation of the former was reported to be negative and non-significant, fruit diameter and fruit weight. At the phenotypic level, fruit yield per plant was positively and significantly correlated with number of primary branches per plant, number of fruits per plant. The trait, number of primary branches exhibited highest positive and significant correlation with fruit yield whereas, maximum negative association was noted to fruit yield.

K**umar *et al*. (2011)** recorded positive significant correlation of fruit length, fruit diameter, average fruit weight, number of nodes per plant and vine length with fruit yield. Whereas, fruit yield showed negative and significant correlation with days to first harvest.

Kumar *et al.* (2011) investigated an experiment and found that fruit yield was positively correlated with total number of fruits per vine, number of good fruits per vine, average fruit weight, fruit length, number of misshaped fruits per vine, fruit diameter, number of branches per vine, number of nodes per vine and vine length. While it was significant and negatively correlated with days to first male flower, days to first female flower and days to first fruit harvest.

Ullah *et al*. (2012) revealed yield per plant were highly significant positive correlation with fruits per plant, fruit weight, flesh thickness, fruit diameter and leaves per plant. Partial correlation was significant for fruits per plant and indicated these traits contributed over 70% to total fruit yield.

Bhardwaj and Kumar (2012) revealed that the analysis of variance indicated significant differences among the genotypes for all the characters under study. Correlation studies indicated that yield was significantly and positively correlated with all the seed characters under study. Hence direct selection on the basis of seed germination, dry seedling weight, seedling length, seed vigour index-I and seed vigour index-II is reliable for yield improvement in cucumber.

Veena *et al.* (2013) investigated thirty eight cucumber genotypes and recorded maximum positive correlation of hundred seed weight with yield per plant. Similarly, number of fruits per plant, average fruit weight, fruit length, flesh thickness and seed cavity length had significant positive correlation with yield.

Khan *et al.* (2015) revealed that yield was positively correlated with fruit length, fruit diameter and vine length. Further, number of fruits per plant had positive and significant association with fruit diameter and vine length.

Kumari (2017) estimated correlation analysis and yield was positively correlated with fruit length (0.523** P≤0.01) and fruit width (0.439* P≤0.01). While fruit per plant showed positive significant correlation with vine length. Present findings are applicable in cucumber cultivation in swat and other areas with similar climatic conditions. This will intern help to improve the economic return and revenue generation of the farmers.

Ene*et al.* (2016) showed a highly significant difference (p<0.01) among the genotypes in all the traits studied in both seasons. ‘Beit Alpha’ genotype gave the highest fruit yield/ha in early season planting, while in the late season, the highest yield producer was ‘Ashely’. In both seasons, vine length, number of branches and leaves, leaf area, number of pistilate and staminate flowers/plant, number of fruit and fruit weight/plant showed positive and significant correlation with total fruit yield/ha.

Kumari *et al.*(2018) proposed the fruit yield per plant had significant and positive correlations, *viz*., both genotypic and phenotypic with traits like average fruit weight (g), number of fruits per plant, number of pistilate flowers per plant, fruit width (cm), vine length (cm), and number of nodes per vine.

2.4 Path coefficients analysis

Path coefficients analysis is a standardized partial regression coefficient, which separate the correlation coefficients into measures of direct and indirect effects and also measures the direct and indirect contribution of various independent variables on dependent variables. Correlation in combination with path analysis would give better insight into cause and effect relationship between different pair of characters. The works of different breeders are reviewed in reference to cucumber:

Singh *et al*. (2002) studied path analysis of ninety eight cucumber hybrids where fruit weight had highest direct effect on fruit yield. Further, fruit length and fruit diameter had also shown direct effect on yield per plot whereas, the indirect effect of other characters like fruit length though negligible, were negative, indicating that selection for high yield via fruit length is likely to show reduction in expression of other characters.

Rao *et al*. (2004) evaluated thirty one cucumber genotypes and revealed that characters namely fruit weight, number of fruits per plant, fruit yield and concluded that these characters are both dependable and reliable for selection in order to improve fruit yield.

Ying *et al*. (2004) carried out path analysis in eight selected inbred lines of gynoecious parthenocarpic cucumber and recorded that the yield was affected mostly by single fruit weight and fruit number per plant and was indirectly affected by vine length.

Dhiman and Chander (2005) carried out path co-efficient analysis in fifteen diverse genotypes of cucumber and reported that yield followed by fruit diameter.

Kumar *et al*. (2008) revealed path analysis at phenotypic level carried that higher and positive direct effect of number of fruits per plant followed by number of primary branches per plant and fruit diameter on fruit yield.

Hanchinamani and Patil (2008) recorded high positive direct effect of average fruit weight through phenotypic path coefficient analysis of forty five genotypes of cucumber. The average fruit weight had the highest positive and direct genotypic effect on fruit yield. Hence, it would be rewarding to lay stress on these characters in selection programmes for increasing fruit yield.

Singh *et al*. (2009) while studying fifteen diverse genotypes of cucumber, recorded positive direct effect of number of fruits per plant and fruit weight on fruit yield per plant. Therefore, they suggested giving high priority to traits *viz*. number of primary branches per plant, number of fruits per plant and fruit weight while selecting for fruit yield.

Hossain *et al*. (2010) evaluated fifty eight long type cucumber accessions and concluded that fruit length, fruit diameter, average fruit diameter and number of fruits per plant had positive and direct effect on fruit yield per plant.

Kumar *et al*. (2011) evaluated six hundred F_2 plants resulting from a cross between Bheemarayana Gudi Local (BGDL) and Hot Season and noted maximum positive direct effect of total number of fruits, number of primary branches and vine length and days to first male flower anthesis on fruit yield whereas, traits namely, days to first female flower anthesis, days to first fruit harvest, and yield.

Kumar *et al.* (2011) revealed that the maximum positive direct effect on yield for total number of fruits per vine, number of branches per vine, number of nodes per vine, vine length and days to first male flower whereas, negative and maximum direct effect on yield was observed for days to first female flower, number of good fruits per vine, fruit diameter, days to first fruit harvest, number of misshaped fruits per vine and fruit length.

Veena *et al*. (2013) recorded positive direct effects of seed cavity breadth, flesh thickness, average fruit weight, fruit days to first female flower anthesis and number of fruits per plant on yield per plant whereas, node number bearing first female flower, days to first male flower anthesis, days to first fruit harvest and fruit diameter had negative direct effect on yield.

Kumar *et al.* (2013) studied path co-efficient analysis for yield and yield contributing characters namely average weight of fruit (g), average diameter of fruit (cm), days to anthesis of first male flower, days to anthesis of first female flower, node number at which first female flower appeared, days to maturity, number of primary branches, vine length (cm), sponge gourd genotypes. Path co-efficient analysis revealed that average diameter of fruit, number of primary branches, number of fruits per vine, average weight of fruit and total soluble solids showed positive direct effects on total yield per vine. Hence, selection for these traits for improving fruit yield per vine in sponge gourd is suggested.

Pal and Sharma (2016) studies path analysis provided a clear picture that, harvest duration had maximum negative indirect effect followed by fruit diameter, number of primary branch per plant, vine length, and fruit harvest duration.

Pal *et al*. (2017) revealed that harvest duration had maximum positive direct effect, followed by marketable fruits per plant while, days to first harvest had maximum negative direct effect followed by severity of downy mildew on yield plant-1. Further, harvest duration exerted maximum positive indirect effect via marketable fruits plant-1 whereas; severity of powdery mildew showed maximum negative indirect effect via harvest duration on yield plant-1. Thus, while conducting selection for yield improvement in cucumber, a breeder will have to emphasize on the early genotypes having more average fruit weight, longer fruits, more fruit diameter, more number of marketable fruits and primary branches plant^{-1}, longer vine as well as harvest duration, more seed length, seed germination percentage, vigour index I and II with minimum severity of economically important foliar diseases**.**

Pushpalatha *et al*. (2017) studied path analysis in twenty four diversified genotypes of cucumber. The results revealed high phenotypic and genotypic co-efficient of variation for yield per plant, number of fruits per plant, number of branches per plant, average fruit weight and vine length. Genotypic correlation co-efficient were higher than phenotypic coefficients further indicating the inherent relationship among the characters studied. The path analysis also showed high direct effects of number of fruits per plant, average fruit weight.

Kumari *et al.*(2018) studied path coefficient analysis and revealed that the traits like number of fruits per plant and average fruit weight (g) have positive and direct genotypic and phenotypic effects towards the fruit yield.

Karthick *et al.* (2019) studied relationship between various horticulture traits and yield per plant in cucumber. Here, how the traits are correlated with yield per plant and also direct and indirect effect of traits on yield per plant was calculated. The yield per plant had genotypic and phenotypic significant positive correlation with length of vine, number of female flower, number of fruit per plant, fruit length, fruit diameter and fruit weight where as significant negative correlation with node number bearing first female flower, number of male flower and sex ratio. The yield per plant also had genotypic significant negative correlation with days to first female flower and days to first harvest. Number of fruits per plant had maximum positive direct and indirect effect on yield per plant.

2.4 Genetic divergence

Genetic diversity is an essential requirement for increasing crop productivity through breeding. Selection of diverse parent in breeding programme helps in isolation of superior recombination using cluster analysis, such as D^2 analysis, principle components analysis and metroglyph analysis which have shown to be useful in selecting genetically distant parent. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advance generation.

D^2 analysis is useful in identification of divergent parent for use in the hybridization programme and it is only possible by replicated data. In

D^2 analysis the genetic diversity is depicted by the cluster representing number of groups in which a population can be classified on the basis of D^2 statistics. A brief review of studies on genetic divergence in cucumber is presented below:

Prasad *et al.* (2001) analyzed diversity pattern using D^2 statistics in sixty inbred lines of cucumber to point out superior parents for a hybridization programme, for thirteen characters involving growth, flowering, fruiting ability and yield. Irrespective of their allelic relationship and area of collection, all inbreds, grouped in ten clusters, showed considerable diversity. Maximum genetic divergence was recorded for the trait number of nodes per plant followed by number of branches per plant and node bearing first female flower. Keeping the diversity pattern in view, seven out of sixty inbreeds were chosen from well separated clusters for hybridization programme. The study revealed that genetic drift and selection in different environments seem to cause greater diversity rather than geographic isolation.

Rao *et al.* (2003) estimated genetic divergence for fifteen quantitative traits in thirty one cucumber cultivars, results recorded significant variation among the cultivars for all the characters. Based on D^2 values, the cultivars were grouped into sixteen highly divergent clusters. The intra-cluster distance ranged from 30.99 to 85.14. The inter-cluster distance was highest between clusters XII and IV. Cluster XII exhibited the lowest number of days to first female flower anthesis, node number bearing first female flower and days to first fruit harvest. Cluster VII was characterized by the maximum maturity period, fruit weight, fruit length and fruit diameter.

Kanwar and Rana (2006) studied twenty six genotypes of cucumber by forming five clusters and recorded wide genetic divergence for all the characters studied namely, days to first female flower anthesis, harvest duration, fruit yield, number of fruits per plant, fruit weight, fruit length, number of primary branches per plant and vine length and days to first harvest and fruit diameter. The genotypes in the clusters were independent of their geographical distribution. Maximum intra-cluster distance was recorded in the genotypes in cluster I followed by cluster number V and II, while maximum inter cluster was noted between cluster I and II followed by clusters II and III. Cluster number IV recorded fruit highest yield followed by cluster number III.

Sharma and Sharma (2006) seven clusters were formed while carrying out genetic divergence study for fruit yield and contributing traits in thirty one diverse indigenous genotypes of cucumber. The genotypes Jorji Local, Bengal 60, JJL and Derabassi Local were promising in terms of fruit yield per plant and fruit length, while Gyn-2, Gyn-3 and Gyn-4 were superior for number of fruits per plant. However, genotypes Chakkimore Local, Farukabad Local, Chamoli Local and Chamba Local were promising for average fruit weight and fruit diameter.

Hossain *et al*. (2010) studied genetic divergence in fifty eight land races of cucumber and D^2 analysis resulted eight clusters, of which, cluster II contained highest number of genotypes followed by clusters III, IV, V, I, VI, VII, VIII. The clustering pattern showed that the genotypes were divergent irrespective of their geographical distribution. Cluster VIII containing only two genotypes recorded highest cluster mean value for fruit length, fruit diameter, average fruit weight and fruit yield per plant, which are considered as main parameters as far as yield is concerned. Cluster VII ranked second in this regard.

Gaikwad *et al.* (2011) conducted genetic diversity studies in eighteen cucumber genotypes for various characters and revealed substantial differences for all characters. The accessions were grouped into eight clusters with Cluster-A and Cluster-B comprising of five genotypes each followed by Cluster F, which contained three genotypes. The maximum inter-cluster distance (D = 11.24) was observed between F and H. Intercrossing among the genotypes belonging to Cluster C, D, F, G and H was suggested to develop high fruit yielding varieties with other desirable characters.

Al-Rawahi *et al*. (2011) while studying genetic diversity on morphological traits in twenty four cucumber genotypes formed two main clusters and sub divided one cluster in five sub groups. Results revealed significant diversity in all accessions and higher diversity index for agronomic, fruit characters.

Manohar and Murthy (2011) studied genetic divergence in thirty genotypes of cucumber for thirty phenotypic characters and powdery mildew resistance. The collections, grouped into five clusters, showed appreciable phenotypic diversity in vine length, fruit length, fruit diameter, average fruit weight. The greater part of diversity was accounted for fruit length, number of nodes per plant, average fruit weight.

Punitha *et al*. (2012) while evaluating forty one genotypes of cucumber confirmed the presence of wide genetic diversity through D^2 analysis. Genotypes were grouped into seven clusters which showed lack of parallelism between geographic and genetic diversities. Among the clusters, inter-crossing the genotypes in the cluster I, II, IV and V had high mean values for many characters studied, is likely to result in an enlargement of spectrum of divergence facilitating the selection for higher fruit yield. Among the characters studied, fruit diameter, average fruit weight showed high genetic divergence.

Kumar *et al.* (2013) estimated genetic divergence and the genotypes were grouped into 4 clusters and the highest (6.168) inter cluster distance was recorded between cluster-II and III. The diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, selection of divergent parents should be based on these cluster distances to obtain favourable hybrids and transgressive segregants in cucumber.

Hasan *et al*. (2015) genetic divergence was studied in seven commercial cultivars of cucumber and genotypes were grouped into three clusters. Highest inter-cluster distance was recorded between cluster I and II whereas lowest inter-cluster distance was recorded between the clusters I and III. Cluster II showed highest mean for vine length, number of nodes per plant, number of primary branches per plant, days to first male flower anthesis, number of fruits per plant and fruit yield per plant whereas cluster III recorded highest mean for fruit length, fruit diameter and average fruit weight.

Pal *et al.* (2017) estimated genetic divergence analysis, using Mahalanobis D^2 statistics, in thirty indigenous cucumber genotypes for twenty four characters. All the character under study showed considerable divergence and the genotypes were grouped into five clusters. The clustering pattern had no parallelism between genetic diversity and geographical distribution, suggesting that the selection of parental genotypes for hybridization will be more appropriate based on genetic diversity. Cluster III contained the maximum (15) number of genotypes, whereas cluster I contained minimum (2) genotypes. The genetic stocks 2 within a cluster had smaller D values among themselves than those belonging to different clusters. Intra-cluster distance was maximum (3.123) in cluster II whereas, it was minimum (1.475) in cluster I. Maximum average inter-cluster distance (10.755) was recorded between cluster II and cluster V, suggesting the greater chances of getting superior hybrids in F or 1 transgressive segregants in subsequent generations. Genotypes in cluster I was superior in seed germination and had minimum seed cavity length and breadth and PDI. Cluster IV had superiority in terms of average fruit weight, fruit length and seed cavity length. Cluster V recorded highest mean value for most of the characters. Considering the diversity pattern and mean performances, the genotypes LC-20 and LC-21 form cluster I, LC-7 from cluster III, LC-28 from cluster IV and LC-2, LC-9, LC-10 and LC-16 from cluster V would be best choice as parents for future hybridization programs.

Ahirwar and Singh (2017) evaluated forty four diverse genotypes with two checks Pant Khira-1 and Pointsette of cucumber through cluster analysis. Results revealed that total genotypes were grouped into six clusters which confirm the presence of wide genetic diversity through the formation of six clusters. The clustering pattern showed the lack of parallelism between geographic and genetic diversities. The Eigen factors of six principal components were interpreted as relative weight of variable in each component. The important variables are those which have high positive or negative weight or values. In first season the first principal component had high positive weight or value to weight of internodal length (0.388) followed by days to first female flowers (0.385) and test weight (0.075). During the second season, high positive weight to days to first fruit harvest (0.459) followed by test weight (0.327) and fruit diameter (0.212). However in pooled data, highest positive weight was due to test weight (0.517) followed by internodal length (0.470) and seed index (0.259) contributed towards high genetic divergence. Hence, these characters could respond favourably for phenotypic selection.

Doddamani *et al.*(2018) undertaken a field experiment during the year 2017-2018 in *Kharif* season at Kittur Rani Channamma College of Horticulture, Arabhavi to study the extent of genetic diversity existing in local cucumber collections. The experiment was laid out in randomized block designs with two replications. A total of 21 local collection of cucumber genotypes were used in the present study. Mahalanobis D^2 analysis indicated considerable diversity and 21 genotypes were grouped into six different clusters. The cluster II showed maximum (2242.20) intra cluster distance. Inter cluster distance revealed the maximum divergence between clusters IV and cluster III (D^2 = 32489.21) followed by cluster III and cluster II (D^2 = 24315.24). Among all the 19 productivity traits studied, flesh thickness, fruit diameter, fruit length and average fruit weight contributed greatly towards divergence. These traits may give more importance in selecting the genotypes the genotype KRCCH-CC-17 in cluster V recorded highest cluster mean. This genotype can be used as a base material for future breeding programme.

Shah *et al.*(2018) evaluated the nature and magnitude of genetic divergence in 13 cucumber genotypes. The results revealed that there is a wide genetic diversity among the 13 genotypes of cucumber. The genotypes were grouped into 4 clusters based on Mahalanobis D^2 statistics using Tocher's method. The clustering pattern of genotypes revealed that among the 4 clusters, maximum numbers of genotypes were found in cluster I and III which comprises 5 genotypes each, while clusters IV was found to be mono-genotypic. Intra clusters distance was highest in II (70.365), while lowest in cluster I (49.748). The inter cluster D^2 values were maximum between cluster II and IV (93.131), whereas, minimum distance observed between cluster I and II (66.512) cluster III was the most diverse as many clusters showed high inter cluster distances with it. From the present studies, cluster I secured first rank which observed maximum mean value for 11 characters followed by clusters II, indicating presence of most promising genotypes in them and these can be extensively used for further breeding programmes to generate new material**.**

Kumar *et al.*(2018)conducted an experiment with an objective to identify divergent genotypes to be used as donor parents in crop improvement. Thirty-two genotypes along with two checks were evaluated in a randomized block design with three replications and the data on 25 yield and yield attributing traits were recorded. The analysis of variance revealed significant differences among all genotypes indicating the presence of sufficient amount of variability for the characters studied. Wide range of variability was observed for number of fruits per plant, fruit weight, fruit yield per plant, powdery mildew incidence and aphid infestation, indicating the scope for selection of suitable initial breeding material for further breeding programme. The genotypes belong to the clusters VI and III, when the D^2 analysis was carried out for 24 characters which partitioned the thirty-two genotypes into 6 clusters, which are genetically divergent and hybridization between these genotypes will likely produce desirable segregants.

Sharma *et al.*(2018)evaluated thirty diverse genotypes of cucumber collected from different indigenous and exotic sources were planted in randomized complete block design, during kharif season of 2016 and were assessed to know the nature and magnitude of genetic divergence for different horticultural traits, using Mahalanobis D2 statistics. All the characters under study showed considerable divergence and the genotypes were grouped into five clusters. Cluster II contained the maximum (12) number of genotypes, whereas cluster V contained minimum (3) genotypes. The intra cluster distance was maximum in cluster IV (3.469) and minimum in cluster III (1.776). Maximum average inter-cluster distance (6.221) was recorded between cluster III and cluster IV. Therefore, the hybridization between the genotypes of cluster III and IV can be made for getting superior hybrids or recombinants in segregating populations. Cluster III performed better for majority of traits viz. node number bearing first female flower, number of marketable fruits per plant, average fruit weight, harvest duration, days to marketable maturity, TSS, seed germination, seed vigour index-I and II, severity of powdery mildew, angular leaf spot and yield per plot. Maximum fruit length (21.42), minimum severity of anthracnose was recorded in cluster V (7.48), while fruit breadth was highest in cluster IV (5.50).

Kumawat *et al*.(2020) carried out an experiment to assess genetic divergence in twenty one cucumber genotypes including one check for fourteen characters. All the characters under study showed considerable divergence and the genotypes were grouped into four clusters. The clustering pattern had no parallelism between genetic diversity and geographical distribution, suggesting that the selection of parental genotypes for hybridization will be more appropriate based on genetic diversity. Cluster III contained the maximum (5) number of genotypes, whereas remaining all clusters I, II and IV contained similar (4) genotypes. The Intra-cluster distance was maximum (306.685) in cluster III whereas, it was minimum (163.11) in cluster II. Maximum average inter-cluster distance (1439.432) was recorded between cluster IV and cluster V, suggesting the greater chances of getting superior hybrids in F1 or transgressive segregants in subsequent generations. Genotypes in cluster IV were superior in node number of first female flower, days to first flowering, shelf-life, TSS, fruit length, fruit weight and fruit yield per plant. Cluster V had superiority in terms of vine length and number of seeds per fruit. Fruit weight, TSS, number of seeds per fruit, node number of first female flower, shelf-life, days to first harvest and days to first flowering contributed towards genetic divergence.

Chapter-III

MATERIALS AND METHODS

The present investigations work entitled **"Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)** was conducted at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during summer season of 2019. The details of materials used and procedures adopted during the course of investigation have been described as follows:

3.1 Experimental site

The experiment was conducted at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) in well levelled field having proper drainage. The farm is situated in the main campus of the university on left side of Ayodhya-Raibareli road at the distance of 42 km away from district head quarter of Ayodhya. The experiment field has sandy loam soil with pH 8.5 and carrying low organic carbon and nitrogen with medium phosphorus and potash with slightly alkaline in nature.

3.2 Environmental conditions

Geographically , this place is located between 24.35° and 26.50° N latitude, 82.12° and 83.95 E longitude and at an altitude of 112 m above from sea mean level in the Gangetic plain of eastern U.P. This area falls in sub-tropical climate zone. The annual rainfall is about 1260 mm. The climate of district Ayodhya is semi-arid with hot summer and cold winter. The metrological data during the crop season is presented in Table 3.1.

Table-3.1 Weekly meteorological parameters during the cropping period(April to July)

Meteorological week	Temperature (^{0}C)		Average RH (%)	Sunshine hours	Total rainfall (mm)
	Max.	Min.			
16	36.57	20.14	61.93	8.03	0.00
17	38.00	22.14	59.43	9.43	0.00
18	41.21	23.29	53.93	10.19	0.00
19	41.43	24.64	46.57	9.43	0.00
20	40.57	24.64	16.57	8.36	0.00
21	40.57	25.21	44.79	9.56	0.00
22	41.50	24.57	44.93	10.56	0.00
23	38.57	36.36	53.64	8.29	0.00
24	40.71	27.36	50.79	8.23	0.00
25	39.79	26.64	49.71	8.00	1.57
26	36.00	26.50	67.25	4.75	2.17
27	37.69	28.56	62.06	7.80	0.00
28	30.71	24.71	88.50	1.47	38.39
29	34.86	24.29	80.21	3.86	2.34
30	33.43	25.50	85.07	4.50	13.74
31	32.79	26.50	78.43	5.29	2.46

Source: Deptt. of Agril. Meteorology, ANDUAT, Ayodhya.

3.3 Experimental materials

The experimental material comprised of 27 variable genotypes of cucumber including two check varieties, selected on the basis of genetic variability from the germplasm stock maintained at Main Experiment Station in the Department of Vegetable Science, A.N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.).

Table-3.2 List of cucumber genotypes used and their source of origin.

S. No.	Name of genotypes	Source of origin
1.	NDCC-9	Sultanpur
2.	NDCC-11	Kumarganj
3.	NDCC-12	Sultanpur
4.	NDCC-13	Ayodhya
5.	NDCC-15	Ayodhya
6.	NDCC-14	Ayodhya
7.	NDCC-10	Sultanpur
8.	NDCC-7	Kanpur
9.	NDCC-8	Lucknow
10.	Cucumber Local	Lucknow
11.	VNCC-4	Varanasi
12.	Khira-1	Kumarganj
13.	VNCC-3	Varanasi
14.	VNCC-2	Varanasi
15.	VNCC-1	Varanasi

16.	JPCC-5	Jaunpur
17.	JPCC-3	Jaunpur
18.	JPCC-1	Jaunpur
19.	JPCC-2	Jauinpur
20.	JPCC-6	Jaunpur
21.	JPCC-4	Jaunpur
22.	Khira-2	Kumarganj
23.	Chandra Arun	Lucknow
24.	Kashi Khira-1	Allhabad
25.	Cucumber Super Best	Sultanpur
26.	Pusa Uday(C)	IARI, New Delhi
27.	Pant Khira-1(C)	Pantnagar, Uttarakhand

3.4 Details of layout

The Experiment was conducted in Randomized Block Design with three replications during the summer (*Zaid)* season of 2019. The details of layout are given below.

a. Number of genotypes : 25
b. Number of checks : 2
c. Number of replications : 3
d. Spacing : 2 m x 0.50 m
e. Plot size : 3 m x 2 m

3.5 Agronomical practices

The soil of experiment field was prepared by tillage operation. The field was levelled and divided in to plot as per layout. The seed of each treatment was sown in rows prepared in a row of 3 m length and spaced 50 cm. The rows were kept at two meter distance. Space sowing was done with 2-3 seeds at each place to assure optimum plant population. A light irrigation was given immediately after seed sowing. The fertilizer was applied @ 100:50:50 (NPK kg/ha) in the form of Urea, DAP and MOP. Well rotten FYM @ 20 t/ha and full dose of phosphorus and potash along with half dose of nitrogen were given in two split doses. Proper plant protection measure i.e. spraying of fungicide and insecticide were used to overcome the problem of disease and insect-pest. The subsequent irrigation was given as and when needed.

3.6 Observations recorded

Observations were recorded on five randomly selected plants from each genotype in each replication, summed up and divided by five to find out the mean value. The procedure of observations is described under the respective sub-heads:

3.6.1 Growth parameter

a. Node to first male flower anthesis
b. Node to first female flower anthesis
c. Days to first male flower anthesis
d. Days to first female flower anthesis
e. Number of primary branches per plant
f. Vine length (m)

3.6.2 Yield characters

a. Days to first fruit harvest
b. Fruit length (cm)
c. Fruit diameter (cm)
d. Number of fruit per plant
e. Average fruit weight (g)

f. fruit yield per plant (kg)

3.6.1 Growth characters

3.6.1.1 Node number to first male flower anthesis

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

3.6.1.2 Node number to first female flower anthesis

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

3.6.1.3 Days to first male flower anthesis

Number of days taken from the date of sowing to the appearance of first male flower in plant.

3.6.1.4 Days to first female flower anthesis

Number of days taken from the date of sowing to the appearance of first male flower in plant.

3.6.1.5 Number of primary branches per plant

The total number of primary branches on the stem of each plant of every treatment was recorded after last picking.

3.6.1.6 Vine length

The vine length was measured from base of the plant at the time of last fruit harvesting stage in each replication and of each genotype.

3.7.2 Yield characters

3.6.2.1Days to first fruit harvest

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

3.6.2.2 Fruit length (cm)

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

3.6.2.3 Fruit diameter (cm)

The diameter of five selected fruits was measured and average was calculated in cm.

3.6.2.4 Number of fruits per plant

Total number of fruits was calculated by adding number of fruits from all harvest of each genotype and in each replication.

3.6.2.5 Average fruit weight (g)

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

3.6.2.6 Fruit yield per plant (kg)

All the fruits are harvested time to time and weight by pan balance after the final harvesting average was calculated.

3.7 Statistical analysis

The experimental data was compiled by taking the mean value of the 28 genotypes of cucumber for all 12 traits from all the three replications. Then it was subjected to the following statisticalanalyses.

3.7.1 Analysis of variance for the design of experiment (Panse and Sukhatme, 1967)

3.7.2 Coefficient of variation, heritability and genetic advance (Burton and deVane, 1953)

3.7.3 Genetic advance in per cent of mean (Johnson *et al*, 1955)

3.7.4 Correlation coefficient (Searle, 1961)

3.7.5 Path coefficient analysis (Dewey and Lu, 1959)

3.7.6. Genetic divergence (D^2)analysis (Mahalanobis, 1928)

3.7.1 Analysis of variance for the design of experiment:

The analysis of variance for the design of experiment (RBD) was carried out according to the procedure outlined by Panse and Sukhatme (1967). The significance of differences among treatments means were tested by 'F' test. To test the hypothesis H_0:t_1=$t_{2.....}$tv, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$Y_{ij} = \mu + t_i + b_i + e_{ij}$

Where,

Y_{ij} = Yield of i^{th} entry in the j^{th} replication

µ = General mean

t_i = Effect of the i^{th} entry (i= 1,2….)

b_i = Effect of the j^{th} replication (j= 1,2….)

e_{ij} = Environment effect

ANOVA of the experiment table

Source of variation	**Degree of freedom**	**Sum of Square**	**Mean sum of square**	**F ratio**
Replications	r-1	SSR	MSR	MSR/MSE
Treatments	t-1	SST	MST	MST/MSE
Error	(r-1) (t-1)	SSE	MSE	
Total	(r.t-1)	TSS		

Where,

r = Number of replications

t = Number of treatments

The standard error, critical difference and coefficient of variation were calculated as follows:

SE of mean= $\sqrt{\frac{2MSE}{R}}$

Critical difference (C.D.) = $\sqrt{\frac{2MSE}{r}}$ x t value at 5% error d.f. Where, Table value of 't' distribution of error d.f. on P<0.5.

Coefficient of variation (C.V. %) = $\sqrt{\frac{MSE}{GM}}$ x 100

3.7.2 Estimation of variance

The mean squares for error was subtracted from the mean squares due to genotypes and the difference was divided by number of replications for obtaining the genotypic variance, which was calculated according to the method suggested by Burton (1952). Environmental variance is the mean squares due to error. Phenotypic variance was calculated by adding genotypic variance and environmental variance, which was suggested by Burton and de Vane (1953).

Environmental variance (σ^2e) = M.S.E.

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{M.S.T.} - \text{M.S.E.}}{\text{r}}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where,

M.S.T. is genotypes / varieties mean square

M.S.E. is error mean square and

r is number of replications.

3.7.2.1Estimation of coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following Burton and deVane (1953).

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

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

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

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

3.7.2.2 Heritability

Heritability in broad sense (h^2_{bs}) was calculated using the formula suggested by Burton and deVane (1953).

$$h^2{}_{bs} = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e} or \frac{\sigma^2 g}{\sigma^2 p}$$

$$h^2{}_{bs}\,(\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

3.7.2.3 Genetic advance

Genetic advance ($\overline{GA}$)was estimated by the method suggested by Johnson *et al*. (1955).

$$Ga. = K.\sigma_p.\frac{\sigma^2 g}{\sigma^2 p}$$

$$= K.\ \sigma_{p.}\ h^2$$

Where,

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

h^2= Heritability

σ_p= Phenotypic standard deviation

$(\overline{Ga}\ \%)$ = Genetic advance in per cent of mean

$$\overline{GA}\ (\%) = \frac{\text{genetic advance}}{\overline{x}} \times 100$$

3.7.3 Correlation coefficient

The correlations between different characters at genotypic (g) and phenotypic (p) levels were worked out between characters as suggested by Searle (1961).

i) Phenotypic correlation coefficient between characters X and Y:

$$r_{xy\,(p)} = \frac{\text{Cov.}_{xy\,(p)}}{\sqrt{\text{Var. X (p). Var. Y (p)}}}$$

ii) Genotypic correlation between characters X and Y:

$$r_{xy\,(g)} = \frac{\text{Cov.}_{xy\,(g)}}{\sqrt{\text{Var. X (g). Var. Y (g)}}}$$

Where,

r_{xy} =Correlation coefficients between X and Y.

Covariance XY= Co-variance between characters X and Y

Var. X= Variance for X character

Var. Y= Variance for Y character.

The significance of phenotypic correlation coefficients was tested against (n-2) degrees of freedom at 5% and 1% probability level. Where, n is the number of genotypes (germplasms) on which the observations were recorded.

3.7.4 Path coefficient analysis

Path coefficient analysis was carried out according to Dewey and Lu (1959). Yield per plant was assumed to be dependent variable (effect) which is influenced by all the characters, the independent variable (causes), directly as well as indirectly through other characters. The residual factor (x) which is uncorrelated with other factors. Path coefficients were estimated by solving the following simultaneous equations indicating the basic relationship between correlation and path coefficient. The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j-1}^{16} r_{iy} P_{jy} \; for i = 1,2 \ldots 16$$

$$r_{iy} = P_{iy} + \sum_{j-1}^{16} r_{iy} P_{jy} \; for r_y = 1.$$

The above equation can be written in the form of matrix:

[A] 16x1= [B] 16x1[C] 16x1

Where,

A is column vector of correlations r_{iy}

B is the correlation matrix of r_{ij}, and

C is the column vector of direct effects, P_{iy}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_j P_{iy} \, r_{iy}$$

The r_{ij}'s i.e., $r_{1.2}$ to $r_{15\text{-}16}$ denote correlations between all possible combinations of independent characters P_{1y} to P_{16y} denote direct effect of various characters on character y.

r_{iy}= Correlation coefficient between 1th and y character.

p_{iy}= Direct effect of ith character on Y.

3.7.5 Estimation of genetic divergence (D^2)

The genetic divergence of forty four genotypes of garden pea was worked out using Mahalanobis (1928) D^2 statistics. The seventeen quantitative characters in garden pea were included for these analyses. For the calculation of D^2 values, following steps involved:

I. A set of uncorrelated linear combinations (y, s) was obtained by pivotal condensation of the common dispersion matrix of set of correlated variables (x, s). The common dispersion matrix was arranged with the help of error mean squares and mean sum of products.

II. Using the relationship between y, s and x, s the mean values of different characters and (X_1 to X_{17} in peas) were transferred in to the mean values of a set of uncorrelated linear combinations (Y_1 toY_{17}) in garden pea.

III. The 'D^2'values between i^{th} and j^{th} genotypes for k^{th} characters were calculated as under:

$D^2 = K (Y_{it} - Y_{it})$

Where, t =1

The K components were calculated separately and added to get $D^2_{ij.}$

IV. The 'K' component and 'D^2_{ij} for each combination were ranked in descending order of magnitude.

V. These ranks were added up for each component D^2_{ij} over combinations of i and j the rank totals were obtained.

VI. **Group constellation:** The D^2 values were arranged in an increasing order of magnitude. The grouping of the strains into different cluster was done using Ward methods. The two most closely associated groups were chosen and third group was found which had the smaller average D^2 value from the first two. Similarly the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 value did not fit with the former group and was, therefore, taken as another cluster.

VII. **Intra and inter-cluster distance:** The intra-cluster D^2 was calculated as the sum of n (n-1)/2 genotypes within a cluster divided by total number of combinations. All possible D^2 values between the groups of two clusters were added and then divided by $n_1 \times n_2$ for computing inter-cluster distance.

Where,

n_1 and n_2 = the number of genotypes in two clusters.

VIII. **Cluster mean:** The cluster mean for the particular character is the summation of mean values of the strains included in a cluster divided by number of strains in the cluster.

IX. **Testing of the significance of D^2 values:** The D^2 values obtained for a pair of population were taken as the calculated value of x^2 and is tested against tabulated value of x for 'P' degree of freedom.

Where,

P = number of characters considered

X. Per cent contribution of each character towards genetic divergence was calculated as below:

$$\text{Percentage contribution of character X} = \frac{N}{C} \times 100$$

Where,

N = Number of genotype combinations which was ranked first for character X.

C = All combinations of genotypes involved in D^2 analysis.

Chapter-IV

EXPERIMENTAL FINDINGS

The present Experiment was carried out during *Zaid* (summer) season of 2019 at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.). The results obtained by analysis of recorded data have been presented and described under following heads:

4.1. Analysis of variance
4.2. Mean performance of genotypes
4.3. Coefficient of variation
4.4. Heritability, genetic advance as percentage of mean
4.5. Genotypic and phenotypic correlation coefficient
4.6. Path coefficient analysis
4.7. Estimation of genetic divergence (D^2)

4.1 Analysis of variance

Analysis of variance for twelve characters in Randomized Block Design is presented in Table 4.1. Significant differences among the genotypes were found for all the characters, namely, node number of first male flower, node number of first female flower, days to first male flower anthesis, days to first female flower anthesis, days to first fruit harvest, number of primary branches per plant, length of fruit, diameter of fruit (cm), vine length (cm), average fruit weight (g), number of fruit per plant and fruit yield per plant (kg).

Table-4.1 Analysis of variance for twelve quantitative characters in cucumber

S. No.	Characters	Source of variation		
		Replications	**Treatments**	**Error**
	d.f.	**2**	**26**	**52**
1.	Node to first male flower anthesis	0.26	0.93**	0.14
2.	Node to first female flower anthesis	3.46*	5.89**	0.93
3.	Day to first male flower anthesis	8.66	30.07**	3.22
4.	Day to first female flower anthesis	5.93	36.69**	6.29
5.	Day to first fruit harvest	0.86	29.31**	7.69
6.	No. of primary branches per plant	0.18*	0.34**	0.04
7.	Fruit length (cm).	0.44	15.55**	0.67
8.	Fruit diameter(cm)	0.31	0.50**	0.16
9.	Average fruit weight	8.26	595.93**	78.91
10.	Vine length(m)	2.04**	0.10*	0.05
11.	No. of fruit per plant	28.13**	1.56**	0.47
12.	Fruit yield per plant (kg).	0.89**	0.06**	0.02

*,** Significant at 5% and 1% level of probability. probability levels,respectively

4.2 Mean performance of genotypes

The mean value of all the genotypes for all 12 characters were computed and have been presented in Table 4.2.1.

4.2.1 Node number of first male flower anthesis

Node number to first male flower anthesis ranged from 5.43 (Cucumber Super best) to 7.50 (Khira-1) with general mean 6.49. The first male flower anthesis at lowest node than its best check Pant Khira-1 (5.67) were found in Cucumber super best (5.43) followed by VNCC-1 (5.47).

4.2.2 Node number to first female flower anthesis

The node number of female flower anthesis varied from 9.53 (VNCC-1) to 15.00 (Kashi Khira-1) with mean value (12.59). The Node number of first female flower anthesis was found lowest with genotypes VNCC-1 (9.53) followed by JPCC-5 (11.13) and VNCC-3 (11.20) than its best check Pant Khira-1 (11.37) while the highest Node number was found in Kashi Khira-1 (15.00).

4.2.3 Days to first male flower anthesis

Days to first male flower anthesis ranged from 37.33 days (Khira-2) to 50.00 days (JPCC-5) and general mean was 42.54 days. The minimum days to male flower anthesis was found 37.33 days (Khira-2) and 38.13 days (Kashi Khira-1), while, Cucumber local (39.00) was at par to its best early check variety Pusa Uday (39.06 days).

4.2.4 Days to first female flower anthesis

The general mean value for days to first female flower anthesis in different genotypes was 50.89 days. The female flower anthesis was found earliest in the Cucumber super best (44.00) days and delayed in NDCC-9 (55.57) days among the genotypes. Some genotypes showed most earlier female flower anthesis *viz.* Cucumber Super best (44.00) followed by Kashi Khira-1 (44.37), Chandra Arun (44.43 days), Khira-2 (47.47 days), Cucumber local (46.43 days) and NDCC-8 (47.57 days) than its best earlier check Pant Khira-1 (48.90 days).

4.2.5 Days to first fruit harvest

Days to first fruit harvest ranged from 54.93 days to 66.27 days in NDCC-8 and VNCC-2, respectively. The general mean was observed 61.53 days. The genotypes i.e. NDCC-8 (54.93) was found earlier than earlies check Pant Khira-1 (57.10 days), while, NDCC-11 (57.53) followed by NDCC-13 (57.57), JPCC-1 (58.90) and JPCC-4 (59.03) showed earliest days to first fruit harvest than second best check Pusa Uday (59.47).

4.2.6 Number of primary branch per plant

Number of primary branch per plant range from 1.60 (NDCC-13) to 2.97 (JPCC-1) with general mean 2.01. There was found maximum primary branch in JPCC-1 (2.97) and NDCC-9 (2.60) to its best check variety Pusa Uday (2.43), while the genotypes Chandra Arun (2.37) followed by NDCC-12 (2.33), VNCC-1 (2.27), VNCC-3 and NDCC-10 (2.20) were found superior than its second best check Pant Khira-1 (2.17).

4.2.7 Fruit length (cm)

The genotypes NDCC-10 was noted to have maximum fruit length (18.68cm), while genotypes Khira-1 had minimum fruit length (10.20 cm) among the genotypes. The general mean for fruit length was 16.07 cm. Genotypes, namely, NDCC-10 (18.68 cm) followed by JPCC-4 (18.47 cm) and Khira-2 (18.33) were found superior than its best check Pant Khira-1 (18.10 cm).

JPCC-4 **NDCC-7**

Flowering in cucumber

JPCC-4 **NDCC-7**

Fruiting in cucumber

Table - 4.2 Mean performance of twenty seven genotypes for twelve characters in cucumber

S. No.	**Characters** **Genotypes**	**Node to first male flower anthesis**	**Node to first female flower anthesis**	**Day to first male flower anthesis**	**Day to first female flower anthesis**	**Day to first fruit harvest**	**No. of primary branches per plant**	**Fruit length (cm)**	**Fruit diameter (cm)**	**Average fruit weight (g)**	**Vine length (cm)**	**Number of fruit per plant**	**Fruit yield per plant (kg)**
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
1	NDCC-9	6.93	13.27	43.26	55.57	65.57	2.60	15.07	4.35	134.33	2.56	7.12	1.47
2	NDCC-11	7.53	13.57	41.10	50.00	57.53	1.80	12.77	4.33	147.33	2.48	6.55	1.40
3	NDCC-12	6.87	14.33	47.13	54.00	59.97	2.33	16.50	4.11	162.00	2.13	6.00	1.13
4	NDCC-13	6.90	13.00	43.30	53.07	57.57	1.60	14.40	3.65	122.47	2.40	7.37	1.41
5	NDCC-15	6.40	12.20	44.10	51.43	65.55	1.70	18.07	3.75	103.00	2.38	7.67	1.47
6	NDCC-14	6.93	13.53	49.30	53.75	65.17	1.97	17.27	4.19	130.00	2.17	8.23	1.36
7	NDCC-10	6.77	11.47	41.66	51.00	65.47	2.20	18.68	3.56	126.00	2.26	7.22	1.33
8	NDCC-7	6.30	12.27	43.03	54.20	64.38	1.73	17.40	3.92	151.00	2.32	8.00	1.63
9	NDCC-8	5.78	13.60	41.20	47.57	54.93	2.10	12.47	4.00	151.33	2.35	8.28	1.30
10	Cucumber Local	6.37	13.67	39.00	46.43	65.88	1.72	17.17	3.80	132.00	2.02	7.59	1.03
11	VNCC-4	6.27	11.73	41.93	55.37	61.60	1.63	14.33	3.85	149.33	2.22	5.92	1.10
12	Khira-1	7.50	11.85	47.00	50.43	60.43	2.10	10.20	4.81	125.00	2.21	7.11	1.22

13	VNCC-3	6.50	11.20	42.83	55.53	64.60	2.20	16.07	3.83	142.67	2.08	7.69	1.44
14	VNCC-2	7.10	11.73	43.13	53.07	66.27	1.63	16.57	3.99	131.00	2.25	6.44	1.35
15	VNCC-1	5.47	9.53	41.00	49.47	59.85	2.27	15.70	4.17	142.27	2.03	8.12	1.32
16	JPCC-5	6.93	11.13	50.00	54.87	63.33	1.97	17.17	5.20	160.67	2.27	7.60	1.40
17	JPCC-3	6.80	14.53	42.13	53.13	62.90	2.10	17.60	4.07	128.20	2.55	7.88	1.26
18	JPCC-1	6.77	12.93	43.66	52.47	58.90	2.97	14.50	4.07	154.47	2.52	7.83	1.47
19	JPCC-2	6.27	12.80	46.36	50.17	60.20	1.90	16.37	4.65	139.00	2.29	7.15	1.28
20	JPCC-6	7.00	9.97	41.06	53.70	59.82	1.63	17.70	4.44	156.33	2.18	7.05	1.36
21	JPCC-4	5.87	13.13	40.66	49.37	59.03	1.87	18.47	4.57	151.40	2.43	7.42	1.53
22	Khira-2	6.13	11.43	37.33	47.47	59.85	1.80	18.33	3.95	153.00	2.37	5.80	1.07
23	Chandra Arun	6.25	11.95	40.06	44.43	61.23	2.37	18.03	4.20	153.00	2.53	6.87	1.34
24	Kashi Khira-1	6.27	15.00	38.13	44.37	61.63	1.97	17.90	4.23	155.67	2.20	6.10	1.20
25	Cucumber Super Best	5.43	14.07	40.53	44.00	63.10	1.63	11.30	4.49	144.00	2.49	6.40	1.38
26	Pusa Uday (C)	6.33	14.60	39.06	50.17	59.47	2.43	15.73	4.19	155.00	2.29	7.29	1.47
27	Pant Khira-1 (C)	5.67	11.37	40.63	48.90	57.10	2.17	18.10	5.11	149.27	2.76	6.97	1.44
Mean		**6.49**	**12.59**	**42.54**	**50.89**	**61.53**	**2.01**	**16.07**	**4.20**	**142.58**	**2.32**	**7.17**	**1.34**
S.E.m ±		0.213	0.556	1.036	1.448	1.602	0.114	0.473	0.234	5.129	0.128	0.395	0.081
C.D. at 5%		0.606	1.582	2.950	4.120	4.560	0.326	1.345	0.667	14.596	0.365	1.125	0.231
Range Lowest		5.43	9.53	37.33	44.00	54.93	1.60	10.20	3.56	103.00	2.02	5.80	1.03
Range Highest		7.53	15.00	50.00	55.57	66.27	2.97	18.68	5.20	162.00	2.76	8.28	1.63

4.2.8Fruit diameter (cm)

The genotypes JPCC-5 was observed maximum diameter of fruit (5.20cm), while NPCC-10 had observed minimum fruit diameter (3.56cm). The general mean was observed to be 4.20 cm. The only genotype JPCC-5 (5.20cm) has more fruit diameter and showed superiority than its best check Pant Khira-1 (5.11cm).

4.2.9 Average fruit weight (g)

Average fruit weight varied from 103.00g (NDCC-15) to 156.33g (NDCC-12) with general mean 142.58g. Some genotypes viz. JPCC-6 (156.33g) followed by JPCC-5 (160.67g) and NDCC-12 (162.00g) were found superior than best check Pusa Uday (155.00g).

4.2.10 Vine length (m)

The longest vine length was found in Pant Khira-1 (2.76m) and the shortest vine length in Cucumber local (2.02m) among the genotypes with a general mean 2.32m. The genotypes such as NDCC-9 (2.56m) followed by JPCC-3 (2.55m), Chandra Arun (2.53m), JPCC-1 (2.52m), Cucumber Super Best (2.49m), NDCC-11 (2.48m), JPCC-4 (2.43m), NDCC-13 (2.40m), NDCC-15 (2.38m), Khira-2 (2.37m), NDCC-8 (2.35m) and NDCC-7 (2.32m) were found superior than second best check Pusa Uday (2.29m)

4.2.11 Number of fruit per plant

Number of fruits per plant ranged from 5.80 to 7.88 for Khira-2 and NDCC-8, respectively. The general mean was observed 7.17. The maximum number of fruits per plant were found in NDCC-8 (8.28) followed by NDCC-14 (8.23), VNCC-1 (8.12), NDCC-7 (8.00), JPCC-3 (7.88), JPCC-1 (7.83), VNCC-3 (7.69), NDCC-15 (7.67), JPCC-5 (7.60), Cucumber local (7.59), JPCC-4 (7.42) and NDCC-13 (7.37) than its best check variety Pusa Uday (7.29).

4.2.12 fruit yield per plant (kg)

The fruit yield per plant varied from 1.63kg (NDCC-7) to 1.03kg (Cucumber local) with general mean 1.34kg. Three genotypes NDCC-7 (1.63kg) and JPCC-4 (1.53kg) were found superior for higher fruit yield per plant than its best check Pusa Uday (1.47kg).

4.3 Coefficient of variation

The estimates of genotypic and phenotypic coefficients of variation for twelve characters of cucumber genotypes has been given in Table 2.The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the characters. The highest phenotypic as well as genotypic coefficients of variation were observed in number of primary branches per plant (18.67% and 15.82%) and fruit length (14.77cm and 13.86cm), while, minimum GCV and PCV were found in days to first fruit harvest (6.27 days and 4.36 days) and days to first female flower anthesis.

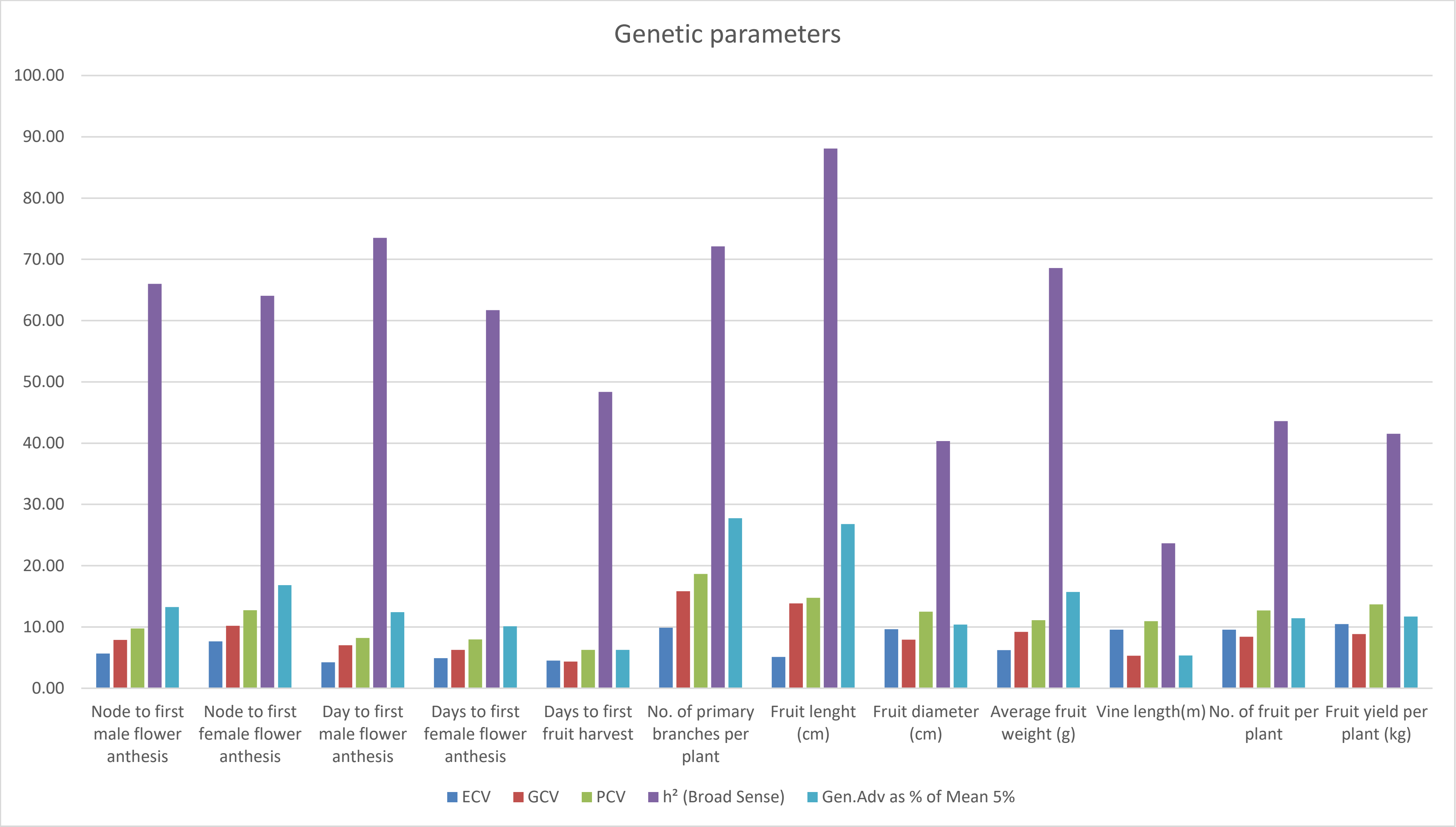
4.4 Heritability, genetic advance as percentage of mean

High heritability was observed for the character fruit length (88.10cm) while, minimum heritability was found for vine length (23.65m) followed by fruit diameter (40.36m), fruit yield per plant (41.54m) and number of fruits per plant (43.61).

High genetic advance in per cent of mean was observed found for number of primary branches per plant (27.74) and fruit length (26.80cm). High heritability coupled with high genetic advance in per cent of mean was found in fruit length (88.10 and 26.80) and number of primary branches per plant (72.11 and 27.74), while lowest was found in vine length (23.65 and 5.34) and days to first fruit harvest (48.35 and 6.25).

Table 4.3 Estimates of range, grand mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense, genetic advance (Ga) and genetic advance in per cent of mean for twelve characters in cucumber.

S. No.	Characters	Range		Grand mean	PCV (%)	GCV (%)	Heritability (h^2_{bs}) in broad sense (%)	Genetic advance	Genetic advance in per cent of mean
		Lowest	Highest						
1.	**Node to first male flower anthesis**	5.43	7.50	6.49	9.74	7.91	66.00	0.86	13.24
2.	**Node to first female flower anthesis**	9.53	15.00	12.59	12.76	10.21	64.07	2.12	16.84
3.	**Day to first male flower anthesis**	37.33	50.00	42.54	8.20	7.03	73.52	5.28	12.42
4.	**Days to first female flower anthesis**	44.00	55.57	50.89	7.96	6.26	61.72	5.15	10.12
5.	**Days to first fruit harvest**	54.93	66.27	61.53	6.27	4.36	48.35	3.84	6.25
6.	**No. of primary branches per plant**	1.63	2.97	2.01	18.67	15.82	72.11	0.56	27.74
7.	**Fruit lenght (cm)**	10.20	18.68	16.07	14.77	13.86	88.10	4.31	26.80
8.	**Fruit diameter (cm)**	3.56	5.11	4.20	12.50	7.94	40.36	0.44	10.39
9.	**Average fruit weight (g)**	103.00	156.33	142.58	11.12	9.21	68.59	22.40	15.71
10.	**Vine length(m)**	2.02	2.76	2.32	10.96	5.32	23.65	0.12	5.34
11.	**No. of fruit per plant**	5.80	7.88	7.17	12.72	8.40	43.61	0.82	11.43
12.	**Fruit yield per plant**	1.03	1.63	1.34	13.70	8.83	41.54	0.16	11.72



Graphical representation of genetic parameters

4.5 Correlation coefficients analysis

The phenotypic correlation coefficient computed among the twelve characters under study has been presented in Table 4.4.

In most cases, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients, suggesting therefore, a strong inherent relationship in different pairs of characters in cucumber genotypes. The most important trait fruit yield per plant had exhibited highly significant positive phenotypic correlation with number of fruit per plant (0.471) and vine length (0.417). Whereas, days to first male flower anthesis was significant positive correlated with node to first male flower anthesis (0.482*) and days to first female flower anthesis was highly positive correlated with node to first male flower anthesis (0.530**) and days to first male flower anthesis (0.597**), while, average fruit weight showed significant negative correlation with days to first fruit harvest (-0.453*).Number of fruits per plant positively correlated with days to first male flower anthesis (0.289) followed by number of primary branches (0.237) and days to first female flower anthesis (0.219).

Table- 4.4Estimates of simple correlation coefficients among twelve characters in cucumber.

Characters	Node to first female flower anthesis	Day to first male flower anthesis	Day to first female flower anthesis	Day to first fruit harvest	No. of primary branches per plant	Fruit length (cm)	Fruit diameter(cm)	Average fruit weight	Vine length (cm)	Number of fruit per plant	Fruit yield per plant (kg)
Node to first male flower anthesis	0.051	0.482*	0.530**	0.205	0.033	-0.137	-0.028	-0.234	-0.113	-0.061	-0.023
Node to first female flower anthesis		-0.073	-0.25	-0.048	0.107	-0.175	-0.108	0.018	0.195	-0.093	-0.087
Day to first male flower anthesis			0.597**	0.216	0.083	-0.143	0.3	-0.192	-0.171	0.289	0.143
Days to first female flower anthesis				0.261	0.075	0.055	-0.096	-0.125	-0.158	0.219	0.26
Days to first fruit harvest					-0.144	0.316	-0.273	-0.453*	-0.293	0.07	0.002
No. of primary branches per plant						-0.035	0.095	0.242	0.214	0.237	0.182
Fruit lenght (cm)							-0.127	0.052	-0.027	0.036	0.036
Fruit diameter (cm)								0.363	0.29	-0.061	0.164
Average fruit weight (g)									0.01	-0.29	-0.034
Vine length(m)										-0.062	0.417*
No. of fruit per plant											0.471*

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

4.6 Path coefficient analysis

The path coefficient analysis was carried out at phenotypic level to resolve direct and indirect effect of twelve characters on fruit yield per plant. The direct and indirect influence of different characters on fruit yield at phenotypic level had been given in Table 4.5

Perusal of Table 4.5 reveals that the higher magnitude of positive direct effect at phenotypic level on fruit yield per plant was exerted by number of fruit per plant (0.558) followed by vine length (0.556) and days to first female flower anthesis (0.264). While, substantial negative direct effect on fruit yield per plant was exerted by number of primary branches per plant (-0.109) and days to first male flower anthesis (-0.103). The positive indirect effect on fruit yield per plant was exerted by days to first female flower anthesis via node to first male flower anthesis (0.140) and days to first male flower anthesis (0.157) followed by vine length via node to first female flower anthesis (0.108), number of primary branches per plant (0.119) and fruit diameter (0.161) whereas, number of fruits per plant exerted positive indirect effect on fruit yield per plant via days to first male flower anthesis (0.161), days to first female flower anthesis (0.122) and number of primary branches per plant (0.132).

The substantial negative indirect effect on fruit yield per plant was exerted by vine length and average fruit weight (-0.163 and 0.111) via days to first fruit harvest.

Table-4.5 Direct and indirect effects of twelve characters on fruit yield per plant (g) in cucumber.

Characters	Node to first male flower anthesis	Node to first female flower anthesis	Day to first male flower anthesis	Day to first female flower anthesis	Day to first fruit harvest	No. of primary branches per plant	Fruit length(cm)	Fruit diameter(cm)	Average fruit weight	Vine length(cm)	Number of fruit per plant	Fruit yield per plant
	1	2	3	4	5	6	7	8	9	10	11	12
Node to first male flower anthesis	**-0.007**	0.000	-0.003	-0.004	-0.001	0.000	0.001	0.000	0.002	0.001	0.000	**-0.023**
Node to first female flower anthesis	-0.004	**-0.077**	0.006	0.019	0.004	-0.008	0.013	0.008	-0.001	-0.015	0.007	**-0.087**
Day to first male flower anthesis	-0.050	0.007	**-0.103**	-0.061	-0.022	-0.009	0.015	-0.031	0.020	0.018	-0.030	**0.143**
Days to first female flower anthesis	0.140	-0.066	0.157	**0.264**	0.069	0.020	0.015	-0.025	-0.033	-0.042	0.058	**0.26**
Days to first fruit harvest	0.044	-0.010	0.047	0.056	**0.215**	-0.031	0.068	-0.059	-0.097	-0.063	0.015	**0.002**
No. of primary branches per plant	-0.004	-0.012	-0.009	-0.008	0.016	**-0.109**	0.004	-0.010	-0.026	-0.023	-0.026	**0.182**
Fruit lenght (cm)	0.012	0.016	0.013	-0.005	-0.029	0.003	**-0.091**	0.012	-0.005	0.002	-0.003	**0.036**
Fruit diameter (cm)	-0.001	-0.006	0.016	-0.005	-0.015	0.005	-0.007	**0.053**	0.019	0.015	-0.003	**0.164**
Average fruit weight (g)	-0.057	0.004	-0.047	-0.031	-0.111	0.059	0.013	0.089	**0.245**	0.002	-0.071	**-0.034**
Vine length(m)	-0.063	0.108	-0.095	-0.088	-0.163	0.119	-0.015	0.161	0.005	**0.556**	-0.034	**0.417***
No. of fruit per plant	-0.034	-0.052	0.161	0.122	0.039	0.132	0.020	-0.034	-0.162	-0.035	**0.558**	**0.471***

R^2-0.8669, Residual effect- 0.3649

4.7 Estimation of genetic divergence (D^2)

Estimation of genetic divergence among the twenty seven genotypes of cucumber were carried out by using Mahalanobis D^2 statistics. Twenty seven genotypes were grouped into 6 different clusters. Maximum number of genotypes were grouped in cluster I (19), whereas, two genotype in cluster II, three genotype in cluster III, and one genotype in cluster Iv, cluster V and cluster VI Table-4.6.

The estimates of intra and inter-cluster distances presented by D^2 values are given in Table-4.7. Maximum intra-cluster distance was recorded in cluster I recorded (47.41) followed by cluster III (41.36). The maximum inter-cluster distance observed between cluster II and cluster V (263.21) followed by cluster I and cluster V (154.27). The minimum inter cluster value was found in cluster IV and VI (67.63) and cluster I and cluster VI (68.86).

A perusal of Table-4.8cluster means for different traits indicated considerable differences among the clusters. The minimum cluster mean value for node number to first male and female flower anthesis were found in cluster II (6.20) and cluster VI (11.13). The minimum days to first male and female flower anthesis and days to first fruit harvest were observed in cluster II (37.73 and 45.92) and cluster III (58.52). The maximum number of primary branches per plant, fruit length and fruit diameter were observed in cluster IV (2.97), cluster II (18.12) and cluster V (4.81), respectively. Maximum average fruit weight and vine length were shown by cluster VI (160.67g) and cluster IV (2.52m), while maximum number of fruits per plant and fruit yield per plant were found in cluster IV (7.83 and 1.47kg).

Table-4.6 Clustering pattern of twenty seven genotypes of cucumber

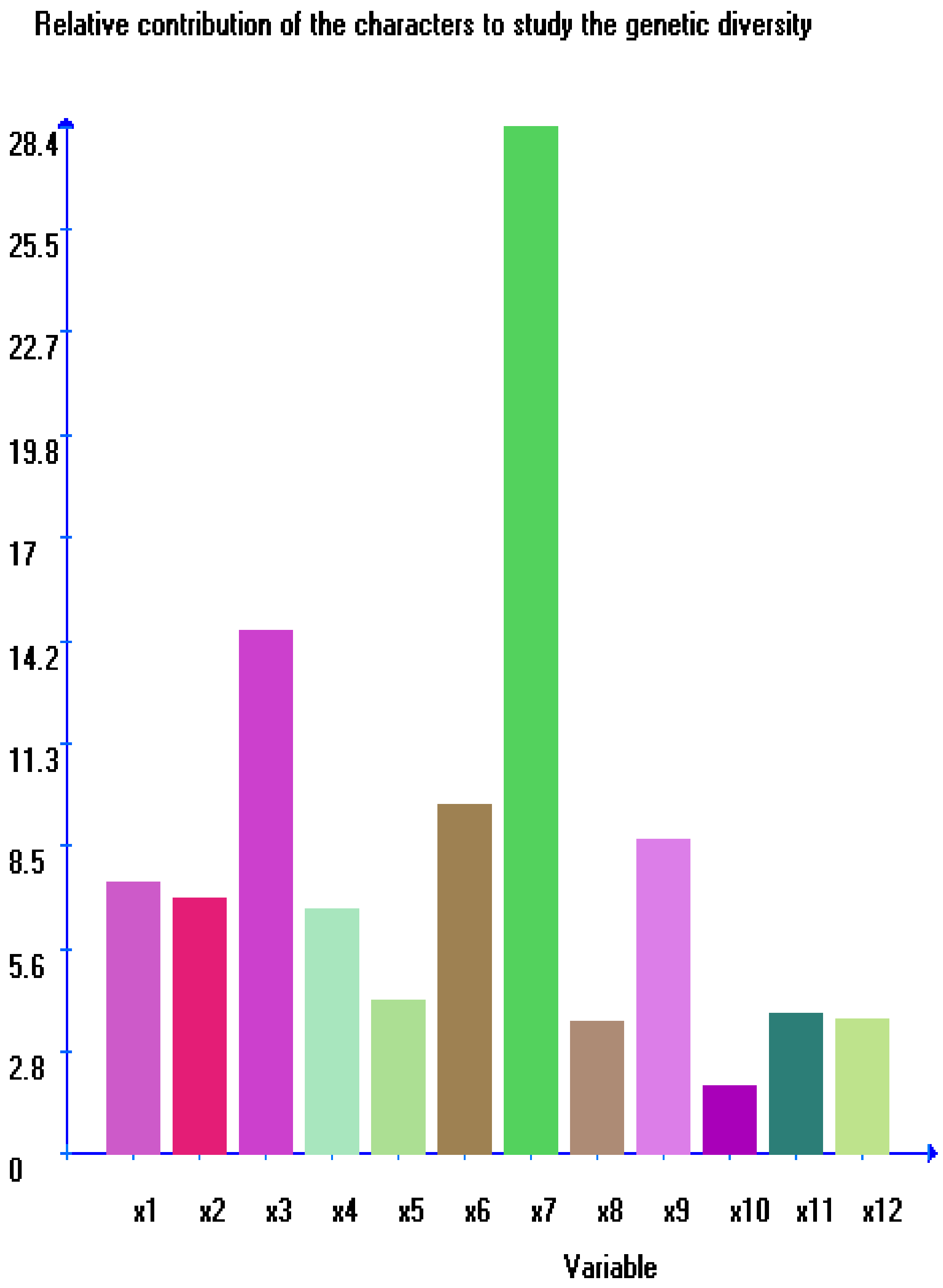
Cluster number	No. of genotypes	Genotypes
I	19	NDCC-9, NDCC-12, NDCC-13, NDCC-15, NDCC-14, NDCC-10, NDCC-7, Cucumber Local, VNCC-4, VNCC-3, VNCC-2, VNCC-1, JPCC-3, JPCC-2, JPCC-6, JPCC-4, Chandra Arun, Pusa Uday (C), Pant Khira-1 (C)
II	2	Khira-2, Kashi Khira-1
III	3	NDCC-8 , Cucumber Super Best, NDCC-11
IV	1	JPCC-1
V	1	Khira-1
VI	1	JPCC-5

Table-4.7 Intra and inter clusters D^2 values for six clusters in cucumber

Cluster number	I	II	III	IV	V	VI
I	**47.41**	69.77	88.59	72.61	154.27	68.86
II		**22.42**	109.32	137.95	263.21	150.18
III			**41.36**	83.48	90.64	134.33
IV				**0.00**	105.60	67.63
V					**0.00**	122.70
VI						**0.00**

Table-4.8 Cluster mean for twelve characters in cucumber

Characters / Cluster No.	Node to first male flower anthesis	Node to first female flower anthesis	Day to first male flower anthesis	Day to first female flower anthesis	Day to first fruit harvest	No. of primary branches per plant	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Vine length (m)	Number of fruit per plant	Fruit yield per plant (kg)
I	6.47	12.44	42.61	51.72	62.19	2.00	16.80	4.13	139.91	2.31	7.26	1.35
II	6.20	13.22	37.73	45.92	60.74	1.88	18.12	4.09	154.33	2.28	5.95	1.14
III	6.25	13.74	40.94	47.19	58.52	1.84	12.18	4.28	147.56	2.44	7.08	1.36
IV	6.77	12.93	43.66	52.47	58.90	2.97	14.50	4.07	154.47	2.52	7.83	1.47
V	7.50	11.85	47.00	50.43	60.43	2.10	10.20	4.81	125.00	2.21	7.11	1.22
VI	6.93	11.13	50.00	54.87	63.33	1.97	17.17	5.20	160.67	2.27	7.60	1.40


Relative contribution of the characters to study the genetic diversity
28.4
25.5
22.7
19.8
17
14.2
11.3
8.5
5.6
2.8
0
x1
x2
x3
x4
x5
x6
x7
x8
x9
x10
x11
x12
Variable

Chapter-V

DISCUSSION

The cucumber (*Cucumis sativus* L.) is grown for its edible fruit. Since, there is wide range of diversity in the germplasm of cucumber in its centre of diversity for yield and its attributing traits. Among the vegetable crops, the cucumber is grown on a large acreage has become necessary to get basic information on genetic variability and other biometrical parameters which will help us in selection as well as genetic manipulations for improvement in the yield.

Genetic variability is the key for any crop improvement programme and effectiveness of selection depends upon the magnitude and kinds of genetic variability present in the population. The genetic variation is heritable one and hence has important in the selection. To achieve this target, the sound biometrical knowledge and major quantitative traits pertaining to variability in the materials, heritability and genetic advance of the economic traits association between the important traits and direct and indirect response on yield per plant will be boon to the plant breeder for making the breeding strategies. The knowledge of genetic divergence will helpful to the breeder for the selection of desirable parents for the hybridization programme.

Most of the economic traits like yield are polygenic in nature and are influenced by environment which sophisticate the success of selection. Keeping in view the importance of different traits related to vegetative growth, quality and yield of fruit, the present investigation was carried out to assess the vastness of variability, correlation coefficients, heritability, expected genetic advance, path coefficient analysis among the characters and clustering pattern of twenty seven genotypes of cucumber for twelve characters. The result obtained from the investigation described in the proceeding chapter attempts have been made to corroborate the findings reported by the present investigations with those of various workers in the past.

5.1 Analysis of variance

The analysis of variance for different characters had been presented in Table 4.1 The mean sum of square due to genotypes/treatments was highly significant for all the characters. In other words, the performance of the genotypes with respect to these characters were statistically different indicating variability among the genotypes due to genetic constitution of materials as well environmental influence for that particular traits. Some researchers such as Gaikwad *et al*. (2011), Shukla *et al.* (2010), Pushpalatha *et al*. (2016) suggested good scope for selection in the available germplasm of cucumber.

5.2 Range and mean performance

The mean of twenty seven genotypes including respective two checks for twelve characters had been presented in Table 4.2. A wide range of variation were recorded in the mean performance of genotypes. The comparison of mean performance of twenty seven genotypes for twelve characters including checks revealed that presence of very high level of variability in the used genotypes. The genotype JPCC-4, and NDCC-7 significantly out yielded the best check. Khan *et al.* (2015), Thakur *et al.* (2017) reported similar results in cucumber for yield.

5.3 Genetic variability

The estimate of coefficient of variation is of prime importance to breeder because genetic variance alone does not allow a decision as to which characters were showing the highest degree of variability.

Phenotypic and genotypic coefficients of variation helps to measure the range of variability in the characters and facilitate a measure to compare the variability present among different quantitative traits. Presented in Table 4.3

In most cases, the phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters under study, indicated the considerable influence of environment on the expression of these characters, Shah *et al.* (2018).

The highest value of phenotypic and genotypic coefficient of variation were observed for number of primary branches per plant followed by fruit length while, the lowest value of phenotypic and genotypic coefficient of variation were observed for days to first fruit harvest followed by days to first male flower anthesis. Therefore, selection of the characters with high PCV may improve through selection on the basis of phenotypic performance of the genotypes. Similar reports were also given by Rajeshwari *et al.* (2014), Kumar *et al.* (2011). which observed high phenotypic coefficient of variation for number of primary branches per plant. Pal *et al.* (2016) also found PCV and GCV values were high for node number bearing first female flower, number of marketable fruits per plant and number of primary branches per plant.

Moderate phenotypic and genotypic coefficient of variability was exhibited by node to first female flower anthesis followed by fruit diameter appears. Similar result was also reported by Kumar *et al.* (2011).

These results indicated that the characters with high GCV and PCV values had maximum improvement opportunity through selection, although difference between PCV and GCV indicates the influence of environment in the expression of these characters.

5.4 Heritability and genetic advance

Heritability in broad sense of a character is important to the breeder. It indicates the possibility and extent to improvement is possible through selection. A high estimate of heritability along with high genetic advance provides good scope for further improvement in advance generations. Thus the degree of success in selection depends upon the magnitude of heritability as well as genetic advance.

In the present investigation, heritability values were ranged from 23.6 to 88.10%. The highest heritability was recorded for fruit length followed by days to first male flower anthesis, number of primary branches. While, lowest heritability was recorded vine length followed by fruit yield per plant. Jat *et al.* (2014) observed high heritability for days to anthesis of first female flower, weight of fruit and diameter of fruit respectively.

The value of expected genetic advance in percent of mean was highest for number of primary branches per plant followed by fruit length and node to first female flower anthesis. The lowest value of genetic advance was recorded for vine length and days to first fruit harvest. Jat *et al.* (2014) estimated high genetic advance in per cent of mean for weight of fruit and total yield per vine.

Shah *et al.* (2018) also reported High heritability coupled with high genetic advance was estimated for most of the traits *viz.*, fruit length, fruit weight, vine length , number of nodes per vine indicated that selection for these traits should be effective for improving economic yield.

5.5 Correlation coefficients

Selection of superior genotypes is the main objective of breeder during improvement for various traits which is dependent on the phenotypic expression. Generally, breeders are selecting the genotypes on the basis of their phenotypic performance. The nature and magnitude of association between yield and its components traits is necessary for effective selection in advance generations.

In the present study, correlation between twelve characters were worked out at phenotypic levels had been presented in Table 4.4 In most cases, the magnitude of genotypic correlation coefficient was higher than the corresponding values of the phenotypic correlation coefficient. This indicated a strong genetic association between the traits and the phenotypic expression which was suppressed due to environmental influence.

The most important trait number of fruit per plant had exhibited highly significant positive phenotypic correlation with number of fruit per plant followed by vine length. Whereas, fruit diameter, number of primary branches per plant, days to first male flower anthesis, days to female flower anthesis and fruit lengthexhibited moderate to low significant positive phenotypic correlation. While, node to first male flower anthesis, node to first female flower anthesis and average fruit weight showing significant negative association with fruit yield per plant. The similar findings were also proposed by Kumar *et al.* (2011), Ullah *et al*. (2012), Veena *et al*. (2013), Khan *et al*. (2015).

5.6 Path coefficient analysis

Fruit yield per plant and yield contributing attributes are interrelated among themselves. This creates hindrance in drawing a clear picture of association between characters. The mutual relationship expressed as correlation coefficient between the traits is either positive or negative but complex in nature and sometimes fails to give a meaningful interpretation. In such situation a biometrical tool path coefficient analysis is used to measure the different ways of contribution of independent traits on the dependent one (yield).

Path coefficient analysis breaks the correlation coefficient into the measures of direct and indirect effect and point out the precise causes of association. In the present investigation, genotypic and phenotypic correlation of yield and yield contributing traits partitioned into their direct and indirect effect through path coefficient analysis. The results of path coefficient are presented in Table 4.5

The higher magnitude of positive direct effect at phenotypic level on fruit yield per plant was exerted by number of fruit per plant followed by vine length and days to first female flower anthesis. The positive indirect effect on fruit yield per plant was exerted by days to first female flower anthesis via node to first male flower anthesis and days to first male flower anthesis followed by vine length via node to first female flower anthesis, number of primary branches per plant and fruit diameter. Similar result were also given by Kumar *et al.* (2011), Pal *et al*. (2017), Karthick *et al.* (2019).

5.7 Genetic divergence

The result of D^2 analysis are presented in Table 4.6, 4.7 and 4.8 The study of genetic divergence twenty seven genotypes of cucumber was carried out by using Mahalanobis D^2 statistics. In present investigation twenty seven genotypes of cucumber were grouped in six distinct non-over lapping clusters. This indicated presence of considerable diversity in the genotypes. The major clusters in the above mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although, the genotypes of same origin or geographic region were also found to be grouped together in the same cluster. The instances of grouping of genotypes of different origin or geographically of same region in same clusters were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity. Cluster I (19) had highest number of genotypes followed by cluster II (2), cluster III (3), cluster IV (1), cluster V (1) and cluster VI (1). The estimates of intra and inter-cluster distance represented by D^2 values. The intra cluster D^2 values ranged from 0.00 to 47.41. Maximum intra-cluster distance was recorded in cluster I recorded (47.41) followed by cluster III (41.36). The maximum inter-cluster distance observed between cluster II and cluster V (263.21) followed by cluster I and cluster V (154.27). The minimum inter cluster value was found in cluster IV and VI (67.63) and cluster I and cluster VI (68.86). Cluster means for different traits indicated considerable differences among the clusters.

The minimum cluster mean value for node number to first male and female flower anthesis were found in cluster II (6.20) and cluster VI (11.13). The minimum days to first male and female flower anthesis and days to first fruit harvest were observed in cluster II (37.73 and 45.92) and cluster III (58.52). The maximum number of primary branches per plant, fruit length and fruit diameter were observed in cluster IV (2.97), cluster II (18.12) and cluster V (4.81), respectively. Maximum average fruit weight and vine length were shown by cluster VI (160.67g) and cluster IV (2.52m), while maximum number of fruits per plant and fruit yield per plant were found in cluster IV (7.83 and 1.47kg). Similar finding were also reported by, Kumar *et al.* (2013), Singh *et al.* (2017), Pal *et al.* (2017).

Chapter-VI

SUMMARY AND CONCLUSION

The present Experiment entitled"Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)"using twenty-seven genotypes of cucumber was carried out to study the extent of variability, heritability (in broad sense), genetic advance, correlation and path coefficient analysis at phenotypic and genotypic levels and genetic divergence for twelve traits.

The experiment was conducted at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.), in Randomized Block Design with three replications during *Zaid*, 2019.

The observations were recorded on twelve quantitative traits. Each treatment consisted of five rows spaced at 2m with plant to plant spacing 0.50m. Each entry was grown in the plot size of 3m × 2m. The following conclusion were found from this study:

1. The mean sum of squares (analysis of variance) due to genotypes were highly significant for all twelve characters representing the variability among the genotypes considered in this study due to diverse genetic constitution of genetic materials.
2. The wide range of variation in mean performance of the genotypes were observed for average fruit weight followed by days to first fruit harvest and days to first female flower anthesis. The minimum difference in range were observed for fruit yield per plant followed by number of primary branches per plant and vine length.
3. Generally, the estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the traits. The higher extent

phenotypicand genotypic coefficients of variation were observed for number of primary branches per plant followed by pod fruit length. Therefore, selection of these characters may improve through selection based on their phenotypic performance.

4. The highest heritability was recorded for fruit length followed by days to first female flower anthesis while, medium to low heritability was observed for remaining of the characters.The expected genetic advance in per cent of mean was highest for number of primary branches per plant followed by fruit length and node to first female flower anthesis whereas, minimum genetic advance was recorded in vine length and fruit yield per plant. High heritability along with high expected genetic advance in per cent of mean was observed for fruit length followed by number of primary branches per plant.

5. The character fruit yield per plant had highly significant positive correlation with number of fruit per plant followed by vine length. It may be concluded that improvement of characters such as number of fruit per plant, number of primary branches, fruit diameter would help in improving the fruit yield and these traits should be considered in fixing selection criteria to improve the fruit yield per plant in cucumber.

6. The highest positive direct effect on fruit yield per plant was exerted by days to first fruit harvest followed by fruit diameter, number of fruit per plant, at genotypic and phenotypic level. However, highest negative direct effect on days to first male flower anthesis was exhibited by fruit length and number of primary branches per plant. These traits may be considered as most reliable selection indices for effective improvement of fruit yield in cucumber.

7. Mahalanobis D^2 statistic distributed all the twenty seven genotypes into six clusters. Maximum number of the genotypes used in this study were grouped in cluster IV, V and VI (each cluster have one), while remaining genotypes were grouped in cluster I (19), cluster II (2) and III (3). The maximum inter-cluster distance was recorded between clusters II and V followed by cluster I and V, which revealed that members of these two clusters were genetically much diverse to each other.While, the minimum inter-cluster D^2 values were observed in case of cluster VI and cluster VI.

Based on the present investigation and findings, it may be concluded that considerable variability exists among the genotypes of cucumber. The genotypes, JPCC-1, NDCC-15 and NDCC-9 were recognized promising genotypes for fruit yield per plant and other traits. Therefore, they may be used for varietal improvement programme in fennel.

Chapter-VII

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DEPARTMENT OF VEGETABLE SCIENCE

Acharya Narendra Deva University of Agriculture & Technology
Kumarganj, Ayodhya-224 229 (U.P.) India

Title: "Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.).

Major Advisor and Chairman	**Name of student**
Dr. C.N. Ram Associate Professor Department of Vegetable Science	**Manisha Kumari** M.Sc. (Horticulture) Vegetable Science Id. No. H-10586/18

ABSTRACT

The present investigations work entitled **"Genetic studies for yield and related traits in cucumber (*Cucumis sativus* L.)** was conducted at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during summer season of 2019. The experiment was conducted in Randomized Block Design with three replications to assess the performance of 27 genotypes of cucumber, to determine nature of variability, character association, path analysis and genetic divergence. Observations were recorded on 12 quantitative characters *viz.,* Days to first male flower anthesis, Days to first female flower anthesis, Node number to first staminate flower appearance, Node number to first pistillate flower appearance, Number of primary branches per plant, Vine length (m), Days to first fruit harvest, Fruit length (cm), Fruit diameter (cm), Number of fruit per plant, Average fruit weight (g), fruit yield per plant (kg). The analysis of variancerevealed significant differences among the genotypes for all the characters except days to maturity. Based on mean performance most promising genotypes *viz.,* NDCC-7, NDCC-15, JPCC-1, JPCC-4 were found as most promising genotypes for high yield per plant. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the characters. The highest phenotypic as well as genotypic coefficients of variation were observed in number of primary branches followed by fruit length.High heritability coupled with low genetic advanced in per cent of mean were observed for fruit length followed by days to first male flower anthesis, number of primary branches, average fruit weight, node to first male flower anthesis had exhibited highly significant and positive phenotypic correlation withnumber of fruit per plant followed by vine length , fruit diameter , number of primary branches per plant , days to first male flower anthesis , days to female flower anthesis and fruit length. High magnitude of positive direct effect at phenotypic level on fruit yield was exerted by number of fruit per plant followed by vine length and days to first female flower anthesis. All genotypes were grouped into six clusters. Cluster I had highest number of genotypes. Maximum inter-cluster distance was observed between clusters III to cluster II which suggested that genotypes of these cluster are genetically very diverse to each other.

(C.N. Ram)	**(Manisha Kumari)**
Major Advisor & Chairman	**Student**