GENETIC VARIABILITY STUDIES IN CUCUMBER (*Cucumis sativus* L.) UNDER LOW HILL REGION OF HIMACHAL PRADESH

Thesis

by

RIYA RANI

(NH-2020-32-M)

submitted to

Dr. YASHWANT SINGH PARMAR UNIVERSITY
OF HORTICULTURE AND FORESTRY
SOLAN (NAUNI) H.P-173230, INDIA

in

partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE
(HORTICULTURE)
VEGETABLE SCIENCE
DEPARTMENT OF VEGETABLE SCIENCE
COLLEGE OF HORTICULTURE AND FORESTRY
NERI (HAMIRPUR) H.P.-177001 INDIA
2022

Dr. B.S Dogra
(Principal Scientist)

Department of Vegetable Science
College of Horticulture and Forestry, Neri
Dr. Yashwant Singh Parmar University of Horticulture and Forestry
Solan (Nauni) H.P -173230 India

CERTIFICATE - I

This is to certify that the thesis entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** submitted in partial fulfillment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES** to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP) – 173230 is a bonafide research work carried out by **Ms. Riya Rani (NH-2020-32-M)** daughter of Shri. Ajay Kumar under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

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

Place: Neri, Hamirpur
Dated:

(Dr. B.S Dogra)
Chairman, Advisory committee

CERTIFICATE - II

This is to certify that the thesis entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** submitted by **Ms. RIYA RANI (NH-2020-32-M)** daughter of Shri. Ajay Kumar to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP) – 173230 India in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

Dr. B.S. Dogra
(Principal Scientist)
Chairman, Advisory Committee

External Examiner

MEMBERS OF ADVISORY COMMITTEE

Dr. Shiv Pratap Singh
(Associate Professor)
Department of Vegetable Science

Dr. Santosh Kumari
(Senior Scientist)
Department of Vegetable Science

Dr. Monica Sharma
(Associate Professor)
Department of Plant Pathology

Professor and Head
Department of Vegetable Science

Countersigned

Dean
College of Horticulture and Forestry,
Neri, Hamirpur (HP)

CERTIFICATE - III

This is to certify that all the mistakes and errors pointed out by external examiner have been incorporated in the thesis entitled **"Genetic variability studies in Cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** submitted by **Ms. RIYA RANI (NH-2020-32-M)** daughter of Shri. Ajay Kumar to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (HP) – 173230 in partial fulfilment of the requirements for the award of degree of **MASTER OF SCIENCE (HORTICULTURE) VEGETABLE SCIENCE** in the discipline of **HORTICULTURAL SCIENCES**.

Dr. B.S Dogra
Chairman
Advisory Committee

Professor and Head
Department of Vegetable Science
College of Horticulture and Forestry
Neri, Hamirpur (H.P.)

ACKNOWLEDGEMENT

First and foremost, I bow my head in front of my lord who gave me everything to pursue this work into completion and bestowing me with divine spirit, essential strength and necessary succor to find my way towards a glorious carrier amidst several hurdles and struggles.

I would like to express my profound sense of gratitude towards my major advisor ***Dr. B.S Dogra*** *(Principal scientist, Department of Vegetable Science), for his valuable and inspiring guidance, everlasting patience, constant encouragement, valuable suggestions, logical and necessary criticisms and close supervision at every step of research work and above all his friendly behavior and sense of forgiveness throughout my association with him. It was great opportunity for me to work under his guidance.*

I sincerely thanks to all the respected members of my advisory committee, ***Dr. Shiv Pratap Singh*** *(Assistant Professor, Department of vegetable science),* ***Dr. Santosh Kumari*** *(Senior Scientist, Department of vegetable science) and* ***Dr. Monica Sharma*** *(Assistant Professor, Department of Plant pathology)* for providing valuable guidance, and timely advice during the most trying times in the tenure of this research work.

I am immensely thankful to ***Dr. Deepa Sharma*** *(Senior Scientist, Department of vegetable science) for her valuable suggestions during the course of investigations. I also express my thanks to Mr. Bali Raj (field assistant), Mr. Hem Raj Sharma (Laboratory assistant) and other non-teaching staff of college for their timely co-operation.*

Nobody has been more important to me in the pursuit of this research work than the member of my family I would like to thank my beloved grandfather ***Late. Shri Kushal Chand****, grandmother* ***Smt. Ishwari Devi,*** *father* ***Shri Ajay Kumar,*** *mother* ***Smt. Reena Rani,*** *brother* ***Saksham,*** *sisters* ***Anshu****,* ***Shreya*** *and* ***Divya,*** *whose blessings, care, love and guidance are with me in whatever I pursue.*

So many people have touched my heart and made an impact on my world. I am thankful for every lesson and learning experience. Rewinding my life that I have spent in Neri, I would like to affectionately remember the company of my friends ***Pallavi, Shivangni, Shilpa, Shivani Dadhwal Manisha, Shivali, Shivalika, Parveen, Anjali and Sandeep.***

It is my honour and privilege to express my gratitude to my senior ***Deeksha mam*** *for their help and guidance. I am also thankful to my seniors* ***Jasdeep mam, Pratibha mam and Rishav sir*** *for their unforgettable company and support.*

At the end, I thank all those whom I am able to recall here and those whom I might have left unknowingly.

Place: Neri, Hamirpur

Dated: **(Riya Rani)**

CONTENTS

ABBREVIATIONS AND SYMBOLS

%	:	Per cent
=	:	Equal to
X	:	Multiplication
^{0}C	:	Degree Celsius
Ha	:	Hectare
H.P.	:	Himachal Pradesh
SE	:	Standard Error
ANOVA	:	Analysis of Variance
C.V.	:	Coefficient of Variation
CD	:	Critical Difference
et al.	:	Co-workers
m^2	:	Meter square
viz.	:	Videlicet (namely)
/	:	Per
UHF	:	University of Horticulture and Forestry
COHF	:	College of Horticulture and Forestry
PCV	:	Phenotypic Coefficient of Variation
GCV	:	Genotypic Coefficient of Variation
m	:	Meter
cm	:	Centimeter
G	:	Gram
mg	:	Milligram
GA	:	Genetic Advance
i.e.,	:	That is
^{0}B	:	Degree Brix
PDI	:	Percent Disease Index
TSS	:	Total soluble solids
Fig.	:	Figure

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

Chapter – 1

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is an important member of the family Cucurbitaceae, having diploid chromosome number 2n=2x=14. Cucumber thought to have originated in the southern Himalayan foothills. India is the primary and China is secondary centre of origin of cucumber. The progenitor of cultivated cucumber is *C. sativus* L.var. *hardwickii.* Cucumber is extensively cultivated in tropics, subtropics and in middle region of temperate zone. It is a thermophilic, day neutral and frost susceptible crop, which require warm weather and bright light for its better growth and development. However, it can be grown in both summer and rainy seasons (Rastogi, 1998).

Globally, cucumber is the second most widely cultivated cucurbits after watermelon and according to Tatlioglu (1993), it ranks fourth in the list of economic vegetables in Asia after tomato, cabbage and onion. The cucumber along with gherkins is cultivated in an area of 2156.04 thousand hectare with production of 84863.93 thousand metric tonnes (Anonymous, 2020a). In India, cucumber is commercially grown in the states of Haryana, Madhya Pradesh, Karnataka, Andhra Pradesh, Uttar Pradesh and Punjab covering an area of about 111 thousand hectares with production of 1638 thousand metric tonnes and average productivity of 14.76 metric tonnes per ha (Anonymous, 2020b). In Himachal Pradesh, cucumber cultivation has spread over from low to mid-hills and fruits are available from June to October, bringing remunerative returns to the farmers of the state.

Cucumber popularly known as ‘khira’ is one of the most important cucurbit vegetables, primarily grown for its tender fruits, which are consumed either raw as salad, cooked as vegetable or as pickling cucumber in its immature stage. Its juice is often recommended as source of silicon to improve the health of skin. It is a rich source of vitamin C (2mg), thiamine 0.03mg, niacin 0.2mg, carbohydrate (2.5%), protein (0.4%), iron (1.5mg), minerals like calcium 10mg and phosphorus 25mg per 100g of fresh weight (Yawalkar, 1985). The fruits and

seed possess astringent, antipyretic and cooling properties. Seed oil is also used as antipyretic. Fruits are beneficial for people suffering from constipation, jaundice and indigestion. Cucumber contains ascorbic and caffeic acids, which assist to alleviate skin irritation and swelling. The slightly bitter taste of cucumbers results from cucurbitacins (Schieberle *et al*. 1990).

Cucumber is a monoecious, annual, trailing or climbing vine (Bailey, 1969). Leaves are triangular-ovate, three lobed with acute curves. The staminate flowers are in clusters with short slender pedicels. The pistillate flower is usually solitary with stout short pedicel. The calyx and corolla of staminate, pistillate and hermaphrodite flowers are five lobed. The staminate flowers have three stamens. Two stamens have two locules each and third is unilocular. The filaments are free, but the stamens are more or less united by their anthers. The pistillate flowers are epigynous and hermaphrodite flowers are perigynous. The pistil consists of one to five (usually three) carpels which in turn, produce ovaries with a corresponding number of locules. The pistillate flowers contain up to five stigmas. The main stem of monoecious cucumber is usually characterized by three phase of sex expressions. Only staminate flowers are produced in the first phase followed by phase of irregularity alternating female, male or mixed nodes and finally a phase of only pistillate flowers. Lateral shoots of monoecious cultivars have stronger female tendencies (Ram, 2012).

India has done little research on varietal production and improvement, despite its economic and nutritional importance. As a result, there is a need to investigate the variability of different horticultural traits in cucumber genotypes in order to identify superior varieties through introduction, selection or hybridization. It is vital to examine variability present in the base population or the genetic material used before beginning any breeding or crop improvement programme. The phenotypic coefficient of variation and genotypic coefficient of variation is helpful in detecting the amount of variation present in the available germplasm. Heritability is the portion of phenotypic variation that is transmitted from parent to progeny. Higher the heritable variation, the greater will be the possibility of fixing the characters through selection. Heritability estimate may not provide clear predictability of the breeding value. Thus, heritability estimates combined with genetic advance are normally more helpful in predicting the

genetic gain under selection than heritability estimates alone (Johnson *et al*. 1955). The understanding of heritability and genetic advances assists the plant breeder in predicting the behaviour of succeeding generations and making desirable selections for improvements. Selection of one character affects a number of associate traits, implying the importance of determining the interrelationship of various yield components, both among themselves and with yield.

Therefore, correlation analysis has an important role in plant breeding programmes as it measures the mutual relationship between yield and its related attributes and among the attributes too. But the relationship between two traits is not so simple. Such a correlation can be resolved into two direct and indirect effects by the path coefficient technique developed by (Wright, 1921). Path coefficient studies are more helpful since it provide a better picture of direct and indirect associations and identify the most efficient yield contributing characters.

Cucumber in India exhibits considerable variation for different traits, but very meagre work has been done for the improvement of local types. Therefore, evaluating locally adopted cucumber genotypes for commercial cultivation is priority area of research in improving the productivity, uniformity, fruit quality and market acceptance. Keeping in view the above discussion, the present investigation entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** was carried out at the Experimental Farm of College of Horticulture and Forestry, Neri with the following objectives:

- To assess the performance and the extent of genetic variability, heritability and genetic advance in various cucumber genotypes.
- To find out the correlation among the various yield and yield contributing characters.
- To estimate direct and indirect effects of different characters on yield using path analysis.
- To identify the promising genotype with desirable horticultural traits.

Chapter – 2

REVIEW OF LITERATURE

A number of studies have been made with regard to variability in important characters of cucumber. Estimating parameters of variability, especially heritability and genetic gain are important indicators for improvement of characters through selection whereas selection for highly heritable characters is more effective. Therefore, heritability along with other parameters of variability can be used in predicting gain of given selection intensity and expected genetic gain further gives idea of extent of improvement in character through selection.

Selection for yield and quality traits can be better achieved if information with respect to correlation between such traits is also available with better understanding of the association between relevant characters with yield which is provided through the path coefficient analysis. A brief review of literature available on various aspects of the present investigation has been presented under the following sub heads:

2.1 Genetic variability

2.2 Heritability and genetic gain/ genetic advance

2.3 Correlation analysis

2.4 Path coefficient analysis

2.1. GENETIC VARIABILITY:

Genetic variability is the raw material on which selection starts to evolve elite genotypes. Therefore, its understanding is very important for its efficient utilization in crop improvement. Greater the genetic variability in the available germplasm, better will be the chances for selecting superior genotypes (Simmonds, 1962). Hence, an insight into magnitude of heritable variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding programme. A review of

information pertaining to genetic variability for different characters in cucumber has been presented below:

Das *et al.* (2003) evaluated eighteen genotypes of cucumber and reported high genetic variability for fruit yield per vine, vine length, number of primary branches per vine, number of fruits per vine, fruit length, fruit diameter and fruit weight. The pooled analysis revealed that highest genotypic coefficient of variation for fruit yield, fruit weight and highest phenotypic coefficient of variation for fruit yield per vine.

Kanwar *et al.* (2003) evaluated twenty-six indigenous cucumber genotypes and observed wide range of variation for all traits, except harvest duration. Genotypic coefficients of variation were higher in magnitude than phenotypic and environmental coefficients of variation for all traits except for harvest duration. Maximum genotypic coefficient of variation observed in sex ratio, node of first female flower and yield per plant. Kanwar and Rana (2006) studied twenty-six genotypes of cucumber and observed that all characters under study showed a wide range of values except days to first pickling and fruit circumference. Phenotypic variability was high for node at which first female flower appears, sex ratio, yield per plant, number of fruits and vine length.

Kumar *et al.* (2008) assessed variability in twenty-five diverse cucumber genotypes for fruit yield and yield attributing traits and observed significant differences among all the genotypes for all the characters. A wide range of variability along with estimates of PCV and GCV was observed for days to first female flower anthesis, number of primary branches/plant, number of fruits/plant, number of node bearing female flowers/plant, fruit length, fruit weight, cavity of fruit at edible stage and fruit yield/plant.

Hossain *et al*. (2010) evaluated fifty-eight cucumber genotypes and observed wide range of variations among the genotypes. Highest genotypic coefficient of variation was recorded in yield per plant, number of fruits per plant, fruit length, number of lateral shoots, average fruit weight, petiole length, node order at which male and female flower opened. Shukla *et al.* (2010) studied the genetic variability for fruit yield and attributing traits in twenty morphologically diverse cucumber genotypes. High estimates of genotypic coefficient of variation

for fruit yield per plant, fruit length, vine length, number of fruit per plant, node number bearing first female flowers, intermodal length, diameter of fruits per plant and number of nodes per vine, indicating their reliability for effective selections.

Gaikwad *et al.* (2011) assessed genetic variability in eighteen genotypes of cucumber and observed wide range of variation for all the traits 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. The high genotypic as well as phenotypic coefficient of variation was observed for characters such as PDI (Percent disease index) followed by length of fruit, number of fruits per vine, weight of fruit and node number of first female flower.

Genetic variability study carried out by Singh *et al*. (2011) in eight genetically diverse cucumber genotypes and recorded maximum variability with respect to yield per vine followed by fruit weight, vine length, days taken to first female flower anthesis and fruit length. Afroz *et al*. (2012) studied twenty two genotypes of cucumber to measure variability for yield and yield contributing characters. High genotypic coefficient of variation was observed for yield per plant, number of male flowers and number of fruits per plant, while it was low for weight and breadth of fruit.

Golabadi *et al*. (2012) studied twenty genotypes of cucumber based on yield related traits. Analysis of variance showed that there was highly significant variation for all the traits among genotypes. Ullah *et al*. (2012) studied the genetic variability and correlation in twelve exotic cultivars of cucumber. Analysis of variance revealed significant differences for all the characters. 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) worked with thirty-eight advanced lines of cucumber for estimating the variability for yield and yield contributing traits. The highest genotypic coefficient of variation as well as phenotypic coefficient of variation were observed for node at which first female flower appear followed by node number of first male flower appearance, yield per plant, seed cavity breadth,

average fruit weight and number of fruits per plant. Kumar *et al.* (2013) evaluated thirty diverse cucumber genotypes to assess the nature and magnitude of variability for different horticultural traits. The genotype LC-1 gave maximum mean value for fruit weight and yield per plot. Both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for seed vigour index-I and yield per plot, indicated the existence of wide range of variations and offers better scope for improvement through selection.

Jat *et al*. (2014) assessed genetic variability for different characters in sixteen genotypes of cucumber and reported considerable amount of genetic variability for all traits in all genotypes. The maximum phenotypic and genotypic coefficient of variation was observed for acidity of fruit followed by weight of fruit, total yield per vine and total soluble solids.

Ene *et al.* (2016) evaluated sixteen cucumber genotypes for estimating the magnitude of their genetic variability and heritability for different horticultural traits. A high coefficient of variation was recorded for most of the traits in both seasons and high variability was observed among genotypes. Pal *et al.* (2016) evaluated thirty cucumber genotypes and observed wide range of variation for different traits. The 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, number of marketable fruits per plant, number of primary branches per plant, seed vigour index II, yield per plant and disease severity of angular leaf spot, anthracnose, downy mildew and powdery mildew.

Pushpalatha *et al*. (2016) investigated twenty four diverse genotypes to assess the variability for different traits. High phenotypic and genotypic coefficient of variation were observed 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, internodal length and vine length.

Kandasamy (2017) evaluated twenty genotypes of cucumber 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. Maximum phenotypic and genotypic co-efficient of variation (PCV and GCV) was observed for yield per plant followed by average fruit weight, fruit diameter and number of fruits per plant.

Kumari *et al*. (2017) evaluated nineteen genotypes of cucumber to study the nature and magnitude of genetic variability for twenty one traits. High estimates of PCV and GCV were obtained for number of node at which first pistillate flower appears, fruit yield (q/ha), fruit length while moderate value was recorded for average fruit weight, indicating the importance of selection for improvement of such traits.

Rajawat and Collis (2017) studied twelve genotypes of cucumber and observed considerable amount of genetic variability for all traits among the genotypes. High PCV and GCV was observed for number of female flowers per vine, number of male flowers per vine, fruit yield per vine, number of branches per vine, number of fruit per vine, node number at which first appears of male flowers, node number at which fist appears of female flowers and fruit length. Sharma *et al*. (2017) evaluated thirty genotypes of cucumber to estimate the nature and magnitude of genetic variability for different horticultural traits in cucumber. For all the characters studied, magnitude of PCV was higher than the corresponding GCV.

Singh *et al.* (2017) reported the nature and magnitude of genetic variability among yield and its contributing traits in cucumber. The estimates of magnitude of phenotypic coefficient of variation (PCV) were higher than corresponding genotypic coefficient of variation (GCV) for all characters. High PCV and GCV value were obtained for the characters *viz*., number of fruit per plant, marketable yield per plant, nodal position of first female flower, internodal length, number of female flower per node, days to anthesis of first female flower, vine length and fruit weight.

Bhagwat *et al.* (2018) evaluated thirty genotypes of cucumber to estimate the nature and magnitude of variability for different horticultural traits. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters. High magnitude of PCV and GCV were observed for node at first female flower appear, total number of fruits per vine, fruit length,

flesh thickness, average fruit weight, fruit yield per vine, fruit yield per hectare, chlorophyll content and rind thickness.

Deepa *et al*. (2018) evaluated thirty cucumber genotypes and found highly significant variation among the genotypes for all the characters. Analysis of variance indicated highly significant variation among the genotypes for all the characters. Estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding values of genotypic coefficient of variation (GCV), though difference was very less in majority of the cases, thus showing these traits were less influenced by environmental factors. High phenotypic and genotypic coefficient of variation were observed for vine length, number of leaves at 90 days after sowing, leaf area, internodal length, number of branches per vine, number of fruits per vine, average fruit weight, fruit length, fruit yield per vine, fruit yield per plot and fruit yield per hectare.

Pradhan *et al*. (2018) studied genetic variability in eleven local cucumber lines. The genotypes exhibited significant differences for all the traits. The range of variation was high for fruit weight, vine length, fruit length and days to first male and female flower bloom. The difference between PCV and GCV were negligible for all the characters except node of first female bloom. Thus showing these characters were less influenced by environmental factors. Shah *et al*. (2018) studied genetic variability in thirteen genotypes of cucumber. The observations were recorded for twenty seven different traits. Analysis of variance showed significant differences among the genotypes for all characters. The PCV was higher than GCV for all traits, indicating the importance of growing environment for the expression of the characters.

Shet *et al.* (2018) evaluated thirty cucumber cultivars for growth and yield traits. Results revealed that significant genetic variability was present among genotypes for node of first female flower, number of male flower, number of female flower, fruit weight, flesh thickness, fruit length and fruit width. Tamang *et al*. (2018) estimated genetic variability in ten genotypes of cucumber. High phenotypic coefficient of variation and genotypic coefficient of variation was observed for fruit weight, fruit length, fruit girth and fruit yield per plant.

Bartaula *et al.* (2019) evaluated eight cucumber genotypes to estimate the magnitude of genetic variability. Analysis of variance revealed significant differences among genotypes for growth and yield traits. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for weight of fruit, whereas traits namely fruit length, fruit diameter and days to maturity had medium value for both GCV and PCV. Chakraborty *et al.* (2019) evaluated twenty-eight diverse landraces of cucumber for seventeen morphological traits. High magnitude of genotypic coefficients of variation were observed for average fruit weight, fruit yield per plant, number of fruits per plant, fruit length, number of branches per plant, number of seeds per fruit and 100 seed weight.

Gangadhara *et al.* (2019) evaluated fifteen gynoecious parthenocarpic lines of cucumber and observed that genotypic and phenotypic coefficient of variation were high for nodal position of first female flower, number of fruits, fruit weight and fruit yield per plant which indicates maximum variability is existing in the genotypes. Karthick *et al.* (2019) evaluated thirty six cucumber genotypes to assess the genetic variability. Phenotypic coefficient of variation (PCV) were higher than the corresponding values of genotypic coefficient of variation (GCV) while the difference between PCV and GCV was very less for length of vine, number of primary branches, number of nodes per vine, node number bearing first male flower, node number bearing first female flower, days for first male flower, days for first female flower, days for first harvest, number of male flower, number of female flower, number of fruits per plant, fruit length, fruit diameter, fruit weight and yield per plant. Hence these traits are less influenced by the environment.

Agashi *et al*. (2020) evaluated eight cucumber genotypes for twelve traits. Analysis of variance showed significant differences among the genotypes for all the traits. High PCV and GCV for number of female flowers per plant, number of branches per plant, vine length, number of leaves per plant, leaf area index, number of fruits per plant and fruit weight. Moderate PCV and GCV for days to 50% flowering, number of male flowers per plant, average leaf area, leaf area index and average fruit length and Low PCV and GCV was recorded for average fruit girth.

Keshari *et al*. (2020) assessed genetic variability in twenty genotypes of cucumber. The analysis of variance revealed significant differences for all traits among the genotypes. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits. The high phenotypic and genotypic coefficient of variation (PCV and GCV) was observed for vine length, number of primary branches, days to 50% flowering, days to first fruit harvest, number of fruits per plant, fruit length, fruit diameter, average fruit weight, fruit yield.

Kumari *et al.* (2020) studied genetic variability in twenty-seven genotypes of cucumber based on twelve quantitive characters. The analysis of variance revealed significant differences among the genotypes for all the characters except days to maturity. The estimates of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters. The highest phenotypic as well as genotypic coefficients of variation were observed for number of primary branches followed by fruit length.

Manivannan *et al.* (2020) assessed the magnitude of genetic variability in twenty four diverse cucumber genotypes for fruit yield and yield attributing traits. The genotypes exhibited significant differences for all traits. The magnitude of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV). High PCV and GCV were recorded for number of primary branches, node at which first female flower appears, number of fruits per plant, yield per vine and yield per hectare.

Mishra *et al.* (2021) conducted genetic evaluation of twelve genotypes of cucumber for yield and related traits. Analysis of variance indicated that twelve diverse genotype of cucumber including one commercial cultivar (Pusa Barkha) significant differences for the seventeen traits among the genotypes. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels was recorded among the genotypes.

Yadav *et al.* (2021) studied genetic variability, heritability and genetic advance in thirty-six genotypes of cucumber. The value of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters, indicating the influence of environmental factors on expression of different characters.

2.2 HERTAIBILITY AND GENETIC ADVANCE:

Heritability and genetic advance are important selection parameters because they determine the impact of environment on character expression and the extent to which improvement is possible after selection (Robinson *et al.* 1951). Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. Genetic advance refers to improvement in the mean genotypic value of the selected plants over parental population. According to, (Liang and Walter, 1968) high heritability along with high genetic advance might be due to action of the additive genes whereas, the high heritability coupled with low genetic advance might be due to the non-additive gene actions which include dominance and epistasis. High heritability coupled with high genetic advance suggests that phenotypic performance based selection could be used to improve character. The studies conducted in cucumber concerning heritability and genetic advance are reviewed below:

Das *et al*. (2003) recorded high heritability coupled with high genetic gain in eighteen cucumber genotypes with respect to fruit yield per vine length, number of primary branches per vine, number of fruits per vine, fruit length, fruit diameter and fruit weight, thus indicating the role of additive genes for the expression of these traits and improvement for these traits can be broad about by selection.

Kanwar *et al*. (2003) reported high heritability for all the characters except harvest duration. The high heritability estimates were associated with high genetic gain for sex ratio, yield per plant and node of first female flower indicating additive gene control for inheritance of these traits.

Kumar *et al.* (2008) evaluated twenty-five genotypes of cucumber for yield and yield attributing traits. High heritability and high expected genetic gain were observed for days to first female flower anthesis, number of primary branches per plant, number of fruits per plant, fruit length and fruit diameter, 100-seed weight, seed cavity at edible stage and fruit yield per plant indicating the importance of additive gene effect. Gaikwad *et al*. (2011) reported high heritability estimates (Broad sense) for all the characters. High heritability along with high genetic advance was recorded for vine length and fruit weight.

Singh *et al*. (2011) reported moderate heritability for node number of first male flower, fruit length, fruit diameter, number of fruits per vine, node number of first female flower and fruit weight. Further, high genetic advance was observed for node number of first male flower, fruit length, number of fruits per vine and average fruit weight indicating additive gene effects and emphasized the effectiveness of selection for improvement.

Afroz *et al.* (2012) recorded high heritability with low genetic advance in percent of mean observed in days to first female flower which indicated the presence of non- additive gene effects for the expression of this character and selection for this trait might not be fruitful. High heritability with high genetic advance in percent of mean was observed for yield per plant and number of fruits per plant showed that these traits can be improved through selection.

Ullah *et al*. (2012) assessed twelve exotic cultivars of cucumber to study genetic variability, heritability and correlation coefficient and observed broad sense heritability estimates for various traits ranged from 42.26 to 89.55%. High to moderate heritability as well as genetic gain observed in fruit weight, fruit length, number of fruits per plant and days to flowering, suggesting the role of additive gene action in their inheritance and the possibility of genetic improvement through selection.

Veena *et al*. (2012) observed high heritability and high genetic advance over mean for number of seeds per fruit, 100 seed weight, days to first male flower opening, fruit length, fruit breadth, seed cavity length, number of fruits per plant, seed cavity breadth, days to first female flower opening, nodes per vine, days to first harvest, node at first female flower appearance. Kumar *et al*. (2013) recorded high heritability estimates coupled with high genetic gain for seed vigour index-I and yield per plot, indicated the existence of wide range of variations and offers better scope for improvement through selection.

Jat *et al.* (2014) reported high estimates of heritability (broad sense) combined with high genetic advance for days to anthesis of first female flower (96.66%), fruit weight (92.67%) and fruit diameter (92.51%) showed the importance of selection for the improvement of these traits.

Pal *et al.* (2016) evaluated thirty genotypes of cucumber and high heritability (>80%) coupled with high genetic gain (>50%) was noted for node number bearing first female flower, number of marketable fruits per plant, number of primary branches per plant, seed vigour index II, yield per plant and diseases severity of angular leaf spot, anthracnose, downy mildew and powdery mildew, which showed the presence of sufficient variability in the germplasm for effective selection. Low estimates for all the variability parameters were reflected by TSS, vine length and seed cavity breadth. Hence, hybridization followed by selection will be promising for improving these traits.

Pushpalatha *et al.* (2016) noted 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 the importance of selection for improvement. Kandasamy (2017) reported high heritability for all the characters except node number of first female flower. Genetic gain was maximum for yield per plant followed by average fruit weight, fruit diameter, number of fruits per plant, number of secondary branches, fruit length, fruit girth and 1000 seed weight.

Kumari *et al*. (2017) reported high heritability coupled with high genetic advance as percentage of mean for number of node at which first pistillate flower appears followed by fruit yield (q/ha), fruit length, average fruit weight, test weight, number of fruits per plant, number of nodes per vine, number of primary branches per vine etc., indicating predominance of additive gene action for these characters. Hence selection based on phenotypic performance of these characters would be more effective.

Rajawat and Collis (2017) recorded high genetic advance coupled with high heritability in number of male flowers per vine, vine length and fruit weight. However, the estimates were moderate for number of female flowers per vine. Higher heritability estimates were accompanied by lower genetic advance for vitamin C, TSS, fruit yield per vine and days to first fruit harvest. The high genetic gain was recorded for fruit yield per vine, 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.

Sharma *et al*. (2017) analysed heritability and genetic gain in thirty cucumber genotypes and reported that high heritability coupled with high genetic gain was observed for severity of anthracnose and angular leaf spot suggested predominant additive gene control for these traits. High to moderate heritability with moderate genetic gain was in node number bearing first female flower, number of marketable fruits per plant, fruit length, days to marketable maturity, harvest duration, seed vigour index I and II, severity of powdery mildew, yield per plot and yield per hectare indicated slightly additive genetic control for these traits. Hence, selection will be less effective in these traits. Fruit breadth, fruit weight, TSS and seed germination showed moderate heritability with low genetic gain, which indicated that these characters are under control of additive gene action, therefore, hybridization will be effective for improving these traits.

Singh *et al*. (2017) recorded high heritability coupled with high genetic advance for marketable yield per plant, number of fruit per plant and intermodal length. High heritability and moderate genetic gain were observed for vine length, days to anthesis of first female flower and fruit weight. The values of heritability along with high genetic advance revealed that these traits are likely to respond to selection.

Bhagwat *et al.* (2018) worked with thirty cucumber genotypes for estimating variability for different horticultural traits. High heritability coupled with high genetic advance was recorded for field emergence, vine length, number of nodes per vine, node at first male flower appear, days to first male flower, node at first female flower appear, days to first female flower, total number of fruits per vine, fruit diameter, fruit length, flesh thickness, fruit weight, yield per vine, yield per hectare, chlorophyll content and rind thickness.

Deepa *et al.* (2018) evaluated thirty cucumber genotypes to assess heritability and genetic advance for various yield and its constituent traits. 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.

Pradhan *et al*. (2018) studied eleven cucumber genotypes and observed high heritability and high expected genetic gain for days to first male and female flower bloom, days to first fruit harvest, fruit yield per hectare, fruit length, fruit girth, fruit weight, vine length, number of branches per vine, internodal length, sex ratio indicating that these characters had additive gene effect and therefore are more reliable for effective selection.

Shah *et al.* (2018) recorded high heritability coupled with high genetic advance for 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%), respectively. Hence, indicating the importance of selection for their improvement.

Shet *et al*. (2018) reported high heritability coupled with high genetic advance for node at first female flower, number of female flower, fruit weight, flesh thickness, fruit length and fruit width indicating the additive gene action for the inheritance of these traits. Tamang *et al.* (2018) evaluated ten genotypes of cucumber to assess the magnitude of variability and genetic association of traits for their improvement. High heritability with high genetic advance was observed for fruit weight, fruit length, fruit girth and fruit yield per plant.

Chakraborty *et al*. (2019) reported high heritability coupled with high genetic gain for average fruit weight, fruit yield per plant, number of fruits per plant, fruit length, number of branches per plant, number of seeds per fruit and 100 seed weight. However, these parameters were moderate for early fruit harvest and total soluble solids (TSS).

Karthick *et al*. (2019) studies heritability in cucumber and observed that all the traits had high heritability coupled with high to moderate genetic advance except days for first male and female flower appearance. Agashi *et al*. (2020) evaluated eight cultivars of cucumber and observed that all the traits were highly heritable implying that these traits are genetically controlled. High heritability

coupled with high genetic advance in eleven parameters implied that selection can be effective method for their improvement.

Keshari *et al*. (2020) evaluated twenty genotypes and heritability estimates high for all the characters. The genetic advancement as a percent of the mean was high for average fruit weight, number of primary branches, number of fruits per plant, fruit length and fruit yield, whereas moderate genetic advance was observed for fruit diameter, vine length, days to first fruit harvest, and days to 50% flowering.

Kumari *et al*. (2020) evaluated twenty-seven genotypes of cucumber and results revealed that high heritability coupled with low genetic advanced in per cent of mean were observed for fruit length, days to first male flower anthesis, number of primary branches, average fruit weight.

Manivannan *et al*. (2020) studied variability, heritability and genetic gain in twenty four diverse cucumber genotypes and reported high heritability and high expected genetic gain for node at which first female flower appear, number of primary branches, number of fruits per plant and yield per vine, demonstrating additive gene effects and highlighted the importance of selection for the improvement of these traits.

Sahoo and Singh (2020) reported high heritability coupled with high genetic advance as percent of mean for fruit length, fruit weigh, number of fruits/plant, plant height, yield per plant, yield per hectare, days to first male flower, node to first male flower, node to first female flower and sex ratio (M/F). These characters had additive gene effect and therefore, these are more reliable for effective selection.

Mishra *et al*. (2021) evaluated twelve diverse cucumber genotypes and results revealed that high heritability coupled with high genetic advance in per cent of mean for average fruit yield, number of fruits per vine, fruit length, node number to first male flower and node number to first female flower. Thus these traits showing additive gene effect and selection for these traits are reliable for developing high yielding cultivar of cucumber.

Yadav *et al*. (2021) reported high heritability for fruit yield per plant and fruit yield per hectare, moderate heritability for days to first male flower, days to last harvest, fruit length, fruit diameter, and low heritability for days to first female flower, days to first harvest and internodal length. High genetic advance was observed for node number to first male flower, fruit yield, node number to first female flower, plant height, fruit weight, fruit length, moderate genetic advance recorded for fruit diameter, days to first male flower, internodal length and low genetic advance for days to last harvest, days to first female flower and days to first harvest. High heritability along with high genetic advance revealed that these characters are controlled by additive gene action. Thus these traits have ample scope for the improvement through selection.

2.3. CORRELATION ANALYSIS:

Correlation coefficient analysis plays an important role in plant breeding programmes as it calculates the mutual relationship between yield and its related attributes and among the attributes too. The association of characters may be due to either genetic linkage or pleiotropy (Harland, 1939).

The studies conducted in cucumber related to correlation analysis are reviewed below:

Dogra (1998) reported positive and significant genotypic correlation of fruit yield per plot with number of fruits per plant. Days to marketable maturity had highly significant and positive association with days to first female flower appearance and node number of first female flower at both phenotypic and genotypic levels.

Rao *et al.* (2004) recorded that fruit yield was positively significantly correlated with fruit weight, fruit length and flesh thickness, whereas it was negatively significantly correlated with node number bearing first female flower and days to first female flower anthesis at both genotypic and phenotypic levels. Ying *et al.* (2004) evaluated eight selected lines of cucumber for six agronomic characters. They observed positive and significant correlation of yield with fruit weight, number of fruits per plant, leaf area and vine length but no significant

genetic correlation was found between yield and number of primary branches per plant.

Hanchinamani and Patil (2009) analysed the correlation coefficient in forty-five cucumber genotypes and recorded positive and significant association of yield with vine length, internodal distances, number of primary branches per plant, number of nodes per plant, fruit length, fruit diameter, flesh thickness, average fruit weight, number of marketable and unmarketable fruits per plant and total number of fruits per plant. Strong association of these traits revealed that selection based on these traits could ultimately improve yield.

Shukla *et al*. (2010) studies twenty morphological diverse cucumber genotypes and observed high significant and positive correlation of fruit yield per plant with number of nodes per vines, vine length, fruit diameter whereas, it was negative and significant with days to first female flower anthesis at both genotypic and phenotypic levels.

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

Kumar *et al*. (2011) studied character association and path analysis in thirty genotypes of cucumber. Correlation studies revealed that yield had positive and significant association with marketable fruits per plant, fruit length, fruit breadth, average fruit weight, harvest duration, total soluble solids, seed germination, seed vigour index I and II, while negative and significant correlations were observed with node number bearing first female flower, days to

marketable maturity, severity of powdery mildew, anthracnose and angular leaf spot, both at phenotypic and genotypic levels.

Afroz *et al*. (2012) evaluated twenty two genotypes for correlation studies and they reported positive and significant association of yield per plant with number of female flowers, number of fruits per plant and fruit length at genotypic level. Ullah *et al*. (2012) reported that fruit diameter, number of fruits per plant, leaf per plant, fruit weight and flesh thickness showed positive and significant correlation with fruit yield. Days to harvest showed negative correlation with yield indicating that early maturing varieties showed lower yields while the late maturing varieties had higher yields in cucumber.

Veena *et al*. (2013) studied thirty eight cucumber genotypes and recorded maximum positive correlation of hundred seed weight with yield per plant. Similarity, number of fruits per plant, average fruit weight, fruit length, flesh thickness and seed cavity length had significant positive correlation with yield. Ahirwar *et al*. (2017) analysed the correlation coefficient in forty-four genotypes of cucumber and revealed that there was a highly significant and positive correlation of yield with number of fruits per plant.

Pal *et al*. (2017) estimated correlation coefficient in thirty cucumber genotypes and observed that yield per plant had positive significant association with average fruit weight, fruit length and diameter, marketable fruit per plant, harvest duration, vine length, primary branches per plant, seed length, hundred seed weight, germination percentage, seed vigour index I and II, whereas yield per plant had negative significant correlation with node number bearing first female flower, days to first harvest, total soluble solids and severity of angular leaf spot, anthracnose, downy mildew and powdery mildew.

Singh *et al*. (2017) assessed genetic variability, heritability, correlation and path coefficient in thirty-eight cucumber genotypes. Correlation studies revealed that yield had significant positive association with number of fruits per plant, fruit girth, fruit weight and vine length and significant negative association with nodal position of first female flower both at phenotypic and genotypic levels.

Deepa *et al*. (2018) studied degree of association of yield with its component traits. Fruit yield per vine had positive and highly significant correlation with average fruit weight, vine length, leaf area, fruit length, number of fruits per vine, circumference of fruit, number of female flowers per vine, number of leaves per vine and intermodal length at both genotypic and phenotypic levels.

Kumar *et al.* (2018) studied correlation and path coefficient analysis for yield and its contributing characters in thirty-two cucumber genotypes. Correlation study showed that the genotypic correlation was higher than phenotypic correlations indicating highly heritable nature of the traits. It was observed that the traits *viz.,* number of fruits per plant, fruit weight, number of primary branches per plant, fruit length and vine length have exhibited highly significant positive association with fruit yield per plant.

Kumari *et al*. (2018) analysed the correlation coefficient in nineteen genotypes of cucumber and observed that fruit yield per plant had significant and positive association with average fruit weight, number of fruits per plant, number of pistillate flowers per plant, fruit width, vine length and number of nodes per vine at both genotypic and phenotypic levels. Tamang *et al.* (2018) studied genetic variation and character association in ten local cucumber genotypes. Correlation study revealed that fruit yield per plant showed highly significant and positively correlation with fruit weight and vine length.

Sharma *et al.* (2018) recorded that yield per plot had positive and significant association with number of marketable fruits per plant, average fruit weight, harvest duration, seed germination and seed vigour index-I, while significant negative correlations with node number bearing first female flower, days to marketable maturity, severity of anthracnose and angular leaf spot at both phenotypic and genotypic levels. Shet *et al*. (2018) studied correlation in thirty genotypes of cucumber and observed that number of female flower, fruit diameter and fruit number per vine had highly significant association with fruit yield.

Bartaula *et al*. (2019) analysed the correlation coefficient in eight cucumber genotypes and recorded that Fruit yield had high significant positive

correlation with fruit diameter and negative significant correlation with days to flowering. Nandi *et al*. (2019) evaluated ten cucumber genotypes and observed that internodal length has highly significant positive association with fruit yield per plant followed by fruit length, fruit weight, number of fruits per plant and vine length. Genotypic correlation was higher than phenotypic correlations indicating highly heritable nature of the traits.

Bhaiya *et al.* (2020) recorded that number of fruits per plant had positive significant phenotypic correlation with fruit yield per plant and diameter of fruit showed negative significant correlation with number of fruits per plant. Manivannan *et al*. (2020) studied correlation in twenty four diverse genotypes of cucumber and observed that yield per plant had positive and significant association with number of primary branches per plant, node at which first female flower appeared and number of fruits per plant.

Manisha *et al.* (2021) evaluated twenty-five cucumber genotypes to assess correlation and path coefficient analysis. Fruit length showed positive and significant correlation with vine length, average fruit weight and fruit diameter. Average fruit weight showed positive and significant correlation with fruit length, fruit yield per plant, vine length and fruit diameter. The number of fruits per plant showed positive and significant correlation with fruit diameter, fruit yield per plant and days at 50% male flower.

2.4. PATH COEFFICIENT ANALYSIS:

Path coefficient analysis allows the partitioning of correlation coefficients into direct and indirect effects, and more useful in achieving effective selection of superior genotypes. It is useful in determining whether the association of characters with yield is due to direct effects on yield or is the result of indirect effects through other component characters. The concept of path analysis was developed by Wright (1921) and the technique was first used by Dewey and Lu (1959) that helps in determining yield contributing characters thus, useful in selection. The path coefficient analysis in cucumber has been studied by several investigators and the same is reviewed below:

Rao *et al*. (2004) evaluated thirty one cucumber genotypes and revealed that fruit weight, number of fruits per plant, flesh thickness and node number bearing first female flower had positive direct effect on yield and concluded that these characters are both dependable and reliable for selection in order to improve yield. Ying *et al*. (2004) analysed the path coefficient analysis in eight selected inbred lines of gynoecious parthenocarpic cucumber and reported that the yield had positive and direct effect via fruit weight and fruit number per plant and was indirectly affected via vine length and leaf area.

Hanchinamani and Patil (2008) observed the path coefficient analysis in forty five genotypes of cucumber and observed that average fruit weight and number of fruits per vine had positive and direct effect on yield per vine at phenotypic level while average fruit weight had highest positive and direct genotypic effect on yield per vine followed by total number of fruits per vine. Hence, it would be rewarding to lay stress on these characters in selection programmes for increasing yield.

Kumar *et al.* (2011) studied path analysis in thirty genotypes of cucumber and revealed that average fruit weight had maximum positive direct effect on yield followed by harvest duration, seed vigour index II, severity of angular leaf spot, anthracnose, powdery mildew, marketable fruits per plant and total soluble solids, whereas negative direct effect of fruit length, fruit breadth, seed vigour index I, days to marketable maturity, seed germination, fruit length, node number bearing first female flower was observed on yield. Hence, selection for fruit weight, harvest duration, number of fruits per plant with minimum disease severity may be reliable for yield improvement in cucumber.

Afroz *et al*. (2012) did path coefficient analysis of cucumber and observed the positive direct effects towards yield per plant through leaf breadth, number of female flowers and fruit weight while leaf length and number of branches per vine showed negative direct effects.

Veena *et al.* (2013) performed path analysis for thirty-eight genotypes of cucumber and revealed that positive direct effects of seed cavity breadth, flesh thickness, average fruit weight, 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 harvest and fruit diameter had negative direct effect on yield.

Hasan *et al*. (2015) observed the path analysis in thirteen genotypes of cucumber. Path analysis revealed that number of fruits per plant, length of main vine, node per plant, leaf length, fruit length, fruit diameter and fruit weight had maximum positive direct effect on yield. Hence, selection is effective for improving yield.

Ahirwar *et al.* (2017) studied forty-two genotypes of cucumber along with two check varieties and observed that direct and indirect contribution of different traits toward yield revealed maximum positive direct effect of number of fruits per plant followed by fruit weight, test weight, days to first male flower, plant height, fruit length, fruit diameter, node number to first female flower. However, days to first female flower, primary branches per plant, seed index, internodal length, node number to first male flower, days to first fruit harvest exerted negative direct effect on yield.

Pal *et al*. (2017) evaluated thirty genotypes of cucumber and 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 per plant.

Kumar *et al.* (2018) evaluated thirty-two genotypes of cucumber and revealed that number of fruits per plant, fruit weight, number of primary branches per plant, fruit length, 100 seed weight, number of seed per fruit, days to last fruit harvest, fruit diameter and number of nodes per vine have direct positive phenotypic and genotypic effect on yield. Hence, selection for these traits can be done for improving fruit yield per plant. Kumari *et al*. (2018) analysed the path coefficient analysis in nineteen genotypes of cucumber. Path coefficient analysis indicated that number of fruits per plant, average fruit weight have positive and direct genotypic and phenotypic effects towards the fruit yield.

Nandi *et al*. (2019) evaluated ten cucumber genotypes and revealed that days to fifty percent flowering, number of fruits per vine, internodal length, fruit weight, fruit length, fruit diameter, TSS and moisture percentage have direct

positive phenotypic and genotypic effect on yield. Vine length, days to first female flower, nodal position of first female flower and days to first fruit pickling have negative direct effect on yield.

Bhaiya *et al.* (2020) estimate path coefficient analysis on phenotypic as well as genotypic levels to resolve direct and indirect effects of different characters on fruit yield per plant. Positive direct effect on fruit yield per plant exerted by days to first male flower anthesis, number of primary branch per plant and days to first fruit harvest. Negative indirect effect on fruit yield per plant exerted by node number of first male flower anthesis, days to first female flower anthesis and diameter of fruit.

Manivannan *et al*. (2020) studied path coefficient in twenty four diverse genotypes of cucumber and observed that positive direct effect on fruit yield was exerted by vine length, number of primary branches, node at which first female flower, fruit length, fruit circumference and number of fruits per plant whereas, days to first female flower have negative direct effect on yield.

Manisha *et al.* (2021) evaluated twenty-five cucumber genotypes and observed that high positive direct effect was exerted by average fruit weight, number of fruits per plant, vine length towards fruit yield per plant at both phenotypic and genotypic level.

Rajawat *et al*. (2022) studied path coefficient in twelve genotypes and observed highest positive direct effect on fruit yield per vine followed by fruits per vine, ascorbic acid, branches per vine whereas, total soluble solids and node number of first female flower showed highest negative direct effect on fruit yield per vine.

Chapter – 3

MATERIALS AND METHODS

The present investigation entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** was conducted from June 2021 to September 2021 at the Experimental Farm of Department of Vegetable Science at College of Horticulture & Forestry, Neri, Hamirpur H.P. The procedures and materials used during the investigation are described in detail in this chapter.

3.1 EXPERIMENTAL SITE

3.1.1. Location

The experiment was conducted at Experimental Farm of Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, H.P. situated in the low hill zone of Himachal Pradesh. The site is located at an altitude of 650 meters above mean sea level, lying between latitude and longitude of **31°41'47.6'' North** and **72°28'6.3''East**, respectively.

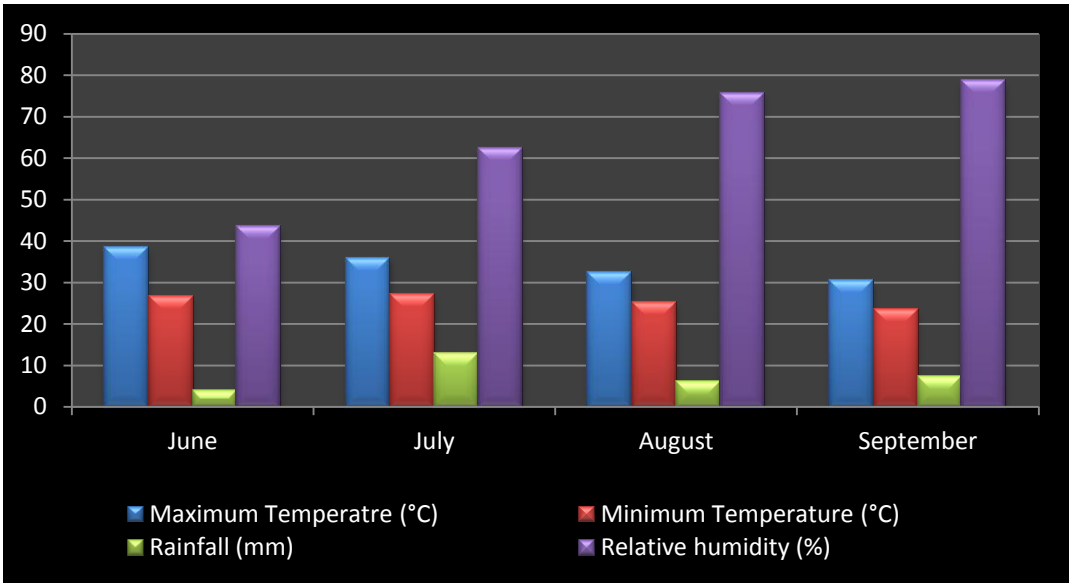
3.1.2. Soil

The soil of experimental field was sandy loam, well-drained, rich in organic matter and had a medium NPK status.

3.1.3. Climate and weather conditions

The experimental farm falls under subtropical condition with an annual rainfall of 60-100 cm. The climate is generally characterized as sub humid, hot summers with mild winters. Generally May and June are the hottest month and December and January are the coldest ones. Maximum rainfall occurs during the month of July. The meteorological data pertaining to the different parameters during the crop season such as maximum and minimum temperatures, relative humidity and rainfall were taken at Meteorological observatory, College of Horticulture and Forestry, Neri, Hamirpur (H.P) are presented in (Appendix-I) and Fig 3.1.

Fig. 3.1 Agro-meteorological data during cropping period



Source: Department of soil science and water management, COHF, Neri, Hamirpur, H.P. (177001)

3.2 EXPERIMENTAL MATERIALS

Experimental material used in for the present investigation comprises of twenty (including the check variety) diverse genotypes of cucumber (*Cucumis sativus* L.). In Table 3.1, the genotypes under study are listed along with their sources.

Table 3.1: List of Genotypes of Cucumber along with their source

Sr.no.	Genotype	Source
1	LC-C-1-21	Department of Vegetable Science COH&F, Neri, Hamirpur
2	LC-C-2-21	Department of Vegetable Science COH&F, Neri, Hamirpur
3	LC-C-3-21	Department of Vegetable Science COH&F, Neri, Hamirpur
4	LC-C-4-21	Department of Vegetable Science COH&F, Neri, Hamirpur

5	LC-C-5-21	Department of Vegetable Science COH&F, Neri, Hamirpur
6	LC-C-6-21	Department of Vegetable Science COH&F, Neri, Hamirpur
7	LC-C-7-21	Department of Vegetable Science COH&F, Neri, Hamirpur
8	LC-C-8-21	Department of Vegetable Science COH&F, Neri, Hamirpur
9	LC-C-9-21	Department of Vegetable Science COH&F, Neri, Hamirpur
10	LC-C-10-21	Department of Vegetable Science COH&F, Neri, Hamirpur
11	LC-C-11-21	Department of Vegetable Science COH&F, Neri, Hamirpur
12	LC-C-12-21	Department of Vegetable Science COH&F, Neri, Hamirpur
13	LC-C-13-21	Department of Vegetable Science COH&F, Neri, Hamirpur
14	LC-C-14-21	Department of Vegetable Science COH&F, Neri, Hamirpur
15	LC-C-15-21	Department of Vegetable Science COH&F, Neri, Hamirpur
16	LC-C-16-21	Department of Vegetable Science COH&F, Neri, Hamirpur
17	Punjab Naveen	PAU Ludhiana
18	Pant Khira	G.B.Pant University, Pantnagar
19	K-75	UHF Nauni, Solan
20	Solan Srijan (Check variety)	UHF Nauni, Solan

3.3 EXPERIMENTAL LAYOUT

The experiment was conducted in the Randomized Complete Block Design (RCBD) with three replications. The details of experimental layout are given below:

Crop	**Cucumber (*Cucumis sativus* L.)**
Number of treatments	20 (including check)
Design	RCBD (Randomized Complete Block Design)
Replication	3
Plot size	2.5 m x 2.5 m
Spacing	1.25 m x 0.5 m
Date of sowing	21 June
Season	Rainy (2021)

3.4 FIELD OPERATIONS

The experimental field was prepared and ploughed thoroughly with the help of power tiller and planked before few days of sowing. Stones, pebbles and crop residues of previous crop were removed manually. The field was brought to the fine tilth and it was levelled for proper drainage of water. Manures and fertilizers N, P, K were applied to the crop as per recommendation of package of practices. After levelling, plots were made according to the layout plan. Seeds of different genotypes of cucumber were directly sown in the field. Three to four seeds per hill were sown at spacing of 1.25 m × 0.5 m in a plot having size of 2.5 × 2.5 m^2 each, accommodating 10 hills per plot. After emergence of seedlings, only one healthy seedling per hill was retained thereby keeping 10 plants per plot. Staking was provided after 30 days of sowing. To ensure healthy crop other cultural operations like thinning, hoeing, weeding, irrigations and plant protection measures were carried out as per package of practices (Anonymous, 2014).

3.5 OBSERVATIONS TO BE RECORDED

The observations were made on five randomly selected plants in each plot for each replication, and the mean was calculated for statistical analysis. Observations were recorded for the following characters:

3.5.1 Days to first female flower

Number of days taken from the date of sowing to the date of first female flower appearance were recorded.

3.5.2 Node number of first female flower

The node number at which first female flower appears was counted.

3.5.3 Fruit length (cm)

Fruit length of randomly selected five fruits was measured during harvesting from the base of calyx to the tip of fruit and was expressed in centimetre (cm).

3.5.4 Fruit breadth (cm)

Fruit breadth of randomly selected fruits was measured by using digital vernier calliper at the middle point of fruit. It was expressed in centimetres (cm).

3.5.5 Fruit weight (g)

After harvesting, the fresh fruit weight was weighed on a digital weighing balance, and the average value was calculated in (g).

3.5.6 Flesh to seed cavity ratio

Breadth of flesh and seed cavity was measured with the help of digital vernier calliper after cutting horizontally into two halves. The following formula was used to work out the flesh to seed cavity ratio:

[Fruit breadth – Seed cavity breadth] / Seed cavity breadth

3.5.7 Internodal length (cm)

Distance between two adjacent nodes at middle portion of vine was measured with the help of scale and expressed in centimetres (cm).

3.5.8 Number of fruits per plant

The number of fruits picked at each harvest was taken into consideration to work out mean number of fruits per plant.

3.5.9 Total yield per plot (kg)

The weight of fruits harvested from each pickling was recorded from each plot (including the tagged plants) and total yield per plot was obtained by adding the yield of all the harvests and was expressed in kilograms (kg).

3.5.10 Harvest duration (days)

Total numbers of days from first fruit harvest to final fruit harvest were counted and average value was expressed as harvest duration.

3.5.11 Fruit colour

The colour of each individual fruit was visually analysed for recording the fruit colour of the genotypes at the end of harvest. Based on visual observation Light Green, Green, Dark Green and White fruits were obtained.

3.5.12 Fruit shape

Fruit shape was determined by using DUS guidelines of cucumber (Anonymous, 2021). Based on visual observation of fruits as elongate, oblong, cylindrical and oval.

Elongate (1) Oblong (2) Cylindrical (3) Oval (4)

3.5.13 Wart colour

The wart colour of each individual fruit was visually analysed at harvesting. Based on visual observation the wart colour on the fruits is expressed

as given by Esquinas-Alcazar and Gulick (1983) as absence of warts, black, brown and white.

3.5.14 Total Soluble Solids (°B)

Total soluble solid was calculated using hand refractometer. The juice from a composite sample of randomly selected fruits was squeezed through a double layer of fine mesh muslin cloth, and a drop of clear juice was dropped in the glass of a hand refractometer to calculate total soluble solids (AOAC 1970).

3.5.15 Ascorbic acid (mg/100g)

The ascorbic acid content of the fresh cucumber fruits was estimated at the time of harvest with the help of the procedure given in Association of Official Agricultural Chemists (AOAC 1980) by using the dye 2, 6- dichlorophenol indophenol.

Reagents used

(a) Metaphosphoric acid

(b) Ascorbic acid

(c) 2, 6- dichlorophenol indophenol

(d) Sodium bicarbonate

Procedure

Take 10 ml of fresh cucumber fruit juice and blend with 90 ml of 3% metaphosphoric acid. Filter rapidly through whatman No. 1 filter paper and take 10 ml of aliquot in a conical flask. Titrate with standard dye (2, 6-dichlorophenol indophenol) to a faint pink colour as an end point which should persist for atleast 15 seconds. The dye was prepared using 50 mg of sodium salt of 2, 6-dichlorophenol indophenol dye in approximately 150 ml of double distilled water containing 42 mg of sodium bicarbonate. It was slightly warmed and the volume was made up to 200 ml. This dye was used for titration and ascorbic acid was calculated by using the following formula:

$$\text{Ascorbic Acid (mg/100g)} = \frac{\text{Dye factor X Titre value X Volume madeup}}{\text{Volume of aliquat X Volume of sample taken for estimation}} \text{X100}$$

3.5.16 Prevalence of disease (s)

Percent Disease Index (PDI) of diseases *viz*., downy mildew, powdery mildew, was recorded periodically. Twelve leaves were randomly selected from three vines of each genotype.

Percent disease index (PDI) of downy mildew was recorded on 0-4 scale, suggested by Thind *et al*. (1991), as given below:

Leaf area infected (%)	Rating/ Score	Symptoms
0.0	0	Plants completely healthy with no downy mildew symptoms
0.1-25.0	1	Plants show slightly infection roughly one in every four leaves infected
25.1-50.0	2	Upto 50 percent of the leaves infected
50.1-75.0	3	Upto 75 percent of the foliage infected, the plants appear to be mildewed
75.1-100.0	4	Almost all the leaves are infected

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

Percent disease index (PDI) of powdery mildew recorded on 0-5 scale adopted by Sen and Kapoor (1974) with slight modifications:

Leaf area infected (%)	Rating/ Score	Category	Symptoms
0.0	0	Immune	No spots
0.1-0.5	1	Resistant	Leaves apparently free from spots or 2-3 specks on the lower leaves only

5.1-15.0	2	Moderately resistant	25 percent leaf area covered with specks, spots restricted
15.1-25.0	3	Moderately susceptible	50 percent leaf area covered on both the surfaces with specks
25.1-50.0	4	Susceptible	75 percent leaf area covered with specks which coalesce at places. Both sides of the leaves affected
Above 50	5	Highly susceptible	Leaves heavily infected with spots coalescing to cover almost the whole leaf on both surfaces; stems and petioles also infected

Percent disease index was calculated (McKinney, 1923) as follows:

$$PDI = \frac{\text{Sum of all disease rating}}{\text{Total no. of ratings x Maximum disease grade}} \text{ x } 100$$

3.6 STATISTICAL ANALYSIS

The analysis of variance will be carried out as per the procedure given by Gomez and Gomez (1984).

3.6.1 ANOVA for RCBD

Source of Variation	Degree of freedom (df)	Sum of Square	Mean sum of square	F_{cal}
Genotypes	(g-1)	S_g	$M_g = S_g/(g-1)$	M_g/M_e
Replications	(r-1)	S_r	$M_r = S_r/(r-1)$	M_r/M_e
Error	(r-1) (g-1)	S_e	$M_e = S_e/(r-1)(g-1)$	
Total	(rg-1)	S_T		

Where,

r = Number of replications,

g = Number of genotypes,

S_r = Sum of squares due to replications,

S_g = Sum of squares due to genotypes,

S_e = Sum of squares due to error,

S_T = Total sum of squares,

M_r = Mean sum of squares due to replications,

M_g = Mean sum of squares due to genotypes,

M_e = Mean sum of squares due to error.

The replication and treatment mean sum of squares was tested against the mean sum of squares due to errors by 'F-test' for(r-1), (r-1) (g-1) and (g-1), (r-1) (g-1) degree of freedom for RCBD at 0.05 level of significance.

The calculated F-values were compared with the tabulated F-value. When F-test will be found significant, the critical difference was calculated to find out the superiority of one genotype over the others.

The standard error and critical differences was calculated as follows:

$$SE\ (m) \pm = \pm\sqrt{\frac{Me}{r}}$$

$$SE\ (d) \pm = \pm\sqrt{\frac{2Me}{r}}$$

$$CD_{0.05} = S.E.\ (d) \times t_{0.05}\ (r-1)\ (g-1)\ df$$

Where,

SE (m) ± = Standard error of mean

SE (d) ± = Standard error of differences

$CD_{0.05}$ = Critical difference at 5% level of significance

3.6.2 Parameters of variability

The genotypic, and phenotypic, coefficients of variation were estimated as suggested by Burton and De Vane (1953) as follows:

3.6.2.1 Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{Genotypicvariance(Vg)}}{General\ mean\ of population\ (GM)} \times 100$$

3.6.2.2 Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{Phenotypicvariance(Vp)}}{General\ mean\ of population\ (GM)} \times 100$$

Where,

$V_e = M_e$

V_g = Genotypic variance $(M_g - M_e)/r$

V_p= Phenotypic variance $(V_g + V_e)$

3.6.2.3. Heritability

Heritability in broad sense was calculated as per formula given by Burton and De Vane (1953) and Allard (1960).

$$\mathbf{H\ (\%) = \frac{Vg}{Vp} \times 100}$$

Where,

H = Heritability (%)

Vg = Genotypic variance $[V_g = (M_g - M_e) / r]$

Vp = Phenotypic variance $(V_g + V_e)$

3.6.2.4. Genetic advance

The expected genetic advance resulting from the selection of five percent superior individuals was calculated as per Allard (1960):

$$\mathbf{GA = H \times \sigma\rho \times K}$$

Where,

H = Heritability (%)

σρ = Phenotypic standard deviation

K = Selection differential at 5% selection index (K = 2.06)

3.6.2.5. Genetic gain (GG)

Genetic advance expressed as per cent of population mean was calculated by the method given by Johnson *et al*. (1955).

$$\mathbf{GG = G_A/G_M \ X \ 100}$$

Where,

GG = Genetic gain

G_A = Genetic advance

G_M = Population mean

For categorization of magnitude of different parameters, following limits were used (Warshamana, 2005).

PCV and GCV

>30%	-	High
15 – 30%	-	Medium
<15%	-	Low

Heritability

>80%	-	High
50 – 80%	-	Medium
<50%	-	Low

Genetic gain

>50%	-	High
25-50%	-	Moderate
<25%	-	Low

3.7. CORRELATION ANALYSIS

The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al*. (1958) which is as follows:

Source of variance	**Degree of freedom**	**Mean sum of squares**		**Mean sum of products**	**Variance ratio (F-value)**
		X	**Y**		
Replications (r)	r-1				
Genotypes (g)	g-1	Mg X	Mg Y	Mg XY = MP_1	MP_1/MP_2
Error (e)	(r-1) (g-1)	Me X	Me Y	Me XY = MP_2	

Genotypic, Phenotypic, and environmental co-variance between X and Y characters worked out as under:

Environmental covariance (V_eXY) = MP_2

Genotypic covariance (V_gXY) = $(MP_1-MP_2)/r$

Phenotypic covariance (V_pXY) = $V_gXY + V_eXY$

Where,

V_eXY = Environmental covariance between X and Y

V_gXY = Genotypic covariance between X and Y

V_pXY = Phenotypic covariance between X and Y

Coefficients of correlation:

3.7.1. Phenotypic correlation between characters X and Y:

$$r_p = \frac{Vp\ XY}{\sqrt{VpX \times VpY}}$$

3.7.2. Genotypic correlation between characters X and Y:

$$r_g = \frac{Vg\ XY}{\sqrt{VgX \times VgY}}$$

3.7.3. Environmental correlation between characters X and Y:

$$r_e = \frac{Ve\ XY}{\sqrt{VeX \times VeY}}$$

Where,

V_pXY, V_gXY, V_eXY denotes phenotypic, genotypic, and environmental covariances between characters X and Y, respectively.

V_pX, V_gX, V_eX denotes phenotypic, genotypic, and environmental variances between characters X, whereas, V_pY, V_gY, V_eY denotes phenotypic, genotypic, and environmental variances between characters Y.

3.8. PATH COEFFICIENT ANALYSIS:

The following formula was used for calculating path coefficient analysis suggested by Dewy and Lu (1959). The path coefficient was obtained by the simultaneous selection of the following equations, which express the basic relationship between genotypic correction (r) and path coefficient (P)

$$r_{14} = P_{14} + r_{12} P_{24} + r_{13} P_{34}$$

$$r_{24} = r_{21} P_{14} + P_{24} + r_{23} P_{34}$$

$$r_{34} = r_{31} P_{14} + P_{32} + r_{24} P_{34}$$

where r_{14}, r_{24} and r_{34} are the genotypic correlation of component characters with yield (dependent variable) and r_{13}, r_{23} and r_{24} are genotypic correlations among the component characters (independent variables) and $r_{12}\,P_{24}$, $r_{13}\,P_{34}$, $r_{21}\,P_{14}$, $r_{23}\,P_{34}$, $r_{31}\,P_{14}$ and $r_{24}\,P_{34}$ indirect effects.

The direct effects will be calculated by the following set of equations:

$$P_{14}= C_{11}\,r_{14}+ C_{12}\,r_{24}+ C_{13}\,r_{34}$$

$$P_{24}= C_{21}\,r_{14} + C_{22}\,r24+ C_{23}\,r_{34}$$

$$P_{34}= C_{31}\,r_{14} + C_{32}\,r_{32} + C_{24}\,r_{34}$$

Where C_{11}, C_{12}, C_{23} and C_{33} are constants and $P_{14,}$ P_{24} and P_{34} are the estimates of direct effects.

3.8.1. Residual effect

It measures the role of other possible independent variables which were not included in the study on dependent variable. The residual effect was estimated with the help of direct effect and simple correlation coefficients as given below:

$$I = P^2x_4 + P^2_{14} + P^2_{24} + P^2_{34} + 2P_{14}r_{12}P_{24} + 2P_{14}r_{13}P_{34} + 2P_{24}r_{22}P_{34}$$

Chapter – 4

RESULTS AND DISCUSSION

The present investigation entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** was carried out to get information on nature and extent of genetic variability, heritability, genetic advance as percent of mean, correlation coefficients and path analysis among twenty genotypes of cucumber for yield and yield contributing characters including quality traits so as to select suitable genotypes either for direct introduction or for further use in breeding programme. The results obtained in the present investigation are presented under the following heads:

4.1 Mean Performance of genotypes

4.2 Variability Parameters

4.2.1 Coefficient of variation

4.2.2 Heritability

4.2.3 Genetic advance (as % of mean)

4.3 Correlation Coefficient analysis

4.4 Path coefficient analysis

4.1 Mean Performance of genotypes:

The analysis of variance revealed highly significant differences among the genotypes for all the characters which reflect good deal of genetic variability as shown in Appendix-II. The mean performance of the twenty genotypes for various characters are depicted and discussed below:

4.1.1 Days to first female flower:

Less number of days to first female flower is an indicative of earliness which in general fetches high price in the market. Significant variations were observed among all the genotypes for days to first female flower (Appendix-II) ranging from 47.66-76.66 days. The genotype Pant Khira took 47.66 days to first female flower which was found statistically at par with four genotypes including

standard check *viz*., Punjab Naveen (50.33), LC-C-1-21 (51.83), LC-C-3-21 (52.00) and Solan Srijan (52.33). While the genotype LC-C-10-21 (76.66) recorded maximum days to first female flower, which was statistically different from other genotypes. These results are in agreement with the earlier findings of Jat *et al*. (2014), Kumari *et al*. (2020) and Yadav *et al*. (2021).

4.1.2 Node number of first female flower:

Node number of first female flowers depicts the earliness of a genotype, lower the node bearing flower, earlier will be the variety in fruit bearing and in getting remunerative returns. Significant variations were observed among all the genotypes for node number bearing first female flower (Appendix-II). The node number for first female flower appearance ranged from 9.50-29.00 with overall mean of 17.54 (Table 4.1). The genotype, Punjab Naveen produced first female flower at the lowermost node (9.50), which was statistically at par with six genotypes including standard check *viz*., Solan Srijan (11.00), Pant Khira (11.83), LC-C-3-21 (12.00), LC-C-1-21 (14.00), LC-C-8-21 (14.00) and LC-C-7-21 (14.66). The first female flower appeared too late in the genotype LC-C-2-21 (29.00) followed by LC-C-13-21 (25.33) and LC-C-10-21 (25.00). Wide range of variability with respect to this trait are also reported by Pal *et al*. (2016), Kumari *et al*. (2017), Kumari *et al*. (2020) and Manivannan *et al*. (2020).

4.1.3 Fruit Length (cm):

Fruit length is an important character affecting the marketable fruit yield and is directly proportional to the yield. The genotypes under study revealed substantial variability as indicated by significant analysis of variance (Appendix-II). It ranged from 11.00 cm to 19.16 cm (Table 4.1) being maximum in LC-C-16-21 which was found to be statistically at par with nine genotypes including standard check *viz*., LC-C-14-21 (19.15 cm), LC-C-7-21 (19.08 cm), LC-C-13-21 (19.04 cm), LC-C-6-21 (18.91 cm), LC-C-11-21 (18.29 cm), Solan Srijan (18.16 cm), LC-C-5-21 (18.04 cm), LC-C-12-21 (17.92 cm) and LC-C-4-21 (17.80 cm). Minimum fruit length of 11.00 cm recorded for LC-C-10-21 which was statistically different from other genotypes. Afroz *et al*. (2012), Rajawat and Collis (2017), Singh *et al*. (2017), Chakraborty *et al*. (2019), Keshari *et al*. (2020)

and Kumari *et al*. (2020) has also reported wide range of variability for fruit length in cucumber.

4.1.4 Fruit breadth (cm):

Fruit breadth is one of the major yield determinating as well as quality traits of fruits. Analysis of variance showed divergence for fruit breadth among the genotypes (Appendix-II). Maximum fruit breadth was recorded in genotype LC-C-4-21 (4.80 cm) which was observed statistically at par with Pant Khira (4.79 cm), LC-C-8-21 (4.78 cm), LC-C-13-21 (4.57 cm) and Punjab Naveen (4.56 cm). While minimum fruit breadth (3.74 cm) was observed in LC-C-2-21. Solan Srijan (standard check) recorded fruit breadth of 4.25 cm which was found statistically at par with thirteen genotypes *viz*., LC-C-1-21 (4.50 cm), LC-C-9-21 (4.49 cm), LC-C-7-21 (4.46 cm), LC-C-5-21 (4.43 cm), LC-C-11-21 (4.42 cm), LC-C-6-21 (4.38 cm), LC-C-14-21 (4.36 cm), LC-C-3-21 (4.34 cm), LC-C-16-21 (4.21 cm), L-C-15-21 (4.17 cm), K-75 (4.15 cm), LC-C-12-21 (4.03 cm) and LC-C-10-21 (4.00 cm). Similar findings are also reported by Veena *et al*. (2012), Kumar *et al*. (2013), Kumari *et al*. (2017), Sharma *et al*. (2017), Shah *et al*. (2018) and Kumari *et al*. (2020).

4.1.5 Fruit weight (g):

Fruit weight is also one of the major yield contributing characters. Genotypes under studies showed variability with respect fruit weight (Appendix-II) ranging from 133.42 g to 307.17 g with a population mean of 213.07 g (Table 4.2).

Maximum fruit weight of 307.17 g was recorded for LC-C-13-21 which was statistically different from other genotypes. While LC-C-2-21 produced minimum fruit weight (133.42 g) which was statistically at par with two genotypes *viz*., LC-C-3-21 (165.77 g) and Punjab Naveen (175.50 g). The check variety, Solan Srijan recorded fruit weight of 233.25 g which was statistically at par with LC-C-15-21 (198.00 g), LC-C-11-21 (200.07 g), LC-C-1-21 (204.39 g), LC-C-7-21 (208.53 g), LC-C-6-21 (211.89 g), LC-C-8-21 (220.42 g), LC-C-5-21 (220.50 g), LC-C-14-21 (221.89 g), LC-C-12-21 (223.00 g), LC-C-4-21 (231.95 g), LC-C-10-21 (237.00 g), LC-C-16-21 (239.00 g) and Pant Khira (263.61 g).

Four genotypes resulted in more fruit weight than that of check Solan Srijan. These findings are in agreement with results obtained by Veena *et al*. (2012), Kumar *et al*. (2013), Singh *et al*. (2017), Kumari *et al*. (2020) and Yadav *et al*. (2021).

4.1.6 Flesh to Seed cavity ratio:

Fruit firmness is related to flesh firmness and seed cavity (endocarp) or locule size. As seed cavity increases, the fruit become less firm. The genotypes bearing maximum flesh to seed cavity ratio are considered ideal. Analysis of variance showed significant variance among genotype for flesh to seed cavity ratio (Appendix-II) ranging from 0.36 to 1.37 (Table 4.2). Maximum flesh to seed cavity ratio was observed in genotype LC-C-2-21 (1.37) which was statistically different from other all genotypes. Minimum flesh to seed cavity ratio of 0.36 was observed in genotype LC-C-10-21. The standard cultivar, Solan Srijan recorded flesh to seed cavity ratio of 0.56 which was statistically at par with LC-C-1-21 (0.57). Results of the present study are in accordance with the findings of Dogra (1998).

4.1.7 Internodal length (cm):

Internodal length is an indicative of vigour of plant and has direct impact on plant spacing. Genotype under study showed significant differences for internodal length indicating the variability for internodal length (Appendix-II). Internodal length varied from 6.23 cm to 9.50 cm among the genotypes. Maximum internodal length was observed in LC-C-13-21 (9.50 cm), which was statistically at par with Pant Khira (9.30 cm), LC-C-14-21 (8.97 cm), LC-C-5-21(8.82 cm), LC-C-7-21 (8.67 cm) and LC-C-16-21 (8.65 cm). While minimum (6.23 cm) value observed in LC-C-2-21. Solan Srijan (standard check) recorded internodal length of 7.67 cm which was found statistically at par with LC-C-4-21 (8.47 cm), LC-C-6-21 (8.08 cm), LC-C-10-21 (7.72 cm), LC-C-15-21 (7.53 cm), LC-C-8-21 (7.38 cm), LC-C-9-21 (7.35 cm), LC-C-11-21 (7.35 cm), LC-C-1-21 (6.98 cm), K-75 (6.92 cm), LC-C-12-21 (6.87 cm) and Punjab Naveen (6.85 cm). The variation for internodal length has also been reported by Pushpalatha *et al*. (2016), Kumari *et al*. (2017), Pradhan *et al*. (2018) and Yadav *et al*. (2021).

4.1.8 Number of fruits per plant:

Number of fruits per plant is one of the direct components which contribute towards yield. All the genotypes studied revealed significant variations for number of fruits per plant (Appendix-II) valued from 1.67 to 11.92 (Table 4.2). Maximum number of fruits per plant was observed in LC-C-14-21 which was statistically at par with LC-C-1-21 (11.57), LC-C-4-21 (11.00) and LC-C-9-21 (10.96). While minimum number of fruits was observed in LC-C-10-21. The standard check Solan Srijan recorded 10.00 number of fruits per plant which was statistically at par with LC-C-9-21 (10.96) and LC-C-4-21 (11.00). Four genotypes resulted in more number of fruits per plant than that of check Solan Srijan. These findings are in agreement with results obtained by Gaikwad *et al*. (2011), Deepa *et al*. (2018), Chakraborty *et al*. (2019), Manivannan *et al*. (2020), Mishra *et al*. (2021) and Yadav *et al*. (2021).

4.1.9 Harvest duration:

The data recorded for harvest duration showed significant differences among all the genotypes (Appendix-II). The average data pertaining to harvest duration is presented in table 4.3. Maximum harvest duration was found in genotype LC-C-9-21 (33.17) which was statistically at par with nine genotypes including check *viz*., LC-C-3-21 (33.00), Solan Srijan (32.67), Pant Khira (32.50), LC-C-1-21 (32.50), Punjab Naveen (32.00), LC-C-7-21 (31.50), LC-C-12-21 (30.17), LC-C-14-21 (29.50) and LC-C-5-21 (27.67). The minimum harvest duration was observed in LC-C-10-21 (16.17).

In general, longer harvest duration, more will be the yield which in turn minimizes the risk of fluctuations in the market. Significant variation in cucumber for harvest duration has also been observed by Kumar *et al*. (2013), Pal *et al*. (2016), Sharma *et al*. (2017) and Kumari *et al*. (2020).

Table: 4.1 Mean performance of cucumber genotypes for days to first female flower, Node number of first female flower, Fruit length (cm), and Fruit breadth (cm) traits:

Genotypes	Days to first female flower	Node number of first female flower	Fruit length (cm)	Fruit breadth (cm)
LC-C-1-21	51.83	14.00	16.43	4.50
LC-C-2-21	67.16	29.00	13.00	3.74
LC-C-3-21	52.00	12.00	14.42	4.34
LC-C-4-21	59.66	15.83	17.80	4.80
LC-C-5-21	57.50	16.00	18.04	4.43
LC-C-6-21	66.50	22.83	18.91	4.38
LC-C-7-21	54.16	14.66	19.08	4.46
LC-C-8-21	58.50	14.00	17.11	4.78
LC-C-9-21	53.50	15.50	16.66	4.49
LC-C-10-21	76.66	25.00	11.00	4.00
LC-C-11-21	63.00	18.16	18.29	4.42
LC-C-12-21	58.33	17.50	17.92	4.03
LC-C-13-21	69.33	25.33	19.04	4.57
LC-C-14-21	58.00	15.83	19.15	4.36
LC-C-15-21	62.33	21.33	12.58	4.17
LC-C-16-21	64.16	19.16	19.16	4.21
Punjab Naveen	50.33	9.50	14.16	4.56
Pant Khira	47.66	11.83	15.96	4.79
K-75	58.66	22.33	14.94	4.15
Solan Srijan	52.33	11.00	18.16	4.25
Mean	**59.08**	**17.54**	**16.59**	**4.37**
Range	**47.66-76.66**	**9.50-29.00**	**11.00-19.16**	**3.74-4.80**
SE(m)	**1.85**	**1.83**	**0.55**	**0.10**
C.V%	**5.43**	**18.06**	**5.71**	**3.79**
C.D.(0.05)	**5.32**	**5.25**	**1.57**	**0.28**

Table: 4.2 Mean performance of cucumber genotypes for fruit weight (g) flesh to seed cavity ratio, internodal length (cm) and Number of fruits per plant traits:

Genotypes	Fruit weight (g)	Flesh to seed cavity ratio	Internodal Length (cm)	Number of fruits per plant
LC-C-1-21	204.39	0.57	6.98	11.57
LC-C-2-21	133.42	1.37	6.23	3.27
LC-C-3-21	165.77	0.81	6.58	5.27
LC-C-4-21	231.95	0.89	8.47	11.00
LC-C-5-21	220.50	0.63	8.82	5.47
LC-C-6-21	211.89	0.67	8.08	7.03
LC-C-7-21	208.53	0.78	8.67	7.47
LC-C-8-21	220.42	0.61	7.38	8.47
LC-C-9-21	189.50	0.66	7.35	10.96
LC-C-10-21	237.00	0.36	7.72	1.67
LC-C-11-21	200.07	1.04	7.35	6.67
LC-C-12-21	223.00	0.94	6.87	5.47
LC-C-13-21	307.17	0.72	9.50	3.53
LC-C-14-21	221.89	0.92	8.97	11.92
LC-C-15-21	198.00	0.80	7.53	3.17
LC-C-16-21	239.00	0.68	8.65	6.01
Punjab Naveen	175.50	0.50	6.85	7.87
Pant Khira	263.61	0.64	9.30	6.67
K-75	176.67	0.88	6.92	5.67
Solan Srijan	233.25	0.56	7.67	10.00
Mean	**213.07**	**0.75**	**7.79**	**6.96**
Range	**133.42-307.17**	**0.36-1.37**	**6.23-9.50**	**1.67-11.92**
SE(m)	**14.72**	**0.01**	**0.32**	**0.52**
C.V%	**11.97**	**2.45**	**7.13**	**12.85**
C.D.(0.05)	**42.31**	**0.03**	**0.92**	**1.48**

4.1.10 Total Yield per plot (kg):

Total yield is one of the utmost important characters in any research programme in which the producers are interested. The observations recorded for this character showed significant variations among various genotypes (Appendix-II), which was ranged from 2.97 kg to 19.00 kg. Ten genotypes gave higher yield per plot than population mean. The highest total yield per plot was recorded in LC-C-4-21 (19.00 kg) which was statistically at par with LC-C-14-21 (18.03). While minimum total yield per plot was observed in LC-C-2-21 (2.97 kg) followed by LC-C-10-21 (3.00 kg). The standard check Solan Srijan recorded total yield of 15.06 kg per plot which was statistically similar to three genotypes *viz*., LC-C-9-21 (15.76 kg), LC-C-8-21 (14.56 kg), Pant Khira (14.38 kg). Four genotypes recorded higher yield per plot than standard check Solan Srijan. These results are similar to the findings of Gaikwad *et al*. (2011), Kumari *et al*. (2017), Deepa *et al*. (2018), Kumari *et al*. (2020) and Mishra *et al*. (2021).

4.1.11 Ascorbic acid (mg/100g):

Ascorbic acid content is also important quality parameters, as high ascorbic acid content would increase the nutritive value of cucumbers, which would help in better retention of colour and flavour. Significant variations were observed in ascorbic acid content among the genotypes (Appendix-II). The data pertaining to ascorbic acid content is presented in Table 4.3, which ranged from 2.03-4.46 mg/100g. Maximum ascorbic acid contents were recorded in standard check Solan Srijan (4.46 mg/100g) which was statistically at par with LC-C-13-21 (4.41 mg/100g), LC-C-4-21 (4.37 mg/100g), Punjab Naveen (4.33 mg/100g) and LC-C-15-21 (4.25 mg/100g) while minimum ascorbic acid content was recorded in LC-C-1-21 (2.03 mg/100g) which was statistically different from other genotypes. These results are in agreement with the findings of Deepa *et al*. (2018), Shah *et al*. (2018) and Mishra *et al*. (2021).

4.1.12 Total soluble solids (^{o}Brix):

A study of total soluble solids is directly related to the sugar content in the genotypes. The observations recorded on total soluble solids showed significant differences among the genotypes as depicted in the analysis of variance

(Appendix-II). The data presented in table 4.3 for total soluble solids varied from 2.12-4.02 ^{o}B. The comparison of mean values for different genotypes revealed that maximum total soluble solids was reflected by LC-C-6-21 (4.02 ^{o}B) which was found statistically at par with LC-C-13-21 (3.95 ^{o}B) and LC-C-10-21 (3.87 ^{o}B). The minimum total soluble solids were recorded in K-75 (2.12 ^{o}B). The standard cultivar Solan Srijan recorded total soluble solids (2.90 ^{o}B) which was statistically similar with ten genotypes LC-C-4-21 (3.28 ^{o}B), LC-C-7-21 (3.18 ^{o}B), LC-C-2-21 (3.15 ^{o}B), LC-C-9-21 (3.05 ^{o}B), Pant Khira (3.02 ^{o}B), LC-C-3-21 (2.98 ^{o}B), LC-C-1-21 (2.97 ^{o}B), LC-C-15-21 (2.95 ^{o}B), LC-C-5-21 (2.77 ^{o}B) and LC-C-12-21 (2.72 ^{o}B). These results are similar to those reported by Pal *et al*. (2016), Singh *et al*. (2017), Deepa *et al*. (2018). Shah *et al*. (2018), Chakraborty *et al*. (2019) and Mishra *et al*. (2021).

4.1.13 Fruit colour:

All the genotypes under study showed wide variations for fruit colour. Fruit colour is an important trait which decides the consumer preferences. The perusal of data based on visual observations presented in (Table 4.4) revealed different colour intensities and were categorised as Light Green, Green, Dark Green and White. Eight genotypes had Dark Green fruits, whereas one genotype had White fruits. While six genotypes had Light Green fruits and another five had Green fruits.

4.1.14 Fruit shape:

Data based on visual observation is presented in Table 4.4 which showed variation w.r.t fruit shape. The fruit shape was categorized as elongate, oblong, cylindrical and oval as per DUS guidelines of cucumber (Anonymous, 2021). Out of twenty genotypes, twelve were cylindrical, one was oblong, and five were elongate and two were oval in shape.

4.1.15 Wart colour:

Data based on visual observation are presented in Table 4.4 and is categorised as absence of warts, black, brown and white (Esquinas-Alcazar and Gulick, 1983). Twelve genotypes had black, and seven genotypes had brown warts whereas the wart colour of the fruits of one genotype was white.

Table: 4.3 Mean performance of cucumber genotypes for harvest duration (days), total yield per plot (kg), ascorbic acid (mg/100g), and TSS (^{0}B) traits:

Genotypes	Harvest duration (days)	Total yield per plot (kg)	Ascorbic acid (mg/100g)	TSS (^{0}B)
LC-C-1-21	32.50	16.34	2.03	2.97
LC-C-2-21	18.33	2.97	4.20	3.15
LC-C-3-21	33.00	7.27	3.58	2.98
LC-C-4-21	26.83	19.00	4.37	3.28
LC-C-5-21	27.67	10.02	3.12	2.77
LC-C-6-21	21.67	12.00	4.09	4.02
LC-C-7-21	31.50	13.79	3.24	3.18
LC-C-8-21	26.33	14.56	3.24	2.28
LC-C-9-21	33.17	15.76	2.44	3.05
LC-C-10-21	16.17	3.00	2.38	3.87
LC-C-11-21	20.17	10.57	2.35	2.25
LC-C-12-21	30.17	10.86	3.46	2.72
LC-C-13-21	19.33	9.27	4.41	3.95
LC-C-14-21	29.50	18.03	3.97	3.33
LC-C-15-21	19.17	4.57	4.25	2.95
LC-C-16-21	18.67	12.36	3.46	3.55
Punjab Naveen	32.00	11.28	4.33	3.35
Pant Khira	32.50	14.38	3.93	3.02
K-75	19.33	8.99	4.02	2.12
Solan Srijan	32.67	15.06	4.46	2.90
Mean	**26.03**	**11.50**	**3.57**	**3.08**
Range	**16.17-33.17**	**2.97-19.00**	**2.03-4.46**	**2.12-4.02**
SE(m)	**2.02**	**0.38**	**0.08**	**0.13**
C.V%	**13.45**	**5.78**	**3.95**	**7.40**
C.D.(0.05)	**5.81**	**1.10**	**0.23**	**0.38**

Table: 4.4 Mean performance of cucumber genotypes for different morphological traits:

Genotypes	Fruit Colour	Fruit Shape	Wart Colour
LC-C-1-21	Dark Green	Cylindrical	Brown
LC-C-2-21	Light Green	Oblong	Brown
LC-C-3-21	Dark Green	Oval	Brown
LC-C-4-21	White	Cylindrical	Black
LC-C-5-21	Dark Green	Elongate	Black
LC-C-6-21	Green	Cylindrical	Black
LC-C-7-21	Dark Green	Elongate	Black
LC-C-8-21	Green	Elongate	Black
LC-C-9-21	Dark Green	Oval	Brown
LC-C-10-21	Light Green	Cylindrical	Brown
LC-C-11-21	Dark Green	Elongate	Black
LC-C-12-21	Green	Cylindrical	Black
LC-C-13-21	Light Green	Cylindrical	Black
LC-C-14-21	Green	Elongate	Black
LC-C-15-21	Light Green	Cylindrical	Black
LC-C-16-21	Light Green	Cylindrical	Black
Punjab Naveen	Green	Cylindrical	Black
Pant Khira	Dark Green	Cylindrical	Brown
K-75	Light Green	Cylindrical	Brown
Solan Srijan	Dark Green	Cylindrical	White

4.1.16 Prevalence of disease (s):

4.1.16.1 Downy mildew:

During the periodic surveys, in the month of July-August downy mildew disease was recorded in the field. Data recorded on PDI of downy mildew, revealed the presence of significant difference among all the genotypes (Appendix-II).

Disease reaction was categorized into four groups *viz*., resistant (0-20%), moderately resistant (21-40%), susceptible (41-60%) and highly susceptible (>60%). Percent Disease Index (PDI) ranged from 9.53-52.77 with a mean of 24.72 (Table 4.5). Minimum PDI (9.53) was recorded in genotype LC-C-9-21, which was statistically at par with Solan Srijan (10.41) and LC-C-7-21 (10.41). Maximum PDI was observed in LC-C-2-21 (52.77) followed by LC-C-10-21 (52.07). Seven genotypes *viz*., LC-C-4-21, LC-C-6-21, LC-C-7-21, LC-C-9-21, LC-C-12-21, LC-C-14-21, Solan Srijan were found resistant while eleven genotypes *viz*., LC-C-1-21, LC-C-3-21, LC-C-5-21, LC-C-8-21, LC-C-11-21, LC-C-13-21, LC-C-15-21, LC-C-16-21, Punjab Naveen, Pant Khira, K-75 recorded moderately resistant and rest of the genotypes *viz*., LC-C-2-21, LC-C-10-21 were susceptible to downy mildew diseases. None of the genotype was found to be highly susceptible to downy mildew diseases (Table 4.6). However, these results are in agreement with the findings of Gaikwad *et al*. (2011), Pal *et al*. (2016) and Pradhan *et al*. (2018) who had also reported significant variation for percent disease index of downy mildew disease in cucumber. The downy mildew disease is usually favoured by high rainfall with moderate temperature and a relative humidity of more than 80% and these conditions are met during the month of July-August at Neri conditions.

4.1.16.2 Powdery mildew:

In the month of September powdery mildew disease was recorded in field. Significant variation was observed among different genotypes under study for PDI of powdery mildew (Appendix-II). Disease reaction was categorized into six categories *viz*., immune (0%), resistant (0.1-5%), moderately resistant (5.1-15%), moderately susceptible (15.1-25%), susceptible (25.1-50%) and highly susceptible

(>50%). Data pertaining to Percent Disease Index (PDI) is presented in table (4.5) and it ranged from 6.78-36.66. The minimum PDI was observed in standard check variety Solan Srijan (6.78) which was statistically at par with LC-C-9-21 (7.52). Maximum PDI was observed in LC-C-10-21 (36.66) which was statistically similar with LC-C-16-21 (35.55) and LC-C-3-21 (32.77).

Two genotypes *viz*., LC-C-9-21, Solan Srijan were found moderately resistant while ten genotypes *viz*., LC-C-1-21, LC-C-5-21, LC-C-6-21, LC-C-8-21, LC-C-11-21, LC-C-12-21, LC-C-13-21, Punjab Naveen, Pant Khira, K-75 were moderately susceptible and eight genotypes *viz*., LC-C-2-21, LC-C-3-21, LC-C-4-21, LC-C-7-21, LC-C-10-21, LC-C-14-21, LC-C-15-21, LC-C-16-21were susceptible to powdery mildew. None of genotype was observed to be immune, resistant and highly susceptible to diseases (Table 4.7). The prevalence of dry weather with moderate to warm temperature in field resulted in causing powdery mildew diseases. Pal *et al*. (2016), Sharma *et al*. (2017), Kumar *et al*. (2018) and Chakraborty *et al*. (2019) had also reported sufficient variation for powdery mildew disease among the different cucumber genotypes.

4.2 Variability Parameters:

The success of any breeding programme for population improvement is determined by the variability in the base population and the effectiveness of selection (Kumari *et al*. 2008). In order to initiate any breeding programme, the nature and extent of genetic variability is one of the essential criteria. The knowledge of various variability parameters i.e. phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), general mean, variation range, heritability (in broad sense), and genetic advance (GA) as per cent of mean are very much useful in predicting the amount of variability present in the given set of genetic material with respect to particular parameter. The variability parameters help to breeder to perform selection judiciously. Therefore, in present study the estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (in broad sense), and genetic advance (GA) as per cent of mean were worked out to see importance and response of selection for various traits (Table 4.8).

Table 4.5 Percent Disease Index of different diseases on genotypes of cucumber

Genotype	Downy Mildew		Powdery Mildew	
	Percent Disease Index *	**Diseases reaction**	**Percent Disease Index ***	**Diseases reaction**
LC-C-1-21	27.08 (31.33)	Moderate resistant	20.89 (27.09)	Moderately susceptible
LC-C-2-21	52.77 (46.57)	Susceptible	25.27 (30.10)	Susceptible
LC-C-3-21	27.50 (31.55)	Moderate resistant	32.77 (34.90)	Susceptible
LC-C-4-21	17.24 (24.52)	Resistant	26.11 (30.69)	Susceptible
LC-C-5-21	22.21 (28.01)	Moderate resistant	20.55 (26.94)	Moderately susceptible
LC-C-6-21	18.75 (25.62)	Resistant	21.66 (27.65)	Moderately susceptible
LC-C-7-21	10.41 (18.76)	Resistant	29.11 (32.59)	Susceptible
LC-C-8-21	23.61 (29.02)	Moderate resistant	17.10 (24.42)	Moderately susceptible
LC-C-9-21	9.53 (17.94)	Resistant	7.52 (15.87)	Moderately resistant
LC-C-10-21	52.07 (46.17)	Susceptible	36.66 (37.25)	Susceptible
LC-C-11-21	31.25 (33.96)	Moderate resistant	18.70 (25.61)	Moderately susceptible
LC-C-12-21	16.66 (23.97)	Resistant	17.22 (24.50)	Moderately susceptible
LC-C-13-21	22.91 (28.57)	Moderate resistant	20.55 (26.92)	Moderately susceptible
LC-C-14-21	16.66 (30.42)	Resistant	27.70 (31.74)	Susceptible
LC-C-15-21	31.94 (34.39)	Moderate resistant	29.44 (32.69)	Susceptible
LC-C-16-21	25.69 (30.42)	Moderate resistant	35.55 (36.58)	Susceptible
Punjab Naveen	25.69 (30.42)	Moderate resistant	19.09 (25.87)	Moderately susceptible
Pant Khira	25.69 (30.38)	Moderate resistant	24.99 (29.92)	Moderately susceptible
K-75	26.39 (30.79)	Moderate resistant	23.33 (28.86)	Moderately susceptible
Solan Srijan	10.41 (18.76)	Resistant	6.78 (14.98)	Moderately resistant
Mean	**24.72**		**23.05**	
Range	**9.53-52.77**		**6.78-36.66**	
SE (m)	**1.34**		**1.32**	
C.V%	**7.96**		**8.07**	
C.D.(0.05)	**3.86**		**3.78**	

*values in the parenthesis are the angular transformed values.

Table 4.6 Disease reaction of downy mildew disease on genotypes of cucumber

Diseases reaction	Genotypes
Resistant (0-20%)	LC-C-4-21, LC-C-6-21, LC-C-7-21, LC-C-9-21, LC-C-12-21, LC-C-14-21, Solan Srijan
Moderately resistant (21-40%)	LC-C-1-21, LC-C-3-21, LC-C-5-21, LC-C-8-21, LC-C-11-21, LC-C-13-21, LC-C-15-21, LC-C-16-21, Punjab Naveen, Pant Khira, K-75
Susceptible (41-60%)	LC-C-2-21, LC-C-10-21
Highly susceptible (>60%)	

Table 4.7 Disease reaction of powdery mildew disease on genotypes of cucumber

Diseases reaction	Genotypes
Immune (0%)	
Resistant (0.1-5%)	
Moderately resistant (5.1-15%)	LC-C-9-21, Solan Srijan
Moderately susceptible (15.1-25%)	LC-C-1-21, LC-C-5-21, LC-C-6-21, LC-C-8-21, LC-C-11-21, LC-C-12-21, LC-C-13-21, Punjab Naveen, Pant Khira, K-75
Susceptible (25.1-50%)	LC-C-2-21, LC-C-3-21, LC-C-4-21, LC-C-7-21, LC-C-10-21, LC-C-14-21, LC-C-15-21, LC-C-16-21
Highly susceptible (>50%)	

4.2.1 Coefficient of variation:

The results recorded on magnitude of both genotypic as well as phenotypic variability. Estimation of genetic parameters of variation for yield and its attributes revealed a wide range of variation for studied characters (Table 4.8). The results showed that the phenotypic coefficient of variation was greater in magnitude than the genotypic coefficient of variation for all of the characters, indicating that there was noticeable variability in the genetic material used, which was not simply due to genotypic effect but also due to environmental effect. The wide difference in phenotypic and genotypic coefficients of variation indicated their sensitivity to environmental fluctuations, whereas the narrow difference indicated less environmental interference on the expression of these characters. Characters with high phenotypic and genotypic coefficients of variation have ample scope for improvement through selection. Narrow difference between PCV and GCV for a trait means the trait is less affected by the environment. The coefficient of variability varied in magnitude from character to character and the characters under study are categorized as low (<15 %), moderate (15-30 %), and high (>30 %) as worked out by Warshamana, 2005.

High magnitude of GCV and PCV were observed for PDI of downy mildew (45.92 and 47.92), number of fruits per plant (42.16 and 44.08), total yield per plot (39.87 and 40.29) and PDI of powdery mildew (33.18 and 36.22 respectively). High phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) were observed for node number of first female flower (33.59 and 28.32 respectively). These characters with high GCV and PCV can be improved effectively through selection. High PCV and GCV for number of fruits per plant have been reported by Ene *et al*. (2016) and Karthick *et al*. (2019). Pal *et al*. (2016) observed high GCV and PCV for PDI of downy mildew and powdery mildew. Pradhan *et al*. (2018) observed high PCV for PDI of downy mildew in cucumber. Veena *et al*. (2012) and Deepa *et al*. (2018) observed high PCV and GCV for total yield per plot.

Moderate magnitude of GCV and PCV were observed for the traits flesh to seed cavity ratio (29.30 and 29.40), harvest duration (22.44 and 26.17), ascorbic acid (21.53 and 21.89), total soluble solids (16.46 and 18.05) and fruit weight

(15.95 and 19.94 respectively). Moderate phenotypic coefficient of variation (PCV) with low genotypic coefficient of variation (GCV) was observed in fruit length (15.59 and 14.51 respectively). Kandasamy (2017), Kumari *et al*. (2017) reported moderate PCV for fruit length and fruit weight. Moderate PCV and GCV for total soluble solids have been reported by Chakraborty *et al*. (2019). Veena *et al*. (2012), Singh *et al*. (2017) and Karthick *et al*. (2019) reported moderate PCV and GCV for fruit weight in cucumber. Moderate GCV and PCV for harvest duration are similar to the findings of Pal *et al*. (2016). Deepa *et al*. (2018) reported moderate GCV and PCV for ascorbic acid.

Low magnitude of GCV and PCV was observed for days to first female flower (11.88 and 13.07), internodal length (11.55 and 13.58) and fruit breadth (5.91 and 7.02 respectively). Pradhan *et al*. (2018) reported low PCV and GCV for days to first female flower, fruit breadth and internodal length in cucumber. Low PCV and GCV for days to first female flower and for internodal length have also been reported by Yadav *et al*. (2021). Veena *et al*. (2012), Pushpalatha *et al*. (2016), Kumari *et al*. (2017) and Kumari *et al*. (2020) has also been reported low PCV and GCV for days to first female flower in cucumber.

4.2.2 Heritability:

Studies on genetic coefficient of variation aid in determining the range of genetic variability for a given character and comparing the variability found in different characters. Although, genetic variability alone cannot be used to determine heritable variation. Burton and De Vane (1953) suggested that GCV along with heritability gives a better idea about the efficiency of selection. Heritability is referred as the portion of phenotypic variation which is transmitted from parent to progeny. Also, it is very essential to have basic information about some necessary and beneficial parameter which might be helpful to increase the efficiency of breeding system. It also provides help to the breeder to select a particular genotype for particular trait efficiently. Selection is more effective for improvement of a trait with high heritability.

Heritability for the characters under study are categorized as high (>80%), moderate (50-80%) and low (<50%). In the present investigation, the range of heritability for various characters under study was observed from 63.99 to 99.31%

(Table 4.8). High heritability was recorded for the characters *viz*., flesh to seed cavity ratio (99.31%), total yield per plot (97.94%), ascorbic acid (96.74%), PDI of downy mildew (91.82%), number of fruits per plant (91.50%), fruit length (86.58%), PDI of powdery mildew (83.91%), total soluble solids (83.18%) and days to first female flower (82.72%). Moderate heritability recorded for harvest duration (73.57%), Internodal length (72.39%), node number of first female flower (71.09%), fruit breadth (70.91%) and fruit weight (63.99%). Characters having high heritability are less influenced by the prevailing environment whereas traits with moderate and low heritability have pronounced effect of environment on their expression. Selection is more effective for improvement for a trait with high heritability.

High heritability for days to first female flower, number of fruits per plant, flesh to seed cavity ratio, fruit length and total yield per plot has been reported by Bhagwat *et al*. (2018). Mishra *et al*. (2021) reported high heritability for ascorbic acid. High heritability for number of fruits per plant and moderate heritability for node number of first female flower recorded by Yadav *et al*. (2021). Pal *et al*. (2016) observed high heritability for PDI of downy mildew, PDI of powdery mildew, fruit length and moderate heritability for harvest duration. High heritability for total yield per plot, fruit length, number of fruits per plant and moderate heritability for internodal length has also been recorded by Kumari *et al*. (2017). Shah *et al*. (2018) observed high heritability for total soluble solids, number of fruits per plant and fruit length. Singh *et al*. (2017) recorded moderate heritability for fruit breadth and node number of first female flower. Veena *et al*. (2012) reported high heritability for fruit length, days to first female flower and moderate heritability for fruit weight.

4.2.3 Genetic advance (as % of mean):

The phenotypic superiority of selected plants over the original population is not solely due to their genotype superiority. It may be due to favourable environmental factors. So, heritability estimates alone are not reliable. Genetic advance in some cases gives good idea for actual position. Improvement in the mean genotypic value of selected plants over base population is known as genetic advance. Genetic gain is the genetic advance as percentage of mean. Genetic

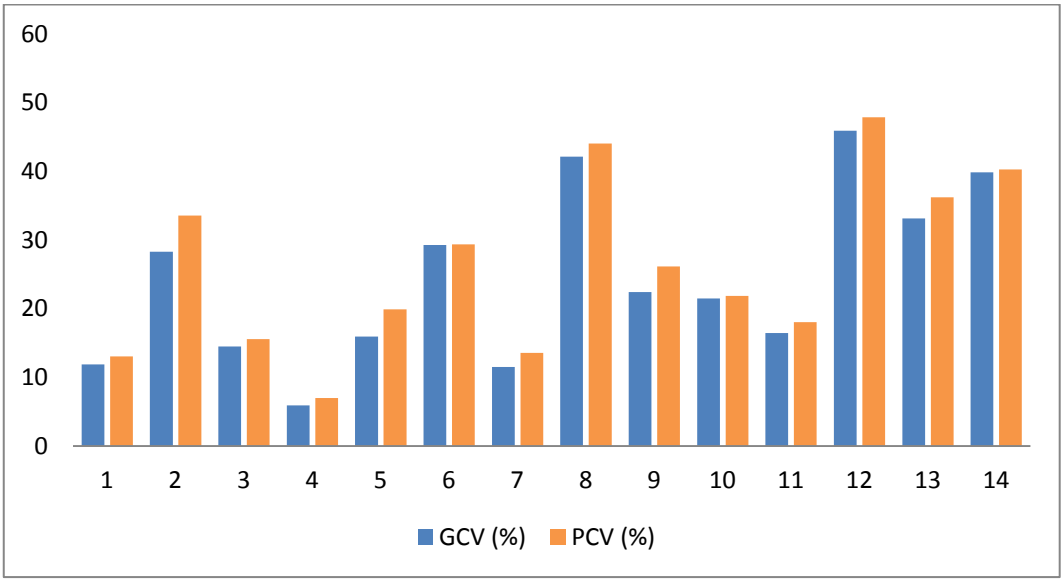
advance depends upon heritability of the character under selection, genetic variability of genotypes and intensity of selection. Johnson *et al*. (1955) suggested that characters with high heritability coupled with high genetic advance would response to selection better than those with high heritability with low genetic advance. High heritability along with high genetic advance shows that characters were governed mainly due to additive gene effect and therefore selection might be effective for improvement of these traits.

Genetic gain for the characters under study are categorized as high (>50%), moderate (25-50%) and low (<25%). Genetic advance was calculated as per cent mean for yield and its components which is presented in Table 4.8 and shown in Fig. 4.2. The highest genetic advance as per cent of mean (genetic gain) was recorded for PDI of downy mildew (90.64%), followed by number of fruits per plant (83.08%), total yield per plot (81.29%), PDI of powdery mildew (62.61%) and flesh to seed cavity ratio (60.15%). Pal *et al*. (2016) reported high genetic gain for PDI of downy mildew and PDI of powdery mildew. High genetic gain for flesh to seed cavity ratio has also been reported by Bhagwat *et al*. (2018). Afroz *et al*. (2012) who observed high genetic advance for number of fruits per plant and total yield per plot.

Moderate genetic gain calculated for node number of first female flower (49.19%), ascorbic acid (43.63%), harvest duration (39.66%), total soluble solids (30.92%), fruit length (27.80%) and fruit weight (26.29%). Mishra *et al*. (2021) reported moderate genetic advance for node number of first female flower and ascorbic acid. Moderate genetic gain for total soluble solids has also been observed by Chakraborty *et al*. (2019). Pal *et al*. (2016) reported moderate genetic advance for fruit length, fruit weight, total soluble solids and harvest duration.

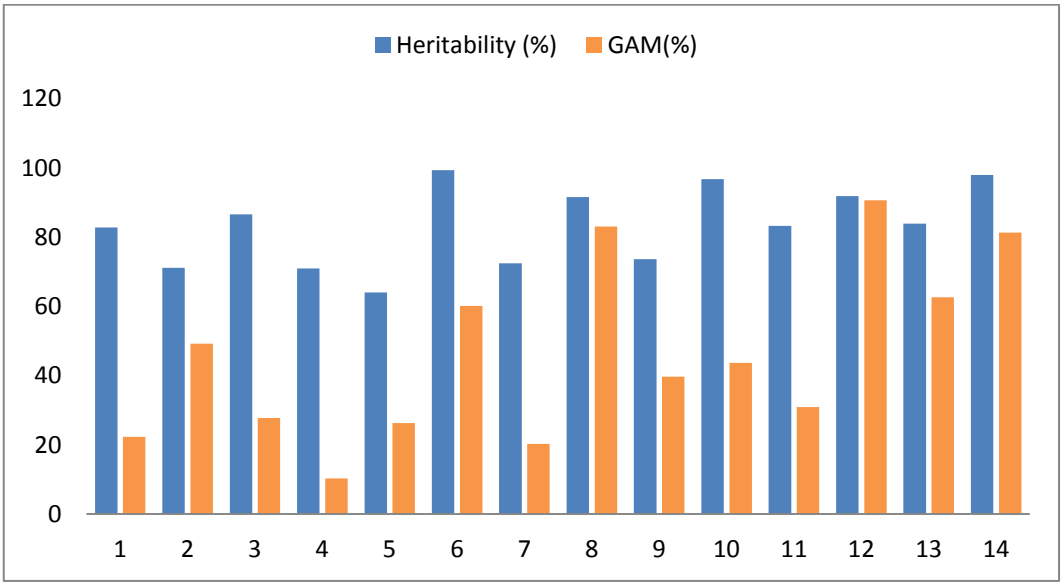
Low genetic advance as per cent of mean was reported for days to first female flower (22.27%), internodal length (20.25%) and fruit breadth (10.26%) which indicates the preponderance of non-additive gene action and improvement in these parameters by selection are not effective. Afroz *et al*. (2012) reported low genetic gain for fruit breadth. Low genetic gain for days to first female flower and fruit breadth has also been recorded by Kumari *et al*. (2017). Yadav *et al*. (2021) reported low genetic advance for internodal length.

Fig. 4.1 Genotypic and Phenotypic coefficient of variability for different traits in cucumber



Where, 1 = Days to first female flower, 2 = Node number of first female flower, 3 = Fruit length (cm), 4 = Fruit breadth (cm), 5 = Fruit weight (g), 6 = Flesh to seed cavity ratio, 7 = Internodal length (cm), 8 = Number of fruits per plant, 9 = Harvest duration (days), 10 = Ascorbic acid (mg/100g), 11 = TSS (^{o}B), 12 = PDI of downy mildew, 13 = PDI of powdery mildew, 14 = Total yield per plot (kg).

Fig. 4.2 Estimates of Heritability and genetic advances as percent of mean for different traits in cucumber



Where, 1 = Days to first female flower, 2 = Node number of first female flower, 3 = Fruit length (cm), 4 = Fruit breadth (cm), 5 = Fruit weight (g), 6 = Flesh to seed cavity ratio, 7 = Internodal length (cm), 8 = Number of fruits per plant, 9 = Harvest duration (days), 10 = Ascorbic acid (mg/100g), 11 = TSS (^{o}B), 12 = PDI of downy mildew, 13 = PDI of powdery mildew, 14 = Total yield per plot (kg).

Table 4.8 Estimation of range, phenotypic and genotypic coefficients of variation, heritability, and genetic advance as % of mean.

Sr. No.	Characters	Mean	Range		Coefficient of variation (%)		Heritability (%)	Genetic Advance as % of mean (%)
			Minimum	Maximum	Genotypic	Phenotypic		
1	Days to first female flower	59.08	47.66	76.66	11.88	13.07	82.72	22.27
2	Node number of first female flower	17.54	9.50	29.00	28.32	33.59	71.09	49.19
3	Fruit length (cm)	16.59	11.00	19.16	14.51	15.59	86.58	27.80
4	Fruit breadth (cm)	4.37	3.74	4.80	5.91	7.02	70.91	10.26
5	Fruit weight (g)	213.07	133.42	307.17	15.95	19.94	63.99	26.29
6	Flesh to seed cavity ratio	0.75	0.36	1.37	29.30	29.40	99.31	60.15
7	Internodal length (cm)	7.79	6.23	9.50	11.55	13.58	72.39	20.25
8	Number of fruits per plant	6.96	1.67	11.92	42.16	44.08	91.50	83.08
9	Harvest duration (days)	26.03	16.17	33.17	22.44	26.17	73.57	39.66
10	Ascorbic acid (mg/100g)	3.57	2.03	4.46	21.53	21.89	96.74	43.63
11	TSS (^{o}B)	3.08	2.12	4.02	16.46	18.05	83.18	30.92
12	PDI of downy mildew	24.72	9.53	52.77	45.92	47.92	91.82	90.64
13	PDI of Powdery mildew	23.05	6.78	36.66	33.18	36.22	83.91	62.61
14	Total yield per plot (kg)	11.50	2.97	19.00	39.87	40.29	97.94	81.29

4.3 Correlation Coefficient analysis:

Correlation is defined as the direction of association between two or more characters. The more directly a character is associated with yield, more will be the success of the selection programme. It gives an idea about relationship among the various characters and determines the component characters for which selection can be done for genetic improvement in the fruit yield. The effect of the component characters on yield can be studied by correlation analysis programme for bringing genetic improvement in the crop. Knowledge of association between traits serves important purpose for the breeder because all the phenotypic traits are the result of interplay of several genetic factors among themselves and their individual and combined interaction with the environmental factors.

The observed correlation coefficients among the different parameters were worked out at both phenotypic as well as genotypic levels. The magnitude and direction of association among characters would be measured by correlation coefficient. The characters that exhibited positive correlations, simultaneous improvement in two or more characters is possible. The negative correlation of some important characteristics may lead to some undesirable selection based on these characters. The negative correlations of these characters pairs tell us about problem in combining important yield components in one genotype.

In the present study, in general, trend revealed that genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients for all the characters, which indicating that environment played lesser role in governing the phenotype of the cucumber genotypes. The correlation coefficients between the characters at both phenotypic and genotypic levels were estimated and are presented in Table 4.9 and 4.10, respectively.

4.3.1 Phenotypic correlations:

Perusal of data from Table 4.9 expressed that total yield per plot showed positive and significant correlation with number of fruits per plant (0.902), fruit length (0.654), fruit breadth (0.622), harvest duration (0.572), internodal length (0.332) and fruit weight (0.272) while total yield per plot had negative and significant association with PDI of powdery mildew (-0.369), days to first female

flower (-0.515), node number of first female flower (-0.567) and PDI of downy mildew (-0.747). PDI of powdery mildew showed positive and significant association with PDI of downy mildew (0.462), days to first female flower (0.333), total soluble solids (0.332) and node number of first female flower (0.258) whereas it showed negatively significant association with fruit length (-0.277), harvest duration (-0.338) and number of fruits per plant (-0.435). PDI of downy mildew had positive and significant association with days to first female flower (0.516) and node number of first female flower (0.483) while negative and significant correlation was observed for internodal length (-0.295), fruit breadth (-0.430), harvest duration (-0.560), number of fruits per plant (-0.632) and fruit length (-0.682).

Total soluble solids exhibited positive and highly significant association with internodal length (0.374), days to first female flower (0.357) and fruit weight (0.312) while negative and significant correlation was obtained for flesh to seed cavity ratio (-0.263). Ascorbic acid was not associated significantly with any of trait under study. Positive and significant association of harvest duration was observed with number of fruits per plant (0.617), fruit breadth (0.427) and fruit length (0.274) while it was significantly and negatively associated with node number of first female flower (-0.735) and days to first female flower (-0.834). Number of fruits per plant had positive and significant association with fruit breadth (0.521) and fruit length (0.489) while it expressed negatively significant association with node number of first female flower (-0.549) and days to first female flower (-0.563). Internodal length was correlated significantly positive with fruit weight (0.637), fruit length (0.485) and fruit breadth (0.406). Positive and significant correlation of flesh to seed cavity ratio was reflected with node number of first female flower (0.362) while it had negative and significant association with fruit breadth (-0.347) and fruit weight (-0.378).

Positive and significant correlation was exhibited by fruit weight with fruit length (0.458) and fruit breadth (0.444). Fruit breadth had positive and significant association with fruit length (0.397) and negatively significant association with days to first female flower (-0.444) and node number of first female flower (-0.526). Node number of first female flower had positive and significant association with days to first female flower (0.807).

4.3.2 Genotypic correlations:

Genotypic correlations provide measures of genetic association between characters and are more reliable than phenotypic correlation and thus help to identify the characters to be utilized in breeding programme.

The data represented in Table 4.10 revealed that total yield per plot was positively and significantly correlated with number of fruits per plant (0.938), fruit breadth (0.738), fruit length (0.715), harvest duration (0.653), internodal length (0.403) and fruit weight (0.321) while PDI of powdery mildew (-0.411), days to first female flower (-0.584), node number of first female flower (-0.675) and PDI of downy mildew (-0.788) showed negative and significant correlation with total yield per plot. PDI of powdery mildew exhibited positive and significant association with PDI of downy mildew (0.536), days to first female flower (0.422), total soluble solids (0.357) and node number of first female flower (0.353) whereas it showed negative significant association with fruit length (-0.342), number of fruits per plant (-0.481) and harvest duration (-0.483). Positive and significant association of PDI of downy mildew was observed with node number of first female flower (0.659) and days to first female flower (0.604) while negative and significant correlation was obtained for fruit weight (-0.322), internodal length (-0.390), fruit breadth (-0.583), harvest duration (-0.683), number of fruits per plant (-0.688) and fruit length (-0.783).

Total soluble solids had positive and highly significant association with days to first female flower (0.476), internodal length (0.449), fruit weight (0.413) and node number of first female flower (0.361) whereas negative and significant association with flesh to seed cavity ratio (-0.295). Ascorbic acid was not associated significantly with any of trait under study. Positive and significant association of harvest duration with number of fruits per plant (0.693) and fruit breadth (0.489) whereas, flesh to seed cavity ratio (-0.256), days to first female flower (-0.927) and node number of first female flower (-0.966) showed negative and significant association. Number of fruits per plant had positive and significant association with fruit breadth (0.552) and fruit length (0.513), while it expressed negative association with days to first female flower (-0.624) and node number of first female flower (-0.694). Internodal length was correlated significantly positive

with fruit weight (0.937), fruit length (0.594) and fruit breadth (0.522) while negatively significant with flesh to seed cavity ratio (-0.278). Positive and significant correlation of flesh to seed cavity ratio was obtained with node number of first female flower (0.429) while it had negative and significant association with fruit breadth (-0.407) and fruit weight (-0.480).

Fruit weight revealed positive and significant association with fruit length (0.465) and fruit breadth (0.423). Positive and significant correlation was exhibited by fruit breadth with fruit length (0.434) while it was negatively and significantly correlated with days to first female flower (-0.493) and node number of first female flower (-0.650). Fruit length had negative and significant association with node number of first female flower (-0.282). Positive and significant association of node number of first female flower was observed with days to first female flower (0.921).

Corresponding to the results of present study, positive and significant correlation of fruit yield with fruit weight, fruit length, harvest duration, number of fruits per plant at both genotypic and phenotypic level has been reported by Pal *et al*. (2017). Sharma *et al*. (2018) revealed positive and significant association of total yield with number of fruits per plant, fruit weight and harvest duration. Similar results exhibiting significant positive association of fruit yield with number of fruits per plant, fruit breadth and fruit length has been reported by Shet *et al*. (2018). Dogra (1998) revealed positive and significant association of yield per plant with number of fruits per plant. Number of fruits per plant and fruit length expressed positive and highly significant association with total yield per plot in cucumber as reported by Afroz *et al*. (2012) and Bhaiya *et al*. (2020). Fruit yield showed positive and significant association with number of fruits per plant, fruit length, fruit breadth and fruit weight which has been similar to the finding of Kumar *et al*. (2018). Singh *et al*. (2017) recorded positive and significant correlation of total soluble solids with days to first female flower and internodal length. Number of fruits per plant showed positive and significant associated with fruit length and internodal length which has been similar to the findings of Nandi *et al*. (2019). Number of fruits per plant expressed positive and significant association with fruit length as reported by Manivannan *et al*. (2020) and Afroz *et al*. (2012).

Positive and significant correlation of internodal length with fruit length and fruit weight has been reported by Nandi *et al*. (2019). Deepa *et al*. (2018) recorded positive and significant correlation of internodal length with total yield per plot, fruit length, fruit breadth and fruit weight. Fruit weight showed positive and significant correlation with fruit breadth and fruit length which has been similar to the results obtained by Singh *et al*. (2017) and Deepa *et al*. (2018). Ahirwar *et al*. (2017) and Manisha *et al*. (2021) recorded positive and highly significant correlation of fruit weight with fruit length. Fruit breadth showed positive and significant correlation with fruit length which has been similar to the results obtained by Shet *et al*. (2018). Node number of first female flower observed positive and significantly correlated with days to first female flower which has been similar to the results obtained by Dogra (1998), Manivannan *et al*. (2020) and Bhaiya *et al*. (2020). Fruit yield showed positive and significant correlation with fruit length, fruit weight whereas, negative and significant association with node number of first female flower, PDI of downy mildew, PDI of powdery mildew, days to first female flower which has been similar to the findings of Pal *et al*. (2017).

4.4 Path coefficient analysis:

Path coefficient analysis is simply a standardized partial regression coefficient which splits the genotypic correlation coefficient into direct and indirect effects on yield. It is useful in finding out whether the association of characters with yield is due to their direct effects or is the consequences of their indirect effects via other component characters. In present investigation, total yield per plot has been used as dependable variable with other traits. Since the values of genotypic path correlation coefficient are more reliable in predicting the correct idea about the direct and indirect effect of the component traits. The estimates of path coefficient analysis at genotypic level are furnished in the Table 4.11 which depicts the direct and indirect effects of various horticultural traits on total yield per plot.

4.4.1 Days to first female flower:

Positive direct effect was observed on total yield per plot through days to first female flower (0.6215). High indirect effect was seen through PDI of downy mildew (0.0906) followed by internodal length (0.0851). Negative indirect effects were observed through ascorbic acid (-0.0049), flesh to seed cavity ratio (-0.0129), fruit length (-0.0169), fruit breadth (-0.0186), PDI of powdery mildew (-0.0453), fruit weight (-0.0933), total soluble solids (-0.1392), node number of first female flower (-0.2181), harvest duration (-0.3729) and number of fruits per plant (-0.4592). Similar finding are also reported by Veena *et al*. (2013), Bhaiya *et al*. (2020) and Ahirwar *et al*. (2017).

4.4.2 Node number of first female flower:

Negative direct effect was observed on total yield per plot (-0.2368). Positive indirect effects were seen via days to first female flower (0.5725), PDI of downy mildew (0.0989), internodal length (0.0151), ascorbic acid (0.0078), fruit weight (0.0028) and negative indirect effects were observed through fruit breadth (-0.0246), fruit length (-0.0279), PDI of powdery mildew (-0.0380), flesh to seed cavity ratio (-0.0394), total soluble solids (-0.1057), harvest duration (-0.3886) and number of fruits per plant (-0.5108) as similar to the findings of Veena *et al*. (2013), Bhaiya *et al*. (2020), Sharma *et al*. (2018), Kumar *et al*. (2011) and Ahirwar *et al*. (2017).

4.4.3 Fruit length (cm):

Positive direct effect of fruit length (0.0989) was observed on yield per plot. Positive indirect effects were seen through internodal length (0.4355), number of fruits per plant (0.3779), harvest duration (0.0970), node number of first female flower (0.0667), PDI of powdery mildew (0.0368), fruit breadth (0.0164), ascorbic acid (0.0045) and negative indirect effects was observed through flesh to seed cavity ratio (-0.0048), total soluble solids (-0.0069), days to first female flower (-0.1065), PDI of downy mildew (-0.1175) and fruit weight (-0.1834) as similar to those of Kumar *et al*. (2011), Veena *et al*. (2013), Manivannan *et al*. (2020) and Bhaiya *et al*. (2020).

4.4.4 Fruit breadth (cm):

Fruit breadth showed positive direct effect (0.0378) on yield per plot. Number of fruits per plant (0.4060), internodal length (0.3827), harvest duration (0.1965), node number of first female flower (0.1539), fruit length (0.0429), flesh to seed cavity ratio (0.0374), PDI of powdery mildew (0.0251), total soluble solids (0.0154), and ascorbic acid (0.0003) had positive indirect effect. Negative indirect effect was observed through PDI of downy mildew (-0.0874), fruit weight (-0.1669) and days to first female flower (-0.3061). Similar results are also reported by Hasan *et al*. (2015), Kumar *et al*. (2018), Sharma *et al*. (2018) and Nandi *et al*. (2019).

4.4.5 Fruit weight (g):

Fruit weight showed negative direct effect on yield per plot (-0.3945). Positive indirect effects were observed via internodal length (0.6863), days to first female flower (0.1471), fruit length (0.0460), flesh to seed cavity ratio (0.0441), fruit breadth (0.0160), ascorbic acid (0.0097), PDI of powdery mildew (0.0022), node number of first female flower (0.0017) and negative effects were observed through number of fruits per plant (-0.0173), PDI of downy mildew (-0.0483), harvest duration (-0.0512) and total soluble solids (-0.1210).

4.4.6 Flesh to seed cavity ratio:

Negative direct effect of flesh to seed cavity was recorded for yield per plot (-0.0919). Positive indirect effect was seen through fruit weight (0.1892), days to first female flower (0.0875), total soluble solids (0.0863), PDI of downy mildew (0.0293), ascorbic acid (0.0261) fruit length (0.0052) and negative indirect effect was observed through PDI of powdery mildew (-0.0070), fruit breadth (-0.0154), number of fruits per plant (-0.0896), node number of first female flower (-0.1016), harvest duration (-0.1029) and internodal length (-0.2038).

4.4.7 Internodal length (cm):

Internodal length showed positive direct effect on yield per plot (0.7326). Positive indirect effect was seen via days to first female flower (0.0722), number

of fruits per plant (0.0716), fruit length (0.0588), flesh to seed cavity ratio (0.0256), ascorbic acid (0.0211), fruit breadth (0.0198) and negative indirect effect was observed through node number of first female flower (-0.0049), harvest duration (-0.0149), PDI of powdery mildew (-0.0192), PDI of downy mildew (-0.0585), total soluble solids (-0.1316) and fruit weight (-0.3695) as similar to the finding of Nandi *et al*. (2019).

4.4.8 Number of fruits per plant:

Positive direct effect of number of fruits per plant was recorded for yield per plot (0.7361). Harvest duration (0.2787), node number of first female flower (0.1643), internodal length (0.0713), PDI of powdery mildew (0.0517), fruit length (0.0508), total soluble solids (0.0453), fruit breadth (0.0209), flesh to seed cavity ratio (0.0112), fruit weight (0.0093) showed indirect positive effect while ascorbic acid (-0.0110), PDI of downy mildew (-0.1033) and days to first female flower (-0.3877) showed negative indirect effect on total yield per plot. These results are in line with Rao *et al*. (2004), Afroz *et al*. (2012), Ying *et al*. (2004), Veena *et al*. (2013), Manivannan *et al*. (2020) and Pal *et al*. (2017).

4.4.9 Harvest duration:

Positive direct effect was observed through harvest duration on yield per plot (0.4022). Number of fruits per plant (0.5101), node number of first female flower (0.2288), total soluble solids (0.0576), PDI of powdery mildew (0.0519), fruit weight (0.0502), fruit length (0.0239), flesh to seed cavity ratio (0.0235), fruit breadth (0.0185) showed positive indirect effects on yield per plot. While negative indirect effect was recorded for ascorbic acid (-0.0079), internodal length (-0.0271), PDI of downy mildew (-0.1025) and days to first female flower (-0.5763). These results are in line with Pal *et al*. (2017), Kumar *et al*. (2011) and Sharma *et al*. (2018).

4.4.10 Ascorbic acid (mg/100g):

Ascorbic acid showed positive direct effect on yield per plot (0.1093). Positive indirect effect was shown by internodal length (0.1417), fruit length (0.0041), fruit breadth (0.0001) and negative indirect effect was observed through PDI of powdery mildew (-0.0007), node number of first female flower (-0.0169),

PDI of downy mildew (-0.0195), flesh to seed cavity ratio (-0.0220), days to first female flower (-0.0280), harvest duration (-0.0292), fruit weight (-0.0351), total soluble solids (-0.0652) and number of fruits per plant (-0.0740) on yield per plot as similar to those of Rajawat *et al*. (2022).

4.4.11 Total soluble solids (^{o}B):

Total soluble solids had negative direct effect on yield per plot (-0.2928). Positive indirect effect was seen through internodal length (0.03291), days to first female flower (0.2956), flesh to seed cavity ratio (0.0271), ascorbic acid (0.0243), PDI of downy mildew (0.0145), fruit length (0.0023) and negative indirect effect was showed through fruit breadth (-0.0020), PDI of powdery mildew (-0.0384), harvest duration (-0.0791), fruit length (-0.0855), number of fruits per plant (-0.1140) and fruit weight (-0.1630). Similar findings are reported by Pal *et al*. (2017) and Rajawat *et al*. (2022).

4.4.12 PDI of downy mildew:

PDI (Percent disease index) of downy mildew had positive and direct effect on yield per plot (0.1501). Days to first female flower (0.3754) and fruit weight (0.1271) showed positive indirect effects while negative indirect effect was observed through ascorbic acid (-0.0142), flesh to seed cavity ratio (-0.0180), fruit breadth (-0.0221), total soluble solids (-0.0284), PDI of powdery mildew (-0.0576), fruit length (-0.0775), node number of first female flower (-0.1561), harvest duration (-0.2747), internodal length (-0.2857), number of fruits per plant (-0.5065). Similar results are also reported by Kumar *et al*. (2011).

4.4.13 PDI of powdery mildew:

Negative direct effect of PDI of powdery mildew was recorded for fruit yield per plot (-0.1074). Positive indirect effect was seen through days to first female flower (0.2622), internodal length (0.1308), PDI of downy mildew (0.0805), fruit weight (0.0080) and ascorbic acid (0.0007).While negative indirect effect was observed through flesh to seed cavity ratio (-0.0060), fruit breadth (-0.0088), fruit length (-0.0339), node number of first female flower (-0.0837), total soluble solids (-0.1046), harvest duration (-0.1944) and number of fruits per plant (-0.3540).

Table 4.9 Estimates of phenotypic correlation coefficients of correlation among different characters in cucumber.

	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	Y14
Y1	**1**													
Y2	0.807**	**1**												
Y3	-0.196	-0.198	**1**											
Y4	-0.444**	-0.526**	0.397**	**1**										
Y5	0.101	-0.025	0.458**	0.444**	**1**									
Y6	0.132	0.362**	0.049	-0.347**	-0.378**	**1**								
Y7	0.029	-0.109	0.485**	0.406**	0.637**	-0.237	**1**							
Y8	-0.563**	-0.549**	0.489**	0.521**	0.022	-0.115	0.077	**1**						
Y9	-0.834**	-0.735**	0.274*	0.427**	0.035	-0.218	0.001	0.617**	**1**					
Y10	-0.012	0.082	0.043	-0.005	0.079	0.234	0.155	-0.109	-0.083	**1**				
Y11	0.357**	0.223	0.037	-0.032	0.312*	-0.263*	0.374**	-0.159	-0.180	0.203	**1**			
Y12	0.516**	0.483**	-0.682**	-0.430**	-0.226	0.184	-0.295*	-0.632**	-0.560**	-0.132	0.095	**1**		
Y13	0.333**	0.258*	-0.277*	-0.230	0.023	0.056	0.173	-0.435**	-0.338**	0.012	0.332**	0.462**	**1**	
Y 14	-0.515**	-0.567**	0.654**	0.622**	0.272*	-0.183	0.332**	0.902**	0.572**	-0.033	-0.081	-0.747**	-0.369**	**1**

*Significance at 5% level **Significance at 1% level

Where Y1 = Days to first female flower, Y2 = Node number of first female flower, Y3 = Fruit length (cm), Y4 = Fruit breadth (cm), Y5 = Fruit weight (g), Y6 = Flesh to seed cavity ratio, Y7 = Internodal length (cm), Y8 = Number of fruits per plant, Y9 = Harvest duration (days), Y10 = Ascorbic acid (mg/100g), Y11 = TSS (^{o}B), Y12 = PDI of downy mildew, Y13 = PDI of powdery mildew, Y14 = Total yield per plot (kg).

Table 4.10 Estimates of genotypic correlation coefficients of correlation among different characters in cucumber.

	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	Y14
Y1	**1**													
Y2	0.921**	**1**												
Y3	-0.171	-0.282*	**1**											
Y4	-0.493**	-0.650**	0.434**	**1**										
Y5	0.237	-0.007	0.465**	0.423**	**1**									
Y6	0.141	0.429**	0.052	-0.407**	-0.480**	**1**								
Y7	0.116	0.021	0.594**	0.522**	0.937**	-0.278*	**1**							
Y8	-0.624**	-0.694**	0.513**	0.552**	-0.023	-0.122	0.097	**1**						
Y9	-0.927**	-0.966**	0.241	0.489**	-0.127	-0.256*	-0.037	0.693**	**1**					
Y10	-0.045	0.072	0.041	0.003	0.089	0.239	0.193	-0.101	-0.073	**1**				
Y11	0.476**	0.361**	0.024	-0.053	0.413**	-0.295*	0.449**	-0.155	-0.197	0.223	**1**			
Y12	0.604**	0.659**	-0.783**	-0.583**	-0.322*	0.195	-0.390**	-0.688**	-0.683**	-0.130	0.097	**1**		
Y13	0.422**	0.353**	-0.342**	-0.233	-0.020	0.065	0.179	-0.481**	-0.483**	0.007	0.357**	0.536**	**1**	
Y 14	-0.584**	-0.675**	0.715**	0.738**	0.321*	-0.189	0.403**	0.938**	0.653**	-0.036	-0.082	-0.788**	-0.411**	**1**

*Significance at 5% level **Significance at 1% level

Where Y1 = Days to first female flower, Y2 = Node number of first female flower, Y3 = Fruit length (cm), Y4 = Fruit breadth (cm), Y5 = Fruit weight (g), Y6 = Flesh to seed cavity ratio, Y7 = Internodal length (cm), Y8 = Number of fruits per plant, Y9 = Harvest duration (days), Y10 = Ascorbic acid (mg/100g), Y11 = TSS (^{o}B), Y12 = PDI of downy mildew, Y13 = PDI of powdery mildew, Y14 = Total yield per plot (kg).

Table 4.11 Genotypic path coefficient analysis for direct and indirect effects of component characters on yield in cucumber.

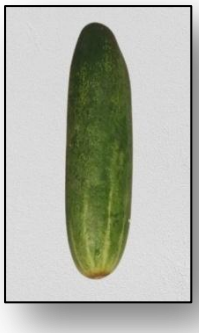
	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	GCCTYP
Y1	**0.6215**	-0.2181	-0.0169	-0.0186	-0.0933	-0.0129	0.0851	-0.4592	-0.3729	-0.0049	-0.1392	0.0906	-0.0453	-0.584**
Y2	0.5725	**-0.2368**	-0.0279	-0.0246	0.0028	-0.0394	0.0151	-0.5108	-0.3886	0.0078	-0.1057	0.0989	-0.0380	-0.675**
Y3	-0.1065	0.0667	**0.0989**	0.0164	-0.1834	-0.0048	0.4355	0.3779	0.0970	0.0045	-0.0069	-0.1175	0.0368	0.715**
Y4	-0.3061	0.1539	0.0429	**0.0378**	-0.1669	0.0374	0.3827	0.4060	0.1965	0.0003	0.0154	-0.0874	0.0251	0.738**
Y5	0.1471	0.0017	0.0460	0.0160	**-0.3945**	0.0441	0.6863	-0.0173	-0.0512	0.0097	-0.1210	-0.0483	0.0022	0.321*
Y6	0.0875	-0.1016	0.0052	-0.0154	0.1892	**-0.0919**	-0.2038	-0.0896	-0.1029	0.0261	0.0863	0.0293	-0.0070	-0.189
Y7	0.0722	-0.0049	0.0588	0.0198	-0.3695	0.0256	**0.7326**	0.0716	-0.0149	0.0211	-0.1316	-0.0585	-0.0192	0.403**
Y8	-0.3877	0.1643	0.0508	0.0209	0.0093	0.0112	0.0713	**0.7361**	0.2787	-0.0110	0.0453	-0.1033	0.0517	0.938**
Y9	-0.5763	0.2288	0.0239	0.0185	0.0502	0.0235	-0.0271	0.5101	**0.4022**	-0.0079	0.0576	-0.1025	0.0519	0.653**
Y10	-0.0280	-0.0169	0.0041	0.0001	-0.0351	-0.0220	0.1417	-0.0740	-0.0292	**0.1093**	-0.0652	-0.0195	-0.0007	-0.036
Y11	0.2956	-0.0855	0.0023	-0.0020	-0.1630	0.0271	0.3291	-0.1140	-0.0791	0.0243	**-0.2928**	0.0145	-0.0384	-0.082
Y12	0.3754	-0.1561	-0.0775	-0.0221	0.1271	-0.0180	-0.2857	-0.5065	-0.2747	-0.0142	-0.0284	**0.1501**	-0.0576	-0.788**
Y13	0.2622	-0.0837	-0.0339	-0.0088	0.0080	-0.0060	0.1308	-0.3540	-0.1944	0.0007	-0.1046	0.0805	**-0.1074**	-0.411**

Where, Y1 = Days to first female flower, Y2 = Node number of first female flower, Y3 = Fruit length (cm), Y4 = Fruit breadth (cm), Y5 = Fruit weight (g), Y6 = Flesh to seed cavity ratio, Y7 = Internodal length (cm), Y8 = Number of fruits per plant, Y9 = Harvest duration (days), Y10 = Ascorbic acid (mg/100g), Y11 = TSS (^{o}B), Y12 = PDI of downy mildew, Y13 = PDI of powdery mildew, Y14 = Total yield per plot (kg), GCCTYP = Genotypic correlation coefficient with total yield per plot.

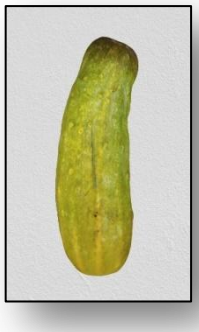
Residual effect 0.02021

Diagonal figures represent the direct effect.

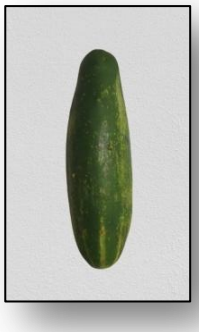
Plate 1: Genetic variability in cucumber genotypes



LC-C-1-21



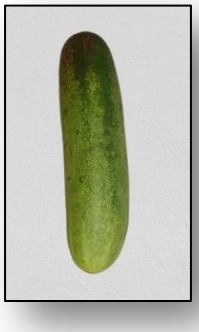
LC-C-2-21



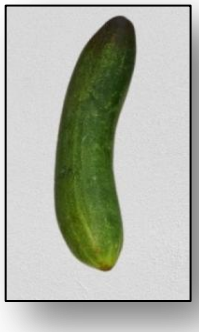
LC-C-3-21

LC-C-4-21

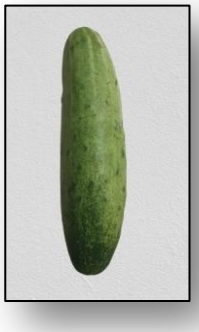
LC-C-5-21



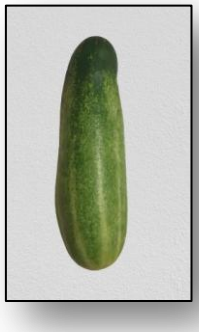
LC-C-6-21



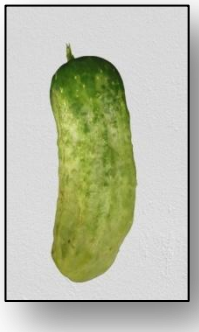
LC-C-7-21



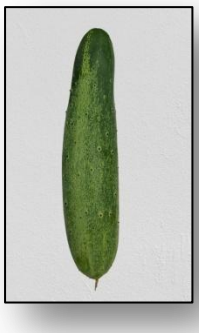
LC-C-8-21



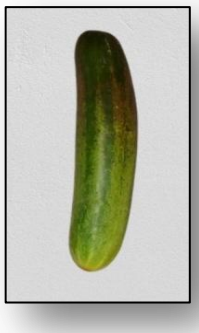
LC-C-9-21



LC-C-10-21

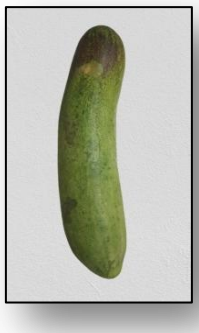


LC-C-11-21

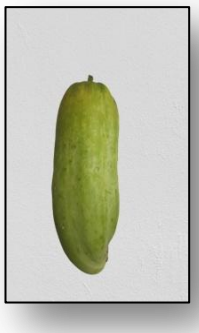


LC-C-12-21

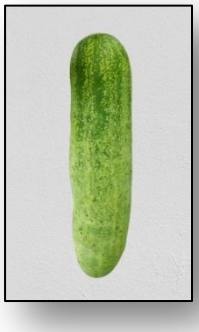
LC-C-13-21



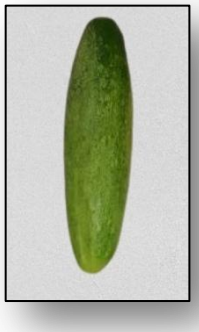
LC-C-14-21



LC-C-15-21

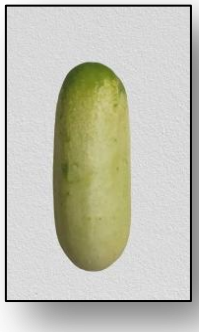


LC-C-16-21



Punjab Naveen

Pant Khira



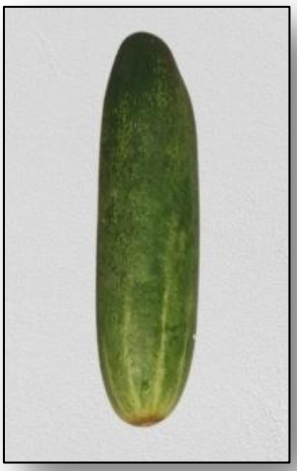
K-75

Solan Srijan

Plate 2: High yielding genotypes of cucumber

LC-C-4-21

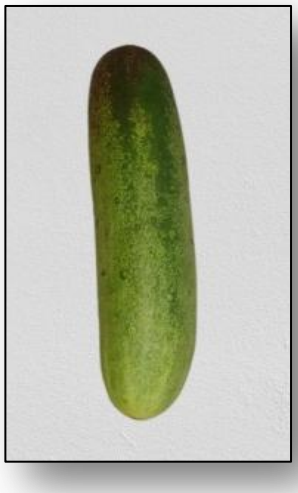
LC-C-14-21



LC-C-1-21

Plate 3: Genotypes rich in ascorbic acid with high TSS

Solan Srijan



LC-C-6-21

LC-C-13-21

Chapter – 5

SUMMARY AND CONCLUSIONS

The present investigation entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** was conducted from June 2021 to September 2021at the Experimental Farm of Department of Vegetable Science at College of Horticulture & Forestry, Neri, Hamirpur, HP. The experimental material consists of twenty genotypes of cucumber and was laid out in randomized complete block design with three replications. Observations were recorded on various characters *viz*., days to first female flower, node number of first female flower, fruit length, fruit breadth, fruit weight, flesh to seed cavity ratio, internodal length, number of fruits per plant, harvest duration, total soluble solids, ascorbic acid, prevalence of diseases and total yield per plot. Morphological characterization of genotypes was done on visual observations. The data was subjected to statistical analysis for variability parameters like mean, genotypic and phenotypic coefficient of variation, heritability, genetic advance as percentage of mean, correlation coefficient and path coefficient analysis.

The major findings of this study are as follows:

- Analysis of variance revealed highly significant differences among the genotypes for all the characters indicating the presence of variability.
- Based on the mean values with respect to characters, the genotype LC-C-4-21 recorded highest total yield per plot followed by LC-C-14-21 and LC-C-1-21. Genotype LC-C-16-21 was found promising for fruit length and LC-C-4-21 for fruit breadth. LC-C-13-21 was also found promising for showing maximum fruit weight and internodal length. LC-C-2-21 recorded maximum flesh to seed cavity ratio and LC-C-14-21 recorded maximum number of fruits per plant. LC-C-9-21 was also found promising for harvest duration and have minimum PDI of downy mildew which found statistically at par with Solan Srijan (standard check). Solan Srijan recorded minimum PDI of powdery mildew followed by LC-C-9-

21. Pant Khira and Punjab Naveen recorded minimum days to first female flower and node number of first female flower, respectively which was statistically at par with Solan Srijan. Solan Srijan and LC-C-6-21 had found promising for ascorbic acid and total soluble solids, respectively. Therefore, these genotypes can be used effectively for further breeding strategies after seeing their performance in other statistical genetic tools such as parameters of variability, correlation and path coefficient analysis.

- Phenotypic coefficient of variation was greater in magnitude than the genotypic coefficient of variation for all the characters, indicating the influence of environment in their expression. High magnitude of GCV and PCV were observed for PDI of downy mildew, number of fruits per plant, total yield per plot and PDI of powdery mildew, indicating wide range of variations and better scope for improvement through selection. Moderate magnitude of GCV and PCV was observed for flesh to seed cavity ratio, Harvest duration, ascorbic acid, total soluble solids and fruit weight. Thereby indicating the role of environmental factors for the expression.
- High heritability accompanied with high or moderate genetic advance as per cent of mean was recorded for the characters *viz*., flesh to seed cavity ratio, total yield per plot, ascorbic acid, PDI of downy mildew, number of fruits per plant, fruit length, PDI of powdery mildew and total soluble solids. This indicates that additive gene action plays an important role in governing these characters and can be improved through selection.
- Genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients for all the characters, which showed that environment played lesser role in governing the phenotype of the genotypes. Results indicated that total yield per plot was positively and significantly correlated with number of fruits per plant, fruit breadth, fruit length, harvest duration, internodal length and fruit weight while negatively significant association was observed with PDI of powdery mildew, days to first female flower, node number of first female and PDI of downy mildew. From the correlations studies, it is concluded that selection should be made on the basis of lowest node number bearing first female flower, early in appearance of first female flower, higher fruit length, breadth and fruit weight, more number of fruits per plant,

Table: 5.1. List of promising genotypes for different characters studied in cucumber (*Cucumis sativus* L.)

Characters	Genotypes	Mean
Days to first female flower	Pant Khira	47.66
	Punjab Naveen	50.33
	LC-C-1-21	51.83
Node number of first female flower	Punjab Naveen	9.50
	Solan Srijan	11.00
	Pant Khira	11.83
Fruit length (cm)	LC-C-16-21	19.16
	LC-C-14-21	19.15
	LC-C-7-21	19.08
Fruit breadth (cm)	LC-C-4-21	4.80
	Pant Khira	4.79
	LC-C-8-21	4.78
Fruit weight (g)	LC-C-13-21	307.17
	Pant Khira	263.61
	LC-C-16-21	239.00
Flesh to seed cavity ratio	LC-C-2-21	1.37
	LC-C-11-21	1.04
	LC-C-12-21	0.94
Internodal length (cm)	LC-C-13-21	9.50
	Pant Khira	9.30
	LC-C-14-21	8.97
Number of fruits per plant	LC-C-14-21	11.92
	LC-C-1-21	11.57
	LC-C-4-21	11.00
Harvest duration (days)	LC-C-9-21	33.17
	LC-C-3-21	33.00
	Solan Srijan	32.67
Ascorbic acid (mg/100g)	Solan Srijan	4.46
	LC-C-13-21	4.41
	LC-C-4-21	4.37
TSS (^{o}B)	LC-C-6-21	4.02
	LC-C-13-21	3.95
	LC-C-10-21	3.87
PDI of downy mildew	LC-C-9-21	9.53
	Solan Srijan	10.41
	LC-C-7-21	10.41
PDI of powdery mildew	Solan Srijan	6.78
	LC-C-9-21	7.52
	LC-C-8-21	17.22
Total yield per plot (kg)	LC-C-4-21	19.00
	LC-C-14-21	18.03
	LC-C-1-21	16.34

maximum internodal length, longer harvest duration with minimum susceptibility to different diseases can bring yield improvement in cucumber.

- Path coefficient analysis revealed that positive direct effects towards total yield per plot was recorded for days to first female flower, fruit length, fruit breadth, internodal length, number of fruits per plant, harvest duration, ascorbic acid and PDI of downy mildew. Negative direct effects on total yield per plot was recorded for node number of first female flower, fruit weight, flesh to seed cavity ratio, total soluble solids and PDI of powdery mildew. Thus, indicating the importance of selection for making improvement in yield.

CONCLUSIONS:

- ✓ On the basis of overall mean performance of the genotypes, LC-C-4-21, LC-C-14-21 and LC-C-1-21 were found superior for total yield per plot and other important horticultural traits. For quality parameters like ascorbic acid and total soluble solids Solan Srijan, LC-C-6-21 and LC-C-13-21 were found promising.

- ✓ Higher estimates of genotypic (GCV) and phenotypic coefficient of variation (PCV) were observed for PDI of downy mildew, number of fruits per plant, total yield per plot and PDI of powdery mildew.

- ✓ High heritability was observed for flesh to seed cavity ratio, total yield per plot, ascorbic acid, PDI of downy mildew, number of fruits per plant, fruit length, PDI of powdery mildew, total soluble solids and days to first female flower.

- ✓ The highest genetic advance as per cent of mean (genetic gain) was recorded for PDI of downy mildew, number of fruits per plant, total yield per plot, PDI of powdery mildew and flesh to seed cavity ratio.

- ✓ Positive and significant correlation of total yield per plot was observed with number of fruits per plant, fruit breadth, fruit length, harvest duration, internodal length and fruit weight.

- ✓ Path coefficient analysis revealed that positive direct effects towards total yield per plot were observed through days to first female flower, fruit length, fruit breadth, internodal length, number of fruits per plant, harvest duration, ascorbic acid and PDI of downy mildew.

LITERATURE CITED

Afroz S, Noman M S, Maleque M A, Hossain M S, Mamun A A and Ara S. 2012. Variability correlation and path coefficient analysis in cucumber (*Cucumis sativus* L.). *Bangladesh Journal of Agricultural Research* **37**:103-08.

Agashi A I, Okporie E O, Chukwu S C and Onyishi G C. 2020. Studies on genetic variability, heritability and genetic advances in cucumber (*Cucumis sativus* L.) cultivars collected from China and Nigeria. *International Journal of Science and Research* **9**:200-04.

Ahirwar C S, Singh D K and Kushwaha M L. 2017. Assessment of genetic divergence in cucumber (*Cucumis sativus* L.) germplasm through clustering and principle component analysis. *Journal of Pharmacognosy and Phytochemistry* **6**:804-07.

Al-Jibouri H A, Miller P A and Robinson H F. 1958. Genotypic and environment variance and covariance in upland cotton crosses of interspecific origin. *Agronomy Journal* **50**:633-37.

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

Anonymous. 2014. *Package of Practices for Vegetable Crops*. YSP University of Horticulture & Forestry, Solan. pp. 54-56.

Anonymous. 2021. http://164.100.60.210/crop-guidelines.htm (2:30 PM, 5th April 2022).

Anonymous. 2020a. http://www.fao.org/faostat/en#data (11:15 AM, 4th June 2022).

Anonymous. 2020b. http://nhb.gov.in/statistics/state_Level/2019-20(Final).pdf (11:50 AM, 4th June 2022).

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

AOAC. 1980. Official Methods of Analysis of the Association of Official Analytical Chemists (Ed. William Horewitz). Benjamin Franklin Station, Washington, D.C.

Bailey L H. 1969. *Manual of cultivated plants*. Macmillan Company, New York. 116p.

Bartaula S, Adhikari A, Panthi U, Karki P and Timalsena K. 2019. Genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.). *Journal of Agriculture and Natural Resources* **2**:215-22.

Bhagwat A, Srinivasa V, Bhammanakati S and Shubha A S. 2018. Evaluation of cucumber (*Cucumis sativus* L.) genotype under hill zone of Karnataka, India. *International Journal of Current Microbiology and Applied Science* **7**:837-42.

Bhaiya R, Singh V B, Yadav G C, Kumar Y and Tiwari D. 2020. Character association and path coefficient analysis of growth, yield and its contributing traits in cucumber (*Cucumis sativus* L.*). International Journal of Chemical Studies* **8**:431-33.

Burton G M and De Vane E H. 1953. Estimating heritability in tall fescue (*Festuca arundineacea*) from replicated clonal material. *Agronomy Journal* **45**:478-81.

Chakraborty D, Kumar M, Wangchu L, Singh S and Pandey A K. 2019. Genetic diversity among landraces of cucumber (*Cucumis sativus* L.) from NorthEast India. *Bangladesh Journal of Botany* **48**:481-88.

Das S, Maurya K R and Choudhary D N. 2003. Heritability studies in cucumber. *Journal of Applied Biology* **13**:54-57.

Deepa S K, Hadimani H P, Hanchinamani C N, Shet R, Koulgi S and Ashok. 2018. Estimation of genetic variability in cucumber (*Cucumis sativus* L.). *International Journal of Chemical* Studies **6**:115-18.

Deepa S K, Hadimani H P, Hanchinamani C N, Shet R, Kougli S and Ashok. 2018. Studies on character association in cucumber (*Cucumis sativus* L.).

International Journal of Current Microbiology and Applied Sciences **7**:1977-82.

Dewey D R and Lu K H. 1959. A correlation and path analysis of components of crested wheatgrass seed production. *Agronomy Journal* **51**:515-18.

Dogra B S. 1998. Studies on heterosis and inheritance of resistance to fruit fly in cucumber (*Cucumis sativus* L.). Ph.D. Thesis. Deparment of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni Solan. 80p.

Ene C O, Ogbonna P E, Agbo C U and Chukwudi U P. 2016. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean Journal of Agricultural Research* **76**:307-13.

Esquinas-Alcazar J T and Gulick P J. 1983. *Genetic resources of Cucurbitaceae; a global report*. IBPGR Secretariat, Rome, Italy. 112p.

Gaikwad A G, Musmade A M, Dhumal S S and Sonawane H G. 2011. Variability studies in cucumber (*Cucumis sativus* L.). *Ecology, Environment and Conservation* **17**:799-02.

Gangadhara K, Kumar R, Selvakumar R, Apparao V V and Yadav L P. 2019. Evaluation of cucumber hybrids/lines for yield and quality under polyhouse. *International Journal of Current Microbiology and Applied Sciences* **8**:1652-61.

Golabadi M, Golkar P and Eghtedary A R. 2012. Assessment of genetic variation in cucumber (*Cucumis sativus* L.) genotypes. *European Journal of Experimental Biology* **2**:1382-88.

Gomez K A and Gomez A A. 1984. *Statistical Procedures for Agricultural Research*. 2nded. John Wiley & Sons Inc, New York. 427p.

Hanchinamani C N and Patil M G. 2008. Path coefficient analysis in cucumber (*Cucumis sativus* L.). *Crop Research Hisar* **36**:270-72.

Hanchinamani C N and Patil M G. 2009. Correlation studies in cucumber (*Cucumis sativus* L.). *The Asian Journal of Horticulture* **4**:121-25.

Harland S C. 1939. *The genetics of cotton*. Janathan Cape, London.

Hasan R, Hossain M K, Alam N, Bashar A, Islam S and Tarafder M J A. 2015. Genetic divergence in commercial cucumber (*Cucumis sativus* L.) genotypes. *Bangldesh Journal of Botany* **44**:201-07.

Hossain M F, Rabbani M G, Hakim M A, Amanullah A S M and Ahsanullah A S M. 2010. Study on variability and character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh Research Publications Journal* **4**:423-28.

Jat R K. Ameta K D and Choudhary R C. 2014. Genetic variability, heritability and genetic advance for yield and yield attributing traits in valan kakri (*Cucumis sativus* var. *ultilismus* L.) *The Ecoscan* **6**:317-22.

Johnson H W, Robinson H F and Comstock R E. 1955. Estimates of genetic and environmental variability in soybeans. *Journal of Agronomy* **47**:314-18.

Kandasamy R. 2017. Variability studies in cucumber (*Cucumis sativus* L.). *The Asian Journal of Horticulture* **12**:84-87.

Kanwar M S and Rana M. 2006. Genetic divergence and gene source studies in cucumber (*Cucumis sativus* L.). *Indian Journal of Plant Genetic Resources* **19**:221-25.

Kanwar M S, Korla B N and Kumar S. 2003. Evaluation of cucumber genotypes for yield and qualitative traits. *Himachal Journal of Agriculture Research* **29**:43-47.

Karthick K, Arumugam T, Rajasree V, Ganesan K N and Karthikeyan M. 2019. Evaluation and assessment of genetic variability of cucumber (*Cucumis sativus* L.). *The Pharma Innovation* **8**:156-60.

Keshari D, Singh B, Singh R, Singh M K, Gangwar L K, Vaishali and Alam K. 2020. Studies on genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies* **8**:641-43.

Kumar A, Kumar S and Pal A K. 2008. Genetic variability and characters association for fruit yield and yield traits in cucumber. *Indian Journal of Horticulture* **65**:423-28.

Kumar P J, Syed S, Reddy S S, Lakshmi M L and Reddy S D. 2018. Studies on correlation and path coefficient analysis for yield and its contributing characters in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies* **6**:1649-53.

Kumar S, Kumar D, Kumar R, Thakur R S and Dogra B S. 2013. Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus*) in North-Western Himalayas. *Universal Journal of Plant Science* **2**:27-36.

Kumar S, Kumar R, Gupta R K and Sephia R. 2011. Studies on correlation and path coefficient analysis for yield and its contributing traits in cucumber. *Crop Improvement* **38**:18-23.

Kumari A, Kumar M and Kohli U K. 2008. Genetic parameters and character association in garden pea (*Pisum sativum* L.) cultivars. *Vegetable Science* **35**:160-64.

Kumari A, Singh A K, Moharana D P, Kumar A and Chandel S S. 2017. Estimation of various genetic parameters among promising genotypes of cucumber for yield and yield attributing traits. *International Journal of Pure Applied Bioscience* **5**:585-89.

Kumari A, Singh A K, Moharana D P, Kumar A and Kumar N. 2018. Character relationship and path coefficient analysis for yield and yield components in diverse genotypes of cucumber. *The Pharma Innovation Journal* **7**:33-38.

Kumari M, Ram C N, Nath S, Maurya N and Kumar S. 2020. Studies on genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry* **9**:481-84.

Liang G H and Walter T L. 1968. Heritability estimates and gene effects for agronomic traits in grain sorghum, sorghum vulgate pers. *Crop Science* **8**:77-81.

Manisha, Singh A K and Pal A K. 2021. Studies on correlation and path-coefficient analysis for yield and its contributing characters in cucumber. *The Pharma Innovation Journal* **10**:551-56.

Manivannan M I, Arulmozhiyan R and Suresh R. 2020. Genetic analysis for quantitative traits in cucumber (*Cucumis sativus* L.). *International Journal of Current Microbiology and Applied Sciences* **9**:1547-52.

McKinney H H. 1923. A new system of grading plant diseases. *Journal of Agricultural Research* **26**:195-18.

Mishra S K, Roy S, Kumar N and Prasad V M. 2021. Genetic evaluation of cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry* **10**:2872-74.

Nandi S, Thapa M, Banerjee S and Mondal R. 2019. Character association and path analysis for fruit yield and it's contributing traits in cucumber genotypes (*Cucumis sativus* L.) under naturally ventilated polyhouse during off season. *Journal of Pharmacognosy and Phytochemistry* **8**:2439-42.

Pal S, Sharma H R, Das A and Pandav A K. 2017. Character association and path analysis for fruit yield and it's contributing traits in cucumber (*Cucumis sativus* L.). *Genetics and Plant* Breeding **10**:163-70.

Pal S, Sharma H R, Rai A K and Bhardwaj R K. 2016. Genetic variability, heritability and genetic gain for yield and quality traits in cucumber (*Cucumis sativus* L.). *The Bioscan* **11**:1985-90.

Pradhan S R, Dharmatti P R, Sahu G S and Sahoo S. 2018. Study of magnitude of genetic variability for yield and yield attributing traits among local cucumber genotypes. *Journal of Pharmacognosy and Phytochemistry* **7**:1315-18.

Pushpalatha N, Anjanappa M, Devappa V and Pitchaimuthu M. 2016. Genetic variability and heritability for growth and yield in cucumber (*Cucumis sativus* L.). *Journal of Horticultural Sciences* **11**:33-36.

Rajawat K S and Collis J P. 2017. Genetic variability, heritability and genetic

advances analysis for quantitative and qualitative traits in cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry* **6**:882-85.

Rajawat K S, Shaktawat S K, Jat S L and Tak J K. 2022. Path analysis and character association of cucumber (*Cucumis sativus* L.). *The Pharma Innovation Journal* **11**:1512-16.

Ram.H.H. 2012. *Vegetable Breeding Principles and Practices.* 3rded. Kalyani Publishers, New Delhi. 791p.

Rao E S, Munshi A D and Verma V K. 2004. Genetic association and interrelationship of yield and its components in cucumber (*Cucumis sativus* L.). *Indian Journal of Horticulture* **61**:315-18.

Rastogi K B. 1998. Cucumber hybrid production. In: *Breeding and Seed Production of Vegetable Crops by Centre of Advanced Studies in Horticulture (Vegetable Science).* Department of Vegetable Science, UHF, Nauni, Solan. pp.76-80.

Reddy N S. 2002. Biochemical mechanism of downy mildew resistance in muskmelon (*Cucumis melo* L.) caused by *Pseudoperonospora cubensis* (Berk and Curt) Rostow. Ph.D. Thesis. University of Agricultural Sciences, Bangalore. 96p.

Robinson H F, Comstock R E and Harvey P H. 1951. Genotypic and phenotypic correlation in corn and their implication in selection. *Agronomy Journal* **43**:282-87.

Sahoo T R and Singh D K. 2020. Estimation of genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.) for yield and its components under protected structure. *International Journal of Current Microbiology and Applied Sciences* **9**:2756-64.

Schieberle P, Ofner S and Grosch W. 1990. Evaluation of potent odorants in cucumbers (*Cucumis sativus* L.) and Muskmelon (*Cucumis melo*) by aroma extract dilution analysis. *Journal of Food Science* **55**:193-95.

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

Shah K N, Rana D K and Singh V. 2018. Evaluation of genetic variability, heritability and genetic advance in cucumber for various quantitative and seed characters. *International Journal of Current Microbiology and Applied Sciences* **7:**3296-03.

Sharma S, Kumar R and Sharma H R. 2017. Studies on variability, heritability and genetic gain in Cucumber (*Cucumis sativus* L.). *Indian Journal of Ecology* **44**:829-33.

Sharma S, Kumar R, Chatterjee S and Sharma H R. 2018. Correlation and path analysis studies for yield and its attributes in cucumber. *International Journal of Chemical Studies* **6**:2045-48.

Shet R M, Shantappa T, Ashok and Gurumurthy S B. 2018. Genetic variability and correlation studies for productivity traits in cucumber. *International Journal of Chemical Studies* **6**:236-38.

Shukla I N, Shunder S, Singh D K, Singh N, Pandey R and Awasti P N. 2010. Genetic variability and selection parameters for fruit yield in cucumber. *Current Advances in Agricultural Sciences* **2**:107-08.

Simmonds N M. 1962. Variability in crop plants, its use and conservation. *Botanical Review* **37**:422-65.

Singh S K, Singh A and Gangwar L K. 2011. Variability and heritability studies in cucumber. *Progressive Agriculture* **11**:166-67.

Singh Y, Safiullah, Verma A, Sharma S and Sekhon B S. 2017. Genetic evaluation of cucumber (*Cucumis sativus* L.) genotypes for yield and its contributing traits under mid hill conditions of Himachal Pradesh, India. *Environment and Ecology* **35**:3621-26.

Tamang B, Bhutia K D, Kumar R, Sharma L and Bamaniya B S. 2018. Genetic variation and character association study in local cucumber genotypes of Sikkim. *Current Journal of Applied Science and Technology* **31**:1-9.

Tatlioglu T. 1993. Cucumber (*Cucumis sativus* L.). In: *Genetic Improvement of Vegetable Crops* (G. Kallo and B.O. Bergh eds.). Pergamo Press Ltd; Tarrytown New York. pp.197-33.

Thind T S, Singh P P, Sokhi S S and Grewal R K. 1991. Application timing and choice of fungicides for control of downy mildew of muskmelon. *Plant Disease Research* **6**:49-53.

Ullah M Z, Hasan M J, Chowdhury A Z M K A, Saki A I and Rahman A H M A. 2012. Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. *Bangladesh Journal of Plant Breeding and Genetics* **25**:17-23.

Veena R, Sidhu A S, Pitchaimuthu M and Souravi K. 2012. Genetic evaluation of cucumber (*Cucumis sativus* L.) genotypes for some yield and related traits. *Electronic Journal of Plant Breeding* **3**:945-48.

Veena R, Sidhu A S, Pitchaimuthu M and Souravi K. 2013. Character association for fruit yield and yield traits in cucumber (*Cucumis sativus* L.). *Electronic Journal of Plant Breeding* **4**:1108-12.

Warshamana I K. 2005. Genetic parameters study for yield and quality traits in tomato. *International Journal of Chemical Studies* **3**:722-25.

Wright S. 1921. Correlation and causation. *Journal of Agricultural Research* **20**:557-85.

Yadav S, Singh D K, Singh S S, Bisht Y S and Bhatt R. 2021. Assessment of genetic variability in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies* **9**:3347-49.

Yadav Y C, Kumar S and Singh R. 2010. Correlation coefficient and path analysis in cucumber (*Cucumis sativus* L.). *Progressive Horticulture* **42**:71-75.

Yawalker K S. 1985. *Vegetable Crops of India*. Agri-Horticultural Publishing House, Nagpur. 300p.

Ying Q Z, Cai R, He H L and Pan J S. 2004. Study on genetic correlation and path

analysis of the main agronomic characters of gynoecious parthenocarpic cucumber. *Journal of Shanghai Jiaotong University Agricultural Science* **20**:133-36.

APPENDIX-I

Mean metrological data during the study period (2021-22)

Month	TEMPERATURE		RELATIVE HUMIDITY (%)	RAINFALL (mm)
	MAX	MIN		
June	38.35	26.49	43.43	3.94
July	35.87	27.00	62.49	12.95
August	32.35	25.14	75.67	6.23
September	30.45	23.56	78.75	7.33

Source: Meteorological Observatory, Department of Soil Science and Water Management, College of Horticulture and Forestry, Neri, Hamirpur HP 177001

APPENDIX-II

Analysis of variance (ANOVA) for various horticultural traits in cucumber

Source	Mean sum of squares		
Character	**Replications**	**Genotype**	**Errors**
Df	**2**	**19**	**38**
Days to first female flower	31.204	158.206	10.296
Node number of first female flower	6.429	84.078	10.034
Fruit length (cm)	1.491	18.277	0.898
Fruit breadth (cm)	0.036	0.228	0.027
Fruit weight (g)	50.259	4,116.437	650.244
Flesh to seed cavity ratio	0.001	0.146	0.001
Internodal length (cm)	0.364	2.741	0.309
Number of fruits per plant	5.817	56.122	2.922
Harvest duration (days)	39.117	114.689	12.266
Ascorbic acid (mg/100g)	0.060	1.791	0.020
TSS (^{o}B)	0.030	0.825	0.052
PDI of downy mildew	3.479	398.114	11.478
PDI of powdery mildew	9.262	186.717	11.221
Total yield per plot (Kg)	1.750	63.560	0.443

Department of Vegetable Science
College of Horticulture and Forestry, Neri
Dr Yashwant Singh Parmar University of Horticulture and Forestry
Nauni, Solan (HP) - 173 230 India

Title of the thesis	**Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh.**
Name of the Student	Riya Rani
Admission Number	NH-2020-32-M
Major Discipline	Vegetable Science
Minor Discipline	a) Genetics and Plant Breeding b) Plant Pathology
Date of Thesis Submission	
Total pages of the Thesis	91+ii
Number of words in abstract	307
Major Advisor	Dr. B.S Dogra

Abstract

The present investigation entitled **"Genetic variability studies in cucumber (*Cucumis sativus* L.) under low hill region of Himachal Pradesh"** was conducted during rainy season, 2021 at the Experimental Farm of Department of Vegetable Science, College of Horticulture & Forestry, Neri, Hamirpur, HP. Twenty genotypes of cucumber comprising of local genotypes including standard check Solan Srijan were evaluated in Randomized Complete Block Design with three replications to assess the nature and the extent of various genetic variability parameters and the association among the traits for yield and its component characters. Analysis of variance showed highly significant differences among all genotypes for all the characters. On the basis of overall mean performance of the genotypes, LC-C-4-21, LC-C-14-21 and LC-C-1-21 were found superior for total yield per plot and other important horticultural traits. They could be the promising parents for utilization in further breeding programmes. Higher estimates of genotypic (GCV) and phenotypic coefficient of variation (PCV) were observed for PDI of downy mildew followed by number of fruits per plant, total yield per plot and PDI of powdery mildew. High heritability accompanied with high or moderate genetic advance as per cent of mean was recorded for flesh to seed cavity ratio, total yield per plot, ascorbic acid, PDI of downy mildew, number of fruits per plant, fruit length, PDI of powdery mildew and total soluble solids. The correlation studies revealed that total yield per plot had positive and significant correlation with number of fruits per plant, fruit breadth, fruit length, harvest duration, internodal length and fruit weight. Further, path coefficient analysis revealed that positive direct effects towards total yield per plot was recorded for days to first female flower followed by fruit length, fruit breadth, internodal length, number of fruits per plant, harvest duration, ascorbic acid and PDI of downy mildew. Thus, indicating the importance of selection for yield improvement.

Signature of the Student
Name: Riya Rani
Date:

Signature of the Major Advisor
Name: Dr. B.S Dogra
Date:

Countersigned
Professor and Head
Department of Vegetable Science
College of Horticulture and Forestry, Neri, Hamirpur

BRIEF BIO- DATA

Name	**:**	Riya Rani
Father's Name	**:**	Shri. Ajay Kumar
Mother's Name	**:**	Smt. Reena Rani
Date of Birth	**:**	05-02-2000
Permanent Address	**:**	Village-Darbelli, P.O.-Jhaniari, Tehsil and District-Hamirpur, H.P – 177001
E-mail	**:**	riyakanungo99@gmail.com
Sex	**:**	Female
Marital Status	**:**	Unmarried
Nationality	**:**	Indian
Educational Qualification	**:**	

Certificate/ degree	Year	Board/University	Marks (%)	Class/grade
10^{th}	2014	H.P.B.O.S.E. Dharamshala	91.1	First
12^{th}	2016	H.P.B.O.S.E Dharamshala	93.2	First
Graduation	2020	DR. Y.S Parmar University of Horticulture and Forestry, Nauni, Solan (H.P)	86.0	First

Whether sponsored by some state/ Central Govt./ Univ./SAARC : NA

Scholarship/ Stipend/ Fellowship, any other Scholarship financial assistance received during the study period : University Scholarship

Dated: **(Riya Rani)**