

ASSESSMENT OF GENETIC VARIABILITY AND DIVERGENCE (D^2) AMONG DIFFERENT CHARACTERS IN BRINJAL (*SOLANUM MELONGENA* L.) GENOTYPES

काशी हिन्दू
विश्वविद्यालय



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UNIVERSITY

THESIS SUBMITTED IN PARTIAL FULFILMENT OF THE
REQUIREMENTS FOR THE AWARD OF DEGREE OF

Master of Science (Agriculture)
in
Horticulture

Supervisor

Prof. Anand Kumar Singh

Submitted by

Monica Sailesh

DEPARTMENT OF HORTICULTURE
INSTITUTE OF AGRICULTURAL SCIENCES
BANARAS HINDU UNIVERSITY
VARANASI 221005
INDIA

I.D. No. 20412HOR010

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Enrolment No. 433629

Dedicated to

*Lord Kashi Vishwanath,
My Beloved Parents*

*&
Advisor*





DEPARTMENT OF HORTICULTURE
INSTITUTE OF AGRICULTURAL SCIENCES
BANARAS HINDU UNIVERSITY
VARANASI – 221005
INDIA



Prof. Anand Kumar Singh
Professor

Department of Horticulture
Institute of Agricultural Sciences

Ref. No.:

Date:

CERTIFICATE

To
The Registrar (Academic)
Banaras Hindu University
Varanasi – 221 005

Through: The Head, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, 221005

Dear Sir,

I have great pleasure in forwarding the thesis entitled “**Assessment of genetic variability and divergence (D^2) among different characters in brinjal (*Solanum melongena* L.) genotypes**” submitted by **Ms. MONICA SAILESH, I.D. No. 20412HOR010, Enrollment Number 433629**, in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in **Horticulture**, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi and placing on record that she has completed the requisite residential requirements as contained in the statute of the University.

I certify that the entire scheme of investigation presented herein was planned and carried out solely by the candidate under my guidance and supervision. The data presented in the thesis, to the best of my knowledge and belief, are genuine and original.

Thanking you.

Forwarded by

Yours faithfully,

Head of Department

(Prof. Anand Kumar Singh)
Supervisor/Advisor



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APPROVED BY MEMBERS OF ADVISORY COMMITTEE

Chairman	Prof. Anand Kumar Singh Professor Department of Horticulture Institute of Agricultural Sciences, BHU, Varanasi
Member	Prof. Binod Kumar Singh Professor Department of Horticulture Institute of Agricultural Sciences, BHU, Varanasi
Member	Dr. Pravin Prakash Professor Department of Plant Physiology Institute of Agricultural Sciences, BHU, Varanasi
External Examiner	

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Date:

Place: Varanasi

(Monica Sailesh)

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LIST OF SYMBOLS AND ABBREVIATIONS

<i>et al.</i>	:	Co workers
%	:	Per cent
Viz.,	:	Namely
/	:	Per
°C	:	Degree Celsius
RBD	:	Randomized Block Design
g	:	gram
CD	:	Critical Difference
SE	:	Standard error
CV	:	Coefficient of variance
kg	:	Kilogram
cm	:	Centimetre
mg	:	Milligram
q/ha	:	Quintal per hectare
q	:	Quintal
etc.	:	Et. cetera
no.	:	Number
F ₁	:	First filial generation
F ₂	:	Second filial generation
h ²	:	Heritability
Vit.	:	Vitamin
&	:	And
mm	:	Millimetre
SE.m	:	Standard error of mean
SI.No.	:	Serial number
mg	:	Milligram
Mor.	:	Morning
Eve.	:	Evening
PCV	:	Phenotypic coefficient of variation
GCV	:	Genotypic coefficient of variation

INTRODUCTION

Vegetables are an essential element of our daily nutrition and the market is brimming with them. Between 2000 and 2019, global vegetable output increased by 65 percent, or 446 million tonnes, to 1128 million tonnes. Tomatoes (16%), onions (9%), cucumbers & gherkins (8%), cabbages (6%) and eggplants (5%) accounted for 42–45 percent of the total over the era. Onions, cucumbers, gherkins and eggplants also gained in popularity (FAO, 2021). With the increased focus on the vegetable sector, there has been a dramatic increase in vegetable yield and availability. India was rated second in the world for vegetable production, contributing 15.8% and 14% of worldwide vegetable acreage and production, respectively. Vegetable production accounts for 60.32% of overall horticulture production in India.

Vegetables are rich in minerals and vitamins and therefore good for health. In our bodies, they help to prevent cancer, diabetes and heart disease. Almost every vegetable is low in fat and calories, cholesterol-free and high in fibre. Vegetables are high in fibre, which maintains our digestive system healthy and prevents constipation. We can eat a lot of veggies without burning out since they are low in calories. Vitamin A (carrot, drumstick, leafy vegetables, tomato), Vitamin B (peas, chillies, fenugreek leaves), Vitamin C (green chillies, drumstick leaves, broccoli and radish leaves) are among the vitamins found in vegetables, as are carbohydrates (leguminous vegetables, sweet potato, potato, onion, garlic, and methi), protein (lima bean, peas and cowpea) and minerals (leafy vegetables, drumstick pods). Vegetables also provide essential amino acids to the body.

Brinjal, also known as "baigan" in Hindi and "eggplant" in English, is a common vegetable crop in India and many other countries. It is a member of the Solanaceae family, which also includes tomato (Daunay, 2008). Within the circle of relations, there are 75 genera and roughly 2000 species, with about 150-200 tuber-bearing species belonging to the tuberarium division. The vast majority of species, around 1800, do not produce tubers. The essential chromosomal number $2n = 24$ has been seen in practically

all forms and species, according to cytological investigations. Brinjal is cultivated in India on 749 (in 000 hectares) of land, yielding 12874 (in 000 MT) every year (Anonymous, 2020). The most important brinjal producing states are West Bengal, Orissa, Gujarat, Bihar, Madhya Pradesh, Chhattisgarh, Andhra Pradesh, Tamil Nadu, Maharashtra, and Assam. Brinjal is cultivated in Uttar Pradesh over an area of 8.01 million hectares, producing 275.40 million tonnes per year with a productivity of 34.08 tonnes per hectare. The districts of Uttar Pradesh that give the most area and production to the nationwide pool are Agra, Meerut, Lucknow, Kanpur, Aligarh, Chitrakoot and Gorakhpur (Anonymous, 2019). Under the species *melongena* has three primary botanical varieties (Choudhury, 1976):

- A. The round or egg-shaped cultivars grouped under variety *esculentum*
- B. The long slender types are included under variety *serpentinum*
- C. The dwarf brinjal plants are put under variety *depressum*

However, due to diverse consumer demand that is unique to the region, the demand-supply gap has yet to be closed. Brinjal comes in a variety of sizes, styles, and colours and may be found all around Southeast Asia. As the source of origin, India has a wide range of plant and fruit morphological features, fruit quality, and cooking quality. Hence, there is scope for development in a variety of horticulture qualities to meet a wide range of consumer needs (Ullah *et al.*, 2014).

Brinjal fruit (unripe) is commonly prepared as a vegetable and dried shoots are used as a source of energy in rural areas. Eggplant has a low calorie content in its fruit, as well as a high mineral content that is beneficial to our health. Brinjal fruits are high in calcium, phosphorus, iron, vitamins and phytochemicals such as caffeine and chlorogenic acid and flavonoids, particularly nasunin, are abundant in eggplant. Nasunin, also known as delphinidin-3-(p-coumaroyl-rutinoside)-5-glucoside, is a major phytochemical found in brinjal peels (Matsuzoe *et al.*, 1999). Moisture (96%), protein (1.4 g), fat (0.3 g), carbohydrates (4 g), and fibre (0.4 g) were determined from edible sections of the fruit (excluding the stem and calyx) (1.3 g). It includes numerous vital elements, such as calcium (18 mg), phosphorus (47 mg), iron (0.38 mg), sodium (3 mg), chromium (0.07 mg) and sulphur (44 mg) per 100 g of fruit. Carotene (74 mg),

riboflavin (0.11), thiamine (0.03 mg), niacin (0.9 mg), folic acid (5 mg), vitamin C (1.2 mg) and chlorine (52 mg) are the vitamins found in a 100 g edible piece of the fruit. Arginine, histamine, lysine, tryptophane, phenylalanine, tyrosine, methionine, cysteine, threonine, leucine and valine are among the necessary amino acids found in the fruit.

Eggplant is one of the top ten vegetables for providing the healthiest diet with the fewest calories, as well as having a high phenolic content that aids in radical absorption (Cao *et al.*, 1996). It has a lot of promise as a raw material in the pickle industry and the fruits have therapeutic benefits. White brinjal particularly claimed to be healthy for diabetic patients (Choudhary, 1976) and also recommended as an ideal cure for individuals suffering from liver problems (Chauhan, 1981). Due to the presence of phenolic compounds, it also possesses anti-obesity, anti-inflammatory, and cardinal protecting properties.

Brinjal flowers are huge, violet-coloured that grow singly or in groups of two or more. Androecium have 5 stamens, alternate with corolla; Gynoecium has carpels which are united, hypogynous and syncarpous that has positioned obliquely to the median, ovary is superior; calyx have 5 sepals, united, persistent; corolla have 5 petals, united, usually cup-shaped. Despite the fact that brinjal is a self-pollinating crop, the heteromorphic flower shape causes a lot of cross pollination (called as heterostyly). Cross pollination has been found to occur to the extent of 29% of the time (Ram, 1999). Four types of flowers have been reported depending on the style length via. (a) long-styled with large size ovary, (b) medium-styled with medium size ovary, (c) Pseudo short-styled with rudimentary ovary and (d) true short-styled with very rudimentary ovary. Long and medium-styled flowers have been known to set fruit, however pseudo-short and short-styled blooms have not. Long style flowers have a higher likelihood of cross pollination. Flowers of various lengths can be found in each variety. A varietal characteristic is the proportion of long and medium-styled flower. The fruit set of long styled blooms varies from 70 to 86.7 percent depending on the variety. The fruit set differs from 12.5 percent to 55.6 percent in medium styled blooms. The position of the stigma about the stamens varies by cultivar and even within the same cultivar's flowers. Stigmas can be located above, below, or on the same level as the stamens, with the stigma above the stamens producing the most fruit set. Androecium is viable in short-

styled flowers, but the stigma is smaller, has underdeveloped papillae, contains less sugar than in long-styled flowers. Pollen germination on the stigma and pollen tube penetration into short styles are not observed (Rylski *et al.*, 1984). Botanically, brinjal is categorised as a berry. The fruit contains a large number of tiny, soft seeds that, while edible, have a bitter flavour due to the presence of nicotinoid alkaloids.

There is so much variability in brinjal in terms of fruit size, shape, colour and quality, that there is a wide scope for improvement, particularly in yield, through breeding. Genetic variability plays an important role in crop in selecting the best genotype for making rapid improvement in yield other desirable characters acted as well as to select the potential for hybridization programme and large variability increases the chances of discovering new forms. In formulating an appropriate breeding strategy aimed at exploiting the inherent variability of the original population, variability parameters such as genotypic and phenotypic coefficients of variations, heritability and genetic advance, as well as degree of association between the various characters and direct effect of yield contributing characters on total yield, are of paramount importance.

Under different environmental conditions, phenotypic variability fluctuates, however genetic variability does not, making genetic variability more valuable to a plant breeder for selection and hybridization. Because yield is a complex trait impacted by numerous yields contributing components and heavily influenced by environmental conditions, estimations of heritability and genetic progress are relevant for selection. Heritability refers to the degree of phenotypic diversity caused by genotypes, which aids breeders in selecting the best varieties for certain traits.

Direct selection based on fruit yield performance may be ineffective, while selection based on its component traits would be more appropriate (Fisher, 1918). To comprehend the direction of selection and maximise production in the shortest time, the correlation coefficient between the yield contributing features must be estimated but only correlation studies, do not offer an accurate degree of direct and indirect influences on yield. The path coefficient is a useful tool for distinguishing between direct and indirect causes of selection association, as well as for determining the relative importance of each causative element (Wright, 1921). Correlation studies combined

with path analysis can reveal more about the cause and effect relationship between distinct traits. As a result, selecting the optimum brinjal genotype for successful genetic improvement in this crop is deemed beneficial.

Genetic diversity is critical in any crop improvement programme because it aids in the selection of appropriate parents for hybridization, resulting in superior hybrids and desirable recombinants (Rathi *et al.*, 2011). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). In this regard, Mahalanobis (1936) D²-analysis is a useful tool for plant breeders to determine the degree of genetic divergence between the parents engaged in hybridization. Furthermore, choosing desired genotypes based on their higher genetic divergence would be extremely useful for exploiting heterosis and producing superior recombinants.

Variability is required for the improvement of these characteristics. Variability for economically important traits is a fundamental requirement for crop development. Germplasm characterization is vital for producing high yielding cultivars and improving fruit production and nutritional quality metrics. Hence, the current experiment was attempted to quantify the genetic diversity existing among the selected brinjal genotypes and to hand-pick suitable parents to use in future hybridization programs.

Keeping all of the foregoing in mind, the current study, which was based on the development of fifteen brinjal genotypes for growth, yield and other relevant attributes, had the following goal:

1. To analyse the genetic variability for yield and its component traits,
2. To determine the heritability and genetic advance of quantitative traits,
3. To estimate the correlation coefficient among the important economic traits,
4. To find out the direct and indirect effect of yield components on yield using path coefficient analysis, and
5. To ascertain the genetic divergence for yield and its component traits.

REVIEW OF LITERATURE

Plant breeders are always seeking for new ways to improve both quantitative and qualitative qualities of their plants. As a result, a full understanding of the inheritable configuration of a variety of fundamental features, as well as their interconnections, is required. Within types, phenotypic and genotypic correlations are useful for determining the extent to which colourful features are linked to lucrative output. Path measure analysis is a reliable statistical method for not only quantifying the interactions of various yield components, but also determining whether the effect is immediately represented in the yield or follows a different path to the final output. Genetic variability, heritability and genetic advance estimations might all be useful in determining parent performance in Brinjal. The proposed investigation of genetic variability, heritability, genetic advance, character association, path coefficient analysis and divergence in brinjal has a gap in the literature.

However, an attempt has been made to review the available works of literature on brinjal under the following sub-heads.

2.1 Genetic variability parameters

2.2 Heritability and genetic advance

2.3 Correlation coefficients

2.4 Path coefficient analysis

2.5 Genetic divergence through D^2 analysis

2.1 Genetic variability

The magnitude of genetic variability and diversity present in the germplasm influences the planning and execution of any breeding programme aimed at improving quantitative traits. As a result, genetic diversity is a requirement for any crop improvement programme.

Patel *et al.* (2004) studied twenty-two genotypes of brinjal and found high genotypic as well as phenotypic coefficients of variation for fruit length, yield per plant and fruit weight.

Singh and Kumar (2005) observed twenty-five genotypes of brinjal and reported high genotypic and phenotypic coefficients of variation for average fruit weight and a number of fruits per plant.

Tripathi *et al.* (2009) scrutinized thirty brinjal genotypes and observed high genotypic and phenotypic coefficients of variation for plant height, fruit length, number of primary branches per plant, average fruit weight, number of fruits per plant, fruit diameter and fruit yield per plant.

Kumar *et al.* (2010) studied eighteen genotypes of brinjal and exhibited highest GCV and PCV for number of fruits per plant followed by fruit yield, fruit length, number of branches per plant and average fruit weight. However, fruit width and plant height showed moderate GCV and PCV.

Dhaka and Soni (2012) examined 20 distinct brinjal genotypes for various traits. The highest phenotypic and genotypic coefficient of variation were found in average fruit weight, followed by yield per plant.

Kumar *et al.* (2013) found considerable variability among the genotypes for all the characters. High phenotypic and genotypic coefficient of variance were observed for fruit length, number of fruits per plant and fruit yield per plant.

Lokesh *et al.* (2013) conducted a study on 60 genotypes of brinjal and observed high PCV and GCV values for plant height, plant spread, number of branches per plant, average fruit diameter and average fruit weight.

Mili *et al.* (2014) studied on 36 genotypes of brinjal and observed high genetic coefficient of variation for single fruit weight, fruit diameter, seed yield per fruit, total fruit yield per plot, number of fruits per plant, fruit yield per plant and fruit length.

Singh *et al.* (2013) looked at eight parents and twenty-eight F₁ and found that PCV was generally higher than GCV for all of the characters studied, including plant height, number of primary branches per plant, fruits per plant, plant spread, fruit

diameter, average fruit weight, fruit length and fruit yield per plant. Fruit length, fruit diameter, fruit yield per plant, average fruit weight and primary branches all had high PCV and GCV (>25 percent), whereas yield per plant, plant spread and plant height all had moderate PCV (10–25 percent).

Gavade and Ghadage (2015) found that the F₂ population (15 crosses and their 6 parents) of brinjal exhibited a broad range of variance for most of the traits except for days to last picking, fruit yield per plant had the greatest phenotypic and genotypic variation, whereas the number of branches per plant had the least. Fruit yield per plant, fruit width, fruit weight and length had the largest phenotypic coefficient of variation, but plant height had the lowest. The highest genotypic coefficient of variation was found in fruit yield per plant, fruit width, fruit length and fruit weight, while the lowest was found in days to last harvesting.

Patel *et al.* (2015) evaluated 35 genotypes of brinjal for 21 characters and revealed that PCV was greater than the corresponding GCV for all traits. Maximum PCV (56.26%) and GCV (55.68%) were registered for fruit length to diameter ratio.

Vidhya and Kumar (2015) studied 30 brinjal genotypes for eleven traits and found that genotypic and phenotypic coefficients of variations were highest for fruit girth followed by the number of fruits per plant.

Koundinya *et al.* (2017) exhibited higher phenotypic and genotypic coefficient of variation values in number of fruits per plant (76.86%, 75.63%), fruit weight (43.88, 41.34%) and fruit yield per plant (53.61%, 51.17%) indicating that a greater amount of genetic variability was present for these characters which provide greater scope for selection.

Variability studies were carried out in 36 brinjal genotypes of Indian and exotic origin and observed high estimates of GCV and PCV for number of fruits per plant, fruits yield per plant, leaf chlorophyll and ascorbic acid. PCV was slightly higher than GCV for all the characters as reported by Rani *et al* (2017).

Sujin *et al.* (2017) in their study on 60 genotypes of brinjal found that the maximum phenotypic and genotypic variation were noted for fruit yield per plant followed by fruit weight, fruit girth and number of fruits per plant. For plant height and

number of flowers per plant, moderate estimates of phenotypic and genotypic coefficients of variation were observed.

Parvati *et al.* (2018) investigated 55 brinjal genotypes and estimated phenotypic coefficients of variability and genotypic coefficients of variability ranging from average fruit weight (18.00-176.70) followed by plant spread (51.70-87.60) respectively. PCV was slightly higher than the corresponding GCV and the difference was very low for the majority of the characters.

Banerjee *et al.* (2018) evaluated 38 genotypes of brinjal and observed a high genotypic coefficient of variation (GCV) in fruit length, fruit diameter, number of fruits per plant and fruit weight. Fruit length, fruit diameter, number of fruits per plant, fruit weight and total yield per plant all had higher phenotypic coefficients of variation.

Kumar *et al.* (2018) looked at 17 eggplant genotypes and discovered that average fruit weight, fruit length, number of fruits per plant, fruit girth, number of branches per plant, and fruit yield per plant had high phenotypic and genotypic coefficients of variation.

Saha *et al.* (2019) investigated on twelve genotypes of brinjal and found that both PCV and GCV were found to be greater for fruit yield per plant, whereas number of fruits per plant was high in PCV only.

Bajpai *et al.* (2020) evaluated 28 F₁ hybrids and 8 parents during two consecutive years and indicated that the high genotypic coefficient of variation as well as phenotypic coefficient of variation were recorded for average fruit weight, number of fruits per plant and yield per plant during both the years.

Konyak *et al.* (2020) experimented on forty-six genotypes of brinjal (IIVR 1 to 45 and local check variety) and were evaluated for their growth, yield, quality and genetic attributes and revealed high phenotypic coefficient of variation and genotypic coefficient of variation for fresh weight of fruit, fruit yield per plant, fruit length and fruit diameter.

Kumar *et al.* (2020) examined 38 locally collected genotypes and revealed that fruit yield per plant (36.51 percent) had the highest PCV, followed by number of fruits per plant (34.11 percent), whereas fruit length (14.40 and 17.72), fruit yield per plant

(34.43 and 36.51) and number of fruits per plant (32.20 and 34.11) had the greatest difference between GCV and PCV, indicating that environmental influence on the expression of these traits was greater than other traits.

Sakriya *et al.* (2020) carried out a study on 180 brinjal genotypes and estimated that PCV was higher than their corresponding GCV for all characters. GCV was found low for all the characters whereas, PCV was moderate for fruit yield per plant (15.69%) followed by number of fruits per plant (15.43%).

Anbarasi and Haripriya (2021) conducted two trials in 2019 and 2020 to analyse the variability among the 112 brinjal genotypes and all characteristics showed extremely significant variations. Fruit yield per plant, fruit girth and number of seeds per fruit all had higher PCV and GCV values.

Sharma *et al.* (2022) assessed the variability among thirty brinjal genotypes and found that the PCV was higher than the GCV for almost all the characters. Both the PCV and GCV were high for number of fruits per plant, fruit girth and seed weight per fruit.

2.2 Heritability and Genetic advance

The concept of heritability is critical for determining whether phenotypic differences between individuals are due to genetic or environmental factors. Heritability refers to the chance and scope of improvement that may be achieved by selection. It is a helpful statistic to use when analysing the genetic variance to total variance ratio, which is generally expressed as a percentage.

Patel *et al.* (2004) evaluated twenty-two genotypes of brinjal for heritability and genetics advance. They reported high estimates of heritability coupled with high genetic advance for fruit length, yield per plant and fruit weight.

Singh and Kumar (2005) studied twenty-five genotypes of brinjal and observed the highest estimates of heritability for average fruit weight, followed by yield per plant. High genetic advance as per cent of mean noted for average fruit weight, number of fruits per plant and yield per plant.

Naik *et al.* (2009) assessed sixty-one genotypes of brinjal for evaluation of heritability and genetic advance. High heritability coupled with high genetic advance as per cent of mean were observed for fruit length, number of fruits per plant and total yield per plant.

Tripathi *et al.* (2009) studied thirty brinjal genotypes and found that plant height, number of primary branches, fruit diameter, fruit length, number of fruits per plant, average fruit weight and fruit yield per plant all had strong heritability and genetic progress as a percentage of mean.

Kumar *et al.* (2010) examined eighteen brinjal genotypes and found that fruit length, number of branches per plant, average fruit weight, number of fruits per plant and fruit yield all had high heritability along with high genetic advance. Fruit yield, number of fruits per plant, fruit length, and average fruit weight were all found to have high heritability values.

Dhaka and Soni (2012) discovered that the 20 brinjal genotypes have different characteristics. Heritability estimates for all of the traits are substantial (above 85 percent). The highest heritability was found in the quantity of fruits per plant and the average fruit weight. The genetic improvement as a percentage of the mean was high for average fruit weight, yield per plant, number of fruits per plant and number of leaves per plant. High GCV and heritability were observed for yield per plant, followed by a number of fruits per plant.

Kumar *et al.* (2013) reported high heritability and genetic advance for fruit length, number of fruits per plant and fruit yield per plant using 14 parents (10 landraces, 4 commercial varieties) and 40 hybrids.

Singh *et al.* (2013) estimated that the heritability was high for all the characters and genetic advance was observed to be high for fruits per plant, average fruit weight, fruit length, fruit diameter, number of primary branches per plant, yield per plant, plant spread and plant height were moderate for days to first flowering, days to first fruit set and days to first harvest.

Lokesh *et al.* (2013) experimented on 60 brinjal genotypes and found that genetic advances were high (>20.00) for plant height (25.00), plant spread (115.07),

average fruit weight (25.23). High heritability accompanied by high genetic advance were noticed for plant height, plant spread and average fruit weight.

Mili *et al.* (2014) estimated 36 genotypes of brinjal and observed high heritability for fruit yield per plant, plant height, seed yield per fruit, single fruit weight, fruits per plant and fruit diameter. High heritability and high genetic advance were observed for traits like seed yield per fruit, single fruit weight, number of fruits per plant, total fruit yield per plot and fruit diameter.

Gavade and Ghadage (2015) observed F₂ population of brinjal and found high heritability coupled with high genetic gain for fruit weight and fruit yield per plant. High heritability and high percentage of genetic advance were recorded in case of fruit yield per plant, fruit weight, fruit length and fruit width.

Patel *et al.* (2015) evaluated 35 genotypes and found high estimate of heritability coupled with high genetic advance for most of the yield and its contributing characters which indicates phenotypic selection would be effective for the genetic improvement in these traits.

Vidhya and Kumar (2015) studied 30 brinjal genotypes for eleven traits and showed that the high heritability and high genetic advance have been observed for fruit girth, single fruit weight and marketable yield per plant.

Senapati *et al.* (2016) estimated high heritability coupled with higher genetic advances were observed for the characters like number of fruits per plant (96.51, 73.26), fruit weight (96.01, 49.30) and fruit yield per plant (92.76, 75.52).

Koundinya *et al.* (2017) observed high heritability with high genetic advance for the characters like plant height, days to 1st flowering, days to 50% flowering, number of fruits per plant, fruit weight, harvest index, fruit yield per plant, total sugar, anthocyanin in the peel, total phenols.

Rani *et al.* (2017) reported that number of fruits per plant, fruit yield per plant, average fruit weight, percent shoot borer infestation, percent fruit borer infestation, days to first flowering and trichome density demonstrated high heredity as a percentage of mean.

Banerjee *et al.* (2018) premeditated 38 genotypes in brinjal and found that the fruit length, fruit diameter, fruit weight, and a number of fruits per plant showed high heritability, along with high genetic advance as percent over mean.

Kumar *et al.* (2018) investigated 17 eggplant genotypes and observed high heritability for fruit length (98.33%) followed by average fruit weight (97.52%), number of fruits per plant (96.11%), fruit yield per plant and fruit yield (q/ha) (90.79%) and number of branches per plant (88.70%). The highest value of genetic advance was recorded for fruit yield q/ha (185.14%), average fruit weight (79.45%) and plant spread (E-W) (14.18%). Whereas, the maximum value of genetic advance as a per cent of mean (genetic gain) was recorded in fruit weight (63.59%), fruit length (52.96%) and number of fruits per plant (49.58%).

Saha *et al.* (2019) studied ten quantitative characters of twelve genotypes of brinjal and showed broad-sense heritability coupled with moderate to low genetic advance were recorded in fruit length, average fruit weight, plant height and days to maturity.

Kumar *et al.* (2020) evaluated 38 locally collected genotypes and observed high heritability and genetic advance for the characters such as fruit yield per plant, number of fruits per plant, fruit weight and fruit girth.

Konyak *et al.* (2020) observed high heritability coupled with high genetic advance were found for anthocyanin content, fresh weight of fruit, yield per plant, fruit length and fruit diameter in forty-six genotypes of brinjal.

Sakriya *et al.* (2020) carried out a study on 180 brinjal genotypes and found that high heritability was noticed for fruit length (86.62%), plant height (76.73%), plant spread (North-South) (72.99%), number of branches per plant (72.12%) and total soluble solids (63.38%). The expected genetic advance was observed below for all the characters.

Bajpai *et al.* (2020) reported that fruit length and circumference have strong heritability in the limited sense over both years. Plant height and dry matter content, on the other hand, were noted as having strong heritability in the limited sense during the

first year. Fruit length and fruit circumference have strong heritability and high genetic advance as a percentage of mean.

Anbarasi and Haripriya (2021) detected high heritability for fruit width, fruit length, fruits per plant, average fruit weight and seeds per fruit. Fruit yield per plant have high genetic advance along with high heritability percentage were observed.

2.3 Correlation analysis

The degree and direction of correlation between two or more variables are measured by correlation. Character association research aids breeders in determining grain yield selection criteria in parental lines, allowing selection to be more effective in isolation than when phenotypic characteristics are correlated and subjected to environmental changes. It takes into account both environmental variation and non-additive gene activity. As a result, understanding the relationships between various traits is critical for developing an effective breeding strategy.

The correlation coefficient of eggplant has been researched by a number of researchers. The following is a synopsis of research on the relationship between eggplant characters:

Reena and Mehta (2007) evaluated 20 genotypes of brinjal and recorded that fruit yield per plant had significant positive association with number of fruits per plant and plant height, whereas negative correlation was observed in number of branches per plant, days to first picking, number of fruits per cluster and days to last picking.

Bansal and Mehta (2008) studied twenty-six genotypes of brinjal and observed that the fruit yield per plant had strong positive association with plant height, number of branches per plant and number of fruits per plant at genotypic level.

Senapati *et al.* (2009) studied correlation in thirty-two genotypes of brinjal and found that fruit yield per plant showed positive and significant association with number of branches per plant, number of fruits per plant and fruit weight.

Singh *et al.* (2011) studied correlation in 30 genotypes of brinjal and revealed that fruit yield (q/ha) showed a positive and significant correlation with number of fruits

per plant, seed yield per plant, weight of 100 seeds, fruit length, fruit width and fruit diameter.

Thangamani and Jansirani (2012) studied the correlation with twenty-five F₁ hybrids in brinjal and revealed that yield per plant showed a positive correlation with number of branches per plant, number of fruits per plant and ascorbic acid content. A significant negative correlation of yield was observed with days to first flowering. Fruit borer incidence had a significant positive association with fruit girth and significant negative correlation with ascorbic acid content.

Kumar *et al.* (2013) evaluated 34 genotypes of brinjal and found that number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight exhibited positive and significant correlation with fruit yield per plant.

Pandey *et al.* (2016) revealed that marketable yield per plant, average fruit weight, number of fruits per plant and primary branches per plant was significantly and positively associated with fruit yield at phenotypic as well as genotypic levels, while negatively correlated with fruit length and total soluble solids.

Fruit weight, fruit girth, and number of fruits per plant were shown to have positive and significant correlations among the sixteen morphological features investigated in 60 brinjal genotypes reported by Sujin *et al.* (2017).

Koundinya *et al.* (2017) carried out a study on 40 brinjal genotypes and revealed that fruit yield per plant showed highly positive significant correlation with number of primary branches per plant and number of fruits per plant significant negative correlation with days to 1st flowering, total soluble solids, total sugars and total protein.

Tirkey *et al.* (2018) evaluated 18 brinjal genotypes and found positive correlation in plant height at genotypic level and showed highly significant and positive correlation in single fruit weight, fruit yield per plot, days to first flowering, days to 50% flowering and fruit yield per plot both at the genotypic and phenotypic level.

Saha *et al.* (2019) reported that fruit length and fruit diameter exhibited positive genotypic correlation with fruit yield per plant in 12 genotypes of brinjal.

Tiwari *et al.* (2019) conducted study on 40 genotypes of brinjal and exhibited that total fruit yield per plant had highly significant and positive phenotypic correlation with marketable fruit yield per plant (0.9635), followed by unmarketable fruit yield per plant (0.6003), fruits per plant (0.5405), primary branches per plant (0.3156) and fruit length (0.2426).

Correlation studies revealed that traits like plant height, number of branches per plant, plant spread, number of fruits per plant, fruit length and fruit diameter had a significant association with fruit yield per plant in 20 genotypes of brinjal and was reported by Gurve *et al.* (2020).

Correlation studies in 38 genotypes of brinjal indicated that there is a strong inherent association between yield per plant with characters like plant height and number of fruits per plant. Further, plant height, number of fruits per plant, fruit weight and fruit girth showed significant positive association both at genotypic and phenotypic levels and suggested that these are important correlated characters contributing towards fruit yield of brinjal was reported by Kumar *et al.* (2020).

Chithra *et al.* (2020) conducted an experiment in 300 F₂ segregating populations of the bi-parental cross of Surya × Harita for 12 different quantitative characters and indicated that the total yield per plant had positive and significant association with plant height, number of primary branches, fruit diameter, fruit length, average fruit weight and number of fruits per plant.

Kumar *et al.* (2020) analysed the association in 17 genotypes of brinjal and expressed that the fruit yield per plant showed a significant positive correlation with number of fruits per plant, yield per hectare at genotypic and phenotypic levels and average fruit weight at genotypic level only.

Nikitha *et al.* (2020) evaluated 33 genotypes of brinjal and observed that fruit yield per plant exhibited maximum positive association with number of fruits per plant (0.8997), number of branches per plant (0.2293), fruit diameter (0.1339) and fruit weight (0.1233).

Kumar *et al.* (2021) indicated the fruit yield per plant had exhibited a highly significant and positive correlation with fruit length (0.837) followed by the number of

fruits per plant (0.716). This result also shows that the genotypic correlation coefficient was higher in magnitude than most of the characters corresponding phenotypic correlation coefficient.

2.4 Path Coefficient Analysis

Path analysis gives you a score for how important each independent variable is in predicting changes in the dependent variable. A path coefficient is a standardized partial regression coefficient and as such measures, the direct effect of one trait upon another and permits the separation of correlation coefficient into direct and indirect effects by Dewey and Lu (1959).

Path coefficient analysis revealed that the number of fruits per plant, mean weight of fruits and diameter of fruits had a maximum direct effect at genotypic level and hence direct selection could be made for these characters for improving the yield, while maximum direct effect at phenotypic level was showed by plant height, number of fruits per plant, mean weight of fruits and diameter of fruit. A number of branches per plant, plant height and length of fruit had a positive indirect effect on yield per plant viz., a number of fruits per plant and hence simultaneous selection for these characters can be made for the improvement of yield was reported by Sharma and Swaroop (2000).

Reena and Mehta (2007) studied 20 genotypes of brinjal and showed that path coefficient analysis of fruit weight, number of fruits per plant, seed weight per fruit, fruit length and number of branches per plant exerted direct positive effect on yield per plant.

Singh *et al.* (2011) studied the path analysis in 30 genotypes of brinjal and showed positive significant direct effect on fruit yield viz., the number of fruits per plant, average fruit weight, number of seeds per fruit, fruit length, fruit diameter and number of branches per plant at both genotypic and phenotypic level.

Thangamani and Jansirani (2012) observed that the number of fruits per plant is the most important yield driver due to its strong direct effect and indirect influence on yield viz., the number of branches per plant and fruit weight. Fruit girth and fruit length had moderate effects on yield.

Path co-efficient analysis studied in 35 genotypes of brinjal indicated the highest positive direct effect of fruit length to diameter ratio (2.4326) on fruit yield per plant followed by number of fruits per plant (1.2644) and fruit diameter (1.2539) was reported by Patel *et al.* (2015).

Koundinya *et al.* (2017) observed path analysis in 40 genotypes of brinjal and found that number of fruits per plant imparted the highest positive direct effect on yield followed by fruit weight. The number of fruits per plant emerged as the main casual factors for positive or negative association of several characters with fruit yield per plant.

Path analysis in 60 genotypes of brinjal reported that the number of fruits per plant and fruit weight have a positive direct effect was reported by Sujin *et al* (2017).

Tirkey *et al.* (2018) studied genotypic path coefficients in brinjal and revealed that fruit yield per plot had exhibited maximum direct effect followed by fruit length (0.153), plant height (0.115) and number of primary branches (0.013). Among the direct negative effects number of fruits per plant (-0.327) showed highest negative direct effect on fruit yield per plot followed by total soluble solids (-0.209), primary branches at (60 days) (-0.108) and plant height (60 days) (-0.088) had exhibited direct negative effect.

Saha *et al.* (2019) evaluated 12 genotypes of brinjal and revealed that secondary branches per plant proposed maximum direct effect on the yield on both genotypic and phenotypic levels followed by average fruit weight and fruit length.

Tiwari *et al.* (2019) revealed that marketable fruit yield per plant exhibited the greater magnitude of positive direct influence on fruit yield at phenotypic level. Plant height and average fruit weight had a significant negative direct influence on total fruit yield per plant.

Bende *et al.* (2019) experimented on 41 genotypes (including one check) and found that maximum positive direct effect on fruit yield per plant was exhibited through number of fruits per plant, number of branches per plant and fruit weight per plant.

Konyak *et al.* (2020) revealed that path analysis had maximum positive direct effect on yield which is exerted by fresh weight of fruit (1.08) and number of fruits per plant (0.407).

Nikitha *et al.* (2020) evaluated 33 genotypes of brinjal for path coefficient analysis and found that maximum positive direct effect on fruit yield per plant depicted through number of fruits per plant (0.8929G, 0.9813P), fruit weight (0.7588G, 0.3485P) and number of branches per plant (0.2278G).

Chithra *et al.* (2020) tested 12 quantitative characters on 300 F₂ segregating populations of the bi-parental cross of Surya and Harita, and found that the characters, such as the number of fruits per plant, average fruit weight, plant height, fruit length and fruit diameter, had a high positive direct effect on fruit yield per plant.

Curve *et al.* (2020) studied 20 genotypes of brinjal and revealed that the traits like number of branches per plant, plant spread (North-South) and number of fruits per plant should be considered essential for developing high yielding genotypes as they had high positive direct effects on fruit yield per plant.

Kumar *et al.* (2020) experimented on 17 genotypes of brinjal and expressed that average fruit weight had highest positive direct effect on fruit yield per plant followed by yield per hectare, number of fruits per plant and plant height.

Pal *et al.* (2021) looked at 60 brinjal genotypes and found that the number of primary branches (0.0694), average fruit weight (0.0632) and quantity of fruit per plant (0.0495) had the greatest positive direct impact on total fruit production. Days to 50% flowering (-0.055) and plant height both had a direct detrimental impact on total fruit yield (-0.0371). Average fruit weight (0.0504), quantity of fruit per plant (0.0038) and fruit length (0.002) all exhibited a significant positive indirect impact on marketable fruit yield per plant. Marketable fruit had a substantial negative indirect effect on the number of primary branches (-0.03) and plant height (-0.008).

Dhaka and Soni (2022) evaluated path analysis of 20 genotypes and found that the highest positive direct effect on fruit yield per plant was exerted by the character i.e., average weight of fruit followed by the number of fruits per plant. The estimated residual effect at the genotypic level was equal to 0.26 and at phenotypic levels was equal to 0.31.

Sakriya *et al.* (2022) carried out path analysis in 180 genotypically diverse indigenous genotypes of brinjal. Analysis showed that the number of fruits per plant

exerted positive direct effect on fruit yield per plant and indirectly influences the yield through plant height and fruit length.

2.5 Genetic divergence through D^2 analysis

P. C. Mahalanobis first proposed the notion of D^2 statistics in 1936. Rao in 1952 conveyed that this approach might be used to measure genetic diversity in plant breeding. For the investigation of genetic divergence in diverse breeding materials, this approach is now widely employed in plant breeding and genetics. This is one of the most effective methods for determining genetic divergence.

Singh *et al.* (2006) studied genetic diversity in 29 brinjal genotypes and the genotypes were grouped into six clusters. Cluster II had the maximum genotypes, with up to fourteen, whereas clusters V and VI had single genotype. Clusters I and VI had the greatest distance between them. Cluster I recorded maximum mean value for fruit yield (q/ha), average fruit yield/plant, fruit length and number of fruits/plant and Cluster V recorded the highest mean values for plant height and plant spread. Number of fruits per plant, plant height, average fruit production per plant and number of branches per plant contributed the most divergence.

Kumar *et al.* (2007) assessed genetic diversity in 57 genotypes of brinjal and all the genotypes were grouped into eight clusters. Cluster I accommodate maximum number of genotypes (12) whereas cluster VIII had least number of genotypes (3). Cluster VIII recorded a maximum intra cluster distance of 2.12 while cluster IV recorded minimum intra cluster distance of 1.44. Maximum inter cluster distance was observed between cluster VIII and VII (6.57), whereas cluster III and V had minimum distance (2.08). Cluster VIII recorded highest mean for fruit yield (303.36 q/ha), number of fruits/plant (18.64), fruit length (12.02 cm), plant spread (94.34 cm) and number of branches/plant (6.59) and cluster III recorded maximum mean value for average fruit weight (86.08 g) and plant height (115.14 cm). The characters contributed maximum to genetic divergence are fruit length, fruit width, average fruit weight and fruit yield per plant.

Using Mahalanobis D^2 statistic, Quamruzzaman *et al.* (2009) studied genetic divergence among nineteen eggplant genotypes. Five clusters were generated in all.

Cluster I had the most genotypes (7), whereas clusters IV and V had the least number of genotypes (2). Cluster V had the greatest intra-cluster distance, whereas Cluster III had the smallest. Cluster IV and Cluster V had the greatest inter-cluster distance. At the time of harvest, Cluster V had the greatest mean plant height. Cluster II had genotypes with high mean values for number of branches per plant, fruit diameter, individual fruit weight and fruit yield.

Rathi *et al.* (2011) studied thirty genotypes of brinjal for genetic diversity. The thirty genotypes were separated into five groups. The highest inter-cluster distance was found between clusters I and IV, while the shortest distance was found between clusters I and II. The maximum inter cluster distance was between cluster I and cluster IV. Cluster V had highest mean for fruit yield per plant and average fruit weight.

Shinde *et al.* (2012) studied genetic divergence in 65 genotypes of brinjal and found that all the genotypes were grouped into seven clusters using Mahalanobis D^2 analysis. Out of these seven clusters, cluster A had largest having thirty-eight and cluster E, F, G had lowest having only one genotypes. The maximum inter cluster divergence was observed between cluster E and G (7.29), while it was lowest between cluster A and E (4.19). The inter cluster distance between cluster G and F (6.62) and G and B (6.92) was high. The yield per plant had highest cluster mean for cluster G (2.10) followed by F (1.80), B (1.73), D (1.42).

Sadarunnisa *et al.* (2015) estimated genetic divergence among 50 genotypes of brinjal for 16 characters using Mahalanobis D^2 statistic. On the basis of the relative magnitude of D^2 values, the genotypes were divided into eight groups. Among the eight clusters, cluster IV was the largest comprising of 17 genotypes. The maximum and minimum intra cluster distances were found in cluster VI and cluster I, respectively. The inter-cluster D^2 values were maximum between cluster VI and VII while the minimum inter-cluster distance was observed between clusters I and II. The mean value for most of the traits was highest in cluster VII. Cluster VII recorded the highest mean for characters like plant height, number of fruits per cluster, fruit width, average fruit weight and fruit yield per plant. The genotypes of cluster VIII recorded maximum number of branches per plant and fruit length. The maximum mean values for characters ascorbic acid content were recorded in cluster I. The genotypes of cluster III

recorded maximum mean values for number of fruits per plant and also revealed that average fruit weight is major contributing character towards genetic divergence.

Yadav *et al.* (2017) estimated genetic divergence among 40 genotypes in brinjal using D^2 statistics. The genotypes were grouped into seven clusters. Average intra and inter-cluster D^2 values revealed that cluster II showed a minimum intra-cluster value of 3.793 indicating that the genotypes within this cluster were similar, while cluster I showed maximum intra-cluster D^2 value (4.681) revealed the existence of diverse genotypes in these clusters. The inter-cluster D^2 values ranged from 4.657 to 7.174. The minimum inter-cluster D^2 value was observed between clusters III and IV (4.657) indicating the close relationship among the genotypes included in these clusters. The maximum inter-cluster value was observed between cluster V and II (7.174) indicating that the genotypes included in these clusters had maximum divergence. The highest mean value for number of branches per plant was possessed by cluster III (6.71), cluster VI (82.08) had the highest for plant height, cluster II (8.71) showed the highest mean value for number of fruits per plant, cluster VII had the highest mean for fruit length, cluster V (106.06) divulged the highest mean value for fruit diameter, cluster I (152.50) showed the maximum mean value for fruit weight and cluster V had highest for fruit yield per plant (589.16).

Arti *et al.* (2018) estimated genetic divergence among 50 eggplant genotypes using Mahalanobis D^2 Statistics. All the genotypes were grouped into eight distinct clusters. Clusters II, V and VIII had the maximum genotypes consist of nine, followed by cluster IV with seven genotypes and clusters I, III, VI and VII with single genotypes each. Cluster VII (164.49) had the greatest intra cluster distance, whereas clusters V, VI and VIII had the smallest (0.00). However, the greatest inter-cluster distance (536.13) was found between clusters VII and VIII, indicating a great deal of variety between these two clusters, whereas the smallest (59.63) was found between clusters IV and V. Ascorbic acid content (18.53 percent) followed by number of marketable fruits per plant (17.88 percent), plant height (14.12 percent), total soluble solids (12.65 percent) and number of branches per plant (11.27 percent) all contributed the most to the expression of genetic divergence. Cluster VIII had the highest plant height, number of branches per plant, fruit breadth, and ascorbic acid content. For the earliest flowering

and harvesting, total harvest time and fruit yield per plant, Cluster I exhibited higher mean values. Cluster V had the highest mean for total soluble solids and number of marketable fruits per plant, whereas Cluster IV had the longest fruit length and Cluster VII had the heaviest fruit weight.

Curve *et al.* (2019) conducted an experiment on genetic divergence among 20 genotypes of brinjal for 25 characters and evaluated in a breeding programme aimed at improving yield potential by using Mahalanobis D^2 statistics. The genotypes were grouped into three clusters i.e., cluster I had maximum 18 genotypes followed by II and III having each single genotype respectively. Cluster I had the greatest intra-cluster distance (110.60). Clusters II and III have the greatest inter-cluster distance between them (452.85). Clusters II and III had high cluster means for plant height, plant spread (North-South) and (East-West), fruit length, fruit yield per plant, fruit yield per plot and ascorbic acid, these clusters can be used successfully in hybridization programmes.

Dash *et al.* (2020) looked at 110 brinjal genotypes. Cluster analysis separated all 110 brinjal genotypes into eight major groups based on their D^2 values. The maximum genotypes were found in Cluster VI which included twenty-eight genotypes. Cluster IV had the largest intra cluster distance (3.784), followed by Cluster VII (3.148), showing the most variety within these clusters, while Cluster II had the smallest intra cluster distance. Cluster II and IV showed greater inter-cluster variability (9.061), while clusters V and VI were smaller (2.426), indicating that members of these two clusters were genetically related. Highest cluster mean for plant height and fruit length were observed in cluster II, plant spread mean was highest in cluster III, number of fruits per plant in cluster IV and maximum mean value for fruit weight observed in cluster I.

Mohanty *et al.* (2021) studied genetic divergence among thirty-eight genotypes using Mahalanobis D^2 statistics. The result revealed that genotypes grouped into 13 clusters. The cluster I was the largest containing 9 genotypes followed by cluster III with 7 genotypes. The diversity among the cluster was measured by inter-cluster distance, highest being observed in between cluster VIII and cluster XIII ($D^2 = 1142.59$) followed by cluster IX and cluster XIII ($D^2 = 941.02$) and cluster V and cluster VIII ($D^2 = 792.97$). Cluster VIII had highest cluster mean for number of fruits per plant,

cluster X exhibited highest mean for plant height, cluster IX showed highest mean for fruit length and fruit yield per plant, cluster XII had high value for number of branches per plant, whereas cluster XIII showed higher for fruit weight. Maximum contribution towards divergence was made by fruit girth (19.19%) followed by fruit length (17.97%), plant height (9.84%), fruit weight (7.59%), number of fruits per plant (6.21%) and number of branches per plant (2.98%).

Anbarasi and Haripriya (2021) investigated 112 brinjal genotypes for genetic diversity. For 10 growth and 9 yield attributing characteristics, Mahalanobis D^2 analysis was used. The 112 genotypes were divided into seven groups. Cluster IV (23.975) had the most intra-cluster distance, whereas cluster II (5.683) had the smallest. The maximum inter-cluster distance was observed for clusters I and IV (24.912). Clusters II and III were found to have the shortest inter-cluster distance (10.431). Fruit yield per plant, fruit width and number of seeds per fruit all contributed the most to overall divergence in that order. Cluster IV had the highest average fruit yield per plant (1647.37).

Verma *et al.* (2021) studied 40 brinjal genotypes and discovered that they were all divided into five clusters showing that there was variability among the genotypes for different attributes. Cluster I had the most genotypes, with 24 genotypes, followed by Cluster II which had 10 genotypes. Clusters III, IV, and V included two genotypes each. Cluster IV had the greatest intra-cluster distance (1034.56). Clusters IV and V had the greatest inter-cluster distance (31520.82). Cluster IV had the highest mean number of main branches per plant (4.20). Cluster IV had the highest mean plant height (75.05 cm). Fruit length was greatest in Cluster IV (22.97 cm). Cluster III had the highest mean values for fruit circumference (4.23) and average fruit weight (81.98), whereas Cluster IV had the highest mean values for number of fruits per plant (9.86) and total fruit yield per plant (770.36). Overall fruit yield per plant provided the most contribution to total genetic divergence (48.24 percent).

MATERIALS AND METHODS

The present experiment entitled “**Assessment of genetic variability and divergence (D²) among different characters in brinjal (*Solanum melongena* L.) genotypes**” was conducted at Vegetable Research Farm of Department of Horticulture, Institute of Agricultural Sciences, B.H.U., Varanasi-221005 Uttar Pradesh during Rabi season in 2021.

The details of materials and methods used in the experiment are given below:

3.1.1 Experimental site

The Vegetable Research Farm is about 10 Km, away from Varanasi railway station in south eastern part of Varanasi city and is geographically situated at 25°31' North latitude and 83° 03' East longitude. The altitude of the location is about 123.23 meter above mean sea level. Keeping in view all the prerequisites for trial work, the field was selected as vegetable farm.

3.1.2 Climate

Varanasi is situated in eastern part of U.P. and lies in the centre of the north alluvial plain on the left side of river Ganga and enjoys a humid sub-tropical climate with large variation in summer and winter temperature i.e., extreme of hot weather in summer and cold in winter. On the basis of climatic condition, the entire year could be divided into three distinct seasons: summer starts from last week of March to third week of June, rainy season from last week of June to middle of October and winter season is from end of October to February. The seasonal temperature ranges in summer from 32°C to 45°C. However, the coldest months in January with mean minimum temperature varying from 6°C to 9°C with occasional fog is common in winter season while hot dry wind, called Lou blow in summer. The average annual rainfall is about 1110 mm. The mean relative humidity is about 68 percent which rises up 81 per cent during July to September and falls down to 39 per cent during the end of April to early June. The mean weekly value of weather data recorded at Meteorological Observatory,

Agronomy Farm, Institute of Agricultural Sciences, Banaras Hindu University shown in table 3.1

Weekly meteorological data, Varanasi, year-2020-21. Source: Meteorological Observatory, Department of Agronomy, Institute of Agricultural Sciences, Banaras Hindu University

Table 3.1: Meteorological data

	Month & Date	Rainfall (mm)	Temperature (°C)		R.H. (%)		Wind Speed (km/hr)	Sunshine hours	Evaporation (mm)
			Max.	Min.	Mor.	Eve.			
1	Nov 05-11 (2020)	0.0	29.6	13.9	90	48	1.2	5.6	2.1
2	12-18	0.0	25.0	18.1	89	54	1.9	5.6	2.2
3	19-25	13.2	26.3	12.5	91	48	1.8	4.5	1.9
4	26-02	0.0	26.3	11.1	92	43	1.2	5.8	1.6
5	Dec 03-09	0.0	27.7	12	93	53	0.9	3.5	1.2
6	10-16	3.6	23.9	14.8	93	64	1.8	2.1	1.4
7	17-23	0.0	20.5	7.5	91	59		5.6	1.3
8	24-31	0.0	22.3	7.8	94	49		5.2	1.2
9	Jan 1-7 (2021)	0.0	25.4	12.3	90	54		3.3	1.1
10	8-14	0.0	21.7	13.0	92	59		2.3	1.6
11	15-21	0.0	19.4	8.1	95	65		0.2	1.0
12	22-28	0.0	17.5	9.2	95	71		2.2	1.0
13	29-04	0.0	22.3	7.3	96	46		4.5	1.25
14	Feb 05-11	0.6	24.6	10.8	91	50		6.5	1.7
15	12-18	0.0	28.4	12.4	90	37		7.6	1.9
16	19-25	0.0	29.0	13.7	85	41		7.3	2.6
17	26-04	0.0	30.7	15.4	79	34		9.1	3.8
18	March 05-11	0.0	32.7	17.0	88	36		6.5	4.5
19	12-18	0.0	32.3	17.7	87	39		4.7	6.3
20	19-25	0.0	34.5	20.7	64	40		4.4	5.1
21	26-01	0.0	36.0	17.8	73	23		5.6	5.6
22	April 02-08	0.0	38.8	18.9	74	20		6.5	6.3

23	09-15	0.0	35.3	20.2	60	25		2.9	6.9
24	16-22	0.0	37.3	22.1	58	38		6.0	6.4
25	23-29	0.0	40.7	20.7	-	-		9.8	4.9
26	30-06	0.0	38.9	23.7	54	46		5.2	6.7
27	May 07-13	10.2	36.1	24.5	80	60		6.4	6.3
28	14-20	77.3	37.0	23.7	65	65		4.1	6.3
29	21-27	4.2	33.9	24.1	-	-		6.2	6.0
30	28-03	48.6	33.8	23.8	-	-		4.8	4.2
31	June 04-10	1.6	36.9	27.0	71	55		6.2	4.6
32	11-17	196.6	34.2	25.8	91	71		0.0	2.9
33	18-24	456.7	32.9	25.3	94	86		1.2	2.4
34	25-01	16.4	34.6	26.8	87	71		2.7	3.3

3.1.3 Soil

The soil of field is light sandy loam. The Physio-chemical compositions obtained by the analysis of soil are presented below in tabular form (Table 3.2).

Table 3.2 Physio-chemical composition of soil

Parameter	Value (%)	Method Employed
1. Mechanical analysis		
a. Coarse sand	5.38	
b. Fine sand	44.82	Bouyoucos Hydrometer method (Boyucos, 1962)
c. Silt	29.59	
d. Clay	18.41	
2. Chemical analysis		
a. Available Nitrogen	0.095	Modified Kjeldahl's method
b. Available Phosphorus	0.081	Bicarbonate extractable 'P' and development of blue colour
c. Available Potash	0.542	Neutral normal ammonium acetate method

3.2 Experimental materials

The experimental materials in the form of seeds were bought from the ICAR Indian Institute of Vegetable Research, Jakhani, Varanasi and the Department of Horticulture, Institute of Agricultural Sciences, BHU, Varanasi. The fifteen genotypes of Brinjal used in the investigation are given below (Table 3.2)

Table 3.3: List of genotypes used in trial work

Sl.No.	Name of cultivar	Symbols used	Source of genotypes
1	HABR-4	L ₁	IIVR, VARANASI
2	JB-9	L ₂	IIVR, VARANASI
3	UR-11	L ₃	IIVR, VARANASI
4	JBL-03-04	L ₄	IIVR, VARANASI
5	Green Long	L ₅	IIVR, VARANASI
6	Sobha	L ₆	IIVR, VARANASI
7	SEP 034	L ₇	IIVR, VARANASI
8	Arka Keshav	L ₈	IIVR, VARANASI
9	NBJ-19	L ₉	IIVR, VARANASI
10	NBH-1156	L ₁₀	IIVR, VARANASI
11	Punjab Nagina	L ₁₁	IIVR, VARANASI
12	PPL-Nepal	L ₁₂	IIVR, VARANASI
13	Annamalai	L ₁₃	IIVR, VARANASI
14	IVB-2	L ₁₄	IIVR, VARANASI
15	KS 331	L ₁₅	IIVR, VARANASI

3.3 Layout plan

The experiment was laid out in Randomized Block Design (RBD) with three replications. For this purpose, 45 plots were made. The details of this experiment are as follows:

1	Design	Randomized Block Design
2	Number of replications	3
3	Number of treatments	15
4	Number of plots	45
5	Number of rows in each plot	5
6	Size of plot	3x3m
7	Spacing	60x60 cm
8	Number of plants in each plot	25
9	Irrigation channel	1
10	Fertilizer dose	N:P: K 120:80:80
11	Date of sowing	26 th September, 2020
12	Date of Transplanting	5th November, 2020

3.4 Preparation of the experimental plot

The experimental field was given repeated ploughings with disc plough and the cultivars followed by planking. The required tilth was obtained before transplanting. Plots were made under marked areas. A basal dose of fertilizer is given.

Table 3.4: Layout plan of experimental field

R₁	Irrigation channel	R₂	Irrigation channel	R₃
L ₁		L ₃		L ₅
L ₂		L ₄		L ₆
L ₃		L ₅		L ₇
L ₄		L ₆		L ₈
L ₅		L ₇		L ₉
L ₆		L ₈		L ₁₀
L ₇		L ₉		L ₁₁
L ₈		L ₁₀		L ₁₂
L ₉		L ₁₁		L ₁₃
L ₁₀		L ₁₂		L ₁₄
L ₁₁		L ₁₃		L ₁₅
L ₁₂		L ₁₄		L ₁
L ₁₃		L ₁₅		L ₂
L ₁₄		L ₁		L ₃
L ₁₅		L ₂		L ₄



Figure 3.1: View of experimental field

3.5 Details of field operations

3.5.1 Nursey raising

Raised nursery beds were prepared with dimensions of 4.0 X 1.1 m and levelled by mixing well-rotted FYM. The seeds were sown treating with Carbendazim @ 3g/kg of seed. After sowing, the seeds were covered with a fine mixture of soil and FYM and light irrigation was given with the help of watering cane just after sowing.

3.5.2 Transplanting

One-month-old healthy seedlings of brinjal were transplanted in the flat beds as per layout plan. Transplanting was done at the spacing of 60 x 60 cm with one seedling per hill. Just after transplanting, the seedlings were gently irrigated with the help of water cane.

3.5.3 Fertilizer application

FYM @ 20 tonnes /ha was applied at the time of field preparation. Fertilizers were applied as 100 kg N, 80 kg P and 80 kg K/ha in the form of urea, single super phosphate and muriate of potash. Half dose of nitrogen and full amount of phosphorus and potassium were applied as basal dose. Rest of half of nitrogen was applied as top dressing 30 days after transplanting.

3.5.4 Weeding and plant protection measures

Hand weeding and shallow hoeing were done at an interval of 30 days to keep the plots free from weeds. Plant protection measures were adopted to control the attack of fruit and shoot borer (*Leucinodes orbonalis* L.). During the cropping period, one protective spray of Endosulfan @ 2 ml/litre of water was done at 60 days after transplanting.

3.5.5 Irrigation

After transplanting, irrigations were given at an interval of 10-12 days looking at the soil condition.

3.5.6 Harvesting

Harvesting of the fruits was done, in morning when they attained proper colour and size.

3.6 Characters studied

The observations were recorded during the crop growth period on five randomly selected plants, which were tagged in each plot of every replication. The border plants in each row were avoided and the tagging was done before flowering. The mean value of these plants was computed and used for statistical analysis. The details of the characters studied are described as under.

3.6.1 Quantitative Characters

3.6.1.1 Plant Height (cm)

The height of five randomly selected plants from each plot was measured in centimetres from the base of the plant to the tip of the emerging leaf at the time of the last harvest.

3.6.1.2 Number of branches per plant

The number of primary branches on the main stem at the time of the last harvest was recorded.

3.6.1.3 Plant spread (East-West) (cm)

Plant spread was measured in centimetres from the east to west direction.

3.6.1.4 Plant spread (North-South) (cm)

Plant spread was measured in centimetres from the north to south direction.

3.6.1.5 Fruit length (cm)

Five fruits from each genotype per replication were selected randomly and fruit length was measured with help of vernier callipers in centimetres.

3.6.1.6 Fruit width (cm)

The width of randomly selected same five plants was measured with the help of vernier callipers in centimetres.

3.6.1.7 Number of fruits per plant

The number of marketable fruits from selected plants from each plot was counted in each picking and sum up after last picking to obtain number of fruits per plant.

3.6.1.8 Average fruit weight (g)

The weight of randomly selected five fruits was measured in grams with help of the electronic balance and average was worked out.

3.6.1.9 Chlorophyll content

The chlorophyll content was measured by the help of spad meter from the fully develop young leaves.

3.6.1.10 Number of seeds per fruit

Five fruits from each genotype were sliced lengthwise at random and seeds were manually removed using the fermentation process. The number of seeds per fruit was manually counted, and the average was calculated.

3.6.1.11 Test weight (1000 seed weight) (g)

The thousand seeds were counted manually and weight was recorded in grams. The average of three replications worked out and expressed as hundred seed weight from a genotype.

3.6.1.12 Fruit yield per plant (kg)

Picking of fresh marketable brinjal fruits was done from selected plants throughout the harvesting period and weighted. An average per plant was worked out from all pickings and expressed in kg per plant.

3.6.1.13 Fruit yield (q/ha)

From fruit yield per plant, fruit yield hectare was determined in quintals.

3.6.2 Biochemical traits

3.6.2.1 Total soluble solids (°Brix)

The total soluble solids were determined by using a digital Refractometer. Homogeneous sample was prepared by blending the fruit in a blender. The sample was thoroughly mixed and a few drops were taken on the prism of refractometer. The readings were recorded as “°Brix”.

3.6.2.2 Ascorbic acid (mg/100g)

Ascorbic acid was determined by titrating a known weight of sample with 2, 6-dichlorophenol indophenol dye using meta-phosphoric acid as a stabilizing agent (Albrecht, 1993).

Known weight of the sample was ground in pestle and mortar with 3 per cent meta-phosphoric acid. Volume was made up to 100 ml and filtered. Ten ml of aliquot was titrated against 2, 6 -dichlorophenol indophenol dye. The dye factor was calculated by titrating standard ascorbic acid solution against dye and ascorbic acid content of sample was expressed as

$$\text{Ascorbic acid} = \frac{\text{Titre value} \times \text{dye factor} \times \text{volume made up}}{\text{Weight of the sample} \times \text{aliquot of the sample}} \times 100(\text{mg } 100\text{g}^{-1})$$

3.6.2.3 pH

Fruit pH was recorded at maturity stage of fruit by using digital pH meter.

Procedure for pH measurement

- The pH meter should be calibrated with the appropriate buffer solution such as pH 07.00, 04.00, and 09.20 to confirm the performance of the pH electrode before pH measurement. The process may look a little variation depending on the pH meter used and the electrode used however in most cases the pH determination process is very similar.
- Clean the electrode and temperature probe with deionized water and wipe gently with soft tissue paper.
- Immerse the electrode in the sample solution.
- Press the pH mode key which is on the board.
- The instrument will display the pH.
- Save the reading or print the reading if the printer is connected.

Reset the instrument and again clean the electrode and temperature probe with distilled water and wipe gently with soft tissue paper.

3.7 Statistical procedure

The replication wise mean values of five randomly selected plants from each genotype formed the basis for statistical analysis for different characters under study. The data was analysed statistically by analysis of variance for the randomized block design model suggested by Panse and Sukhatme (1985) was followed to test the significance of differences among the genotypes for all the characters under study.

3.7.1 Analysis of variance for the experimental design

The form of analysis of variance as given in Table 3.5 provides a comparison by partitioning of variance into various sources. The statistical model used for analysis of variance was based on the following linear model.

Replication	Treatment			Total	
	1	2	3	T	
1.	X ₁₁	X ₁₂	X ₁₃	X ₁	R ₁
2.	X ₂₁	X ₂₂	X ₂₃	X _{2t}	R ₂
3.	X ₃₁	X ₃₂	X ₃₃	X _{3t}	R ₃
r	Xr ₁	Xr ₂	Xr ₃	Xrt	Rr
Total	T ₁	T ₂	T ₃	T _t	GT

Model:

$$X_{ij} = \mu + t_i + b_j + \sigma_{ij}$$

Where, X_{ij} = Yield of j^{th} genotype from i^{th} replication.

μ = General mean

b_j = Effect of j^{th} replication

t_i = Effect of i^{th} genotype

σ_{ij} = Uncontrolled random error associated with j^{th} replication in i^{th} genotype

i = Number of genotypes (1, 2...60)

j = Number of replication (1, 2, 3)

$$\text{Grand mean} = \frac{(\text{Grand total})}{N}$$

Where, N = Total number of Treatment X Replication

$$\text{Correction factor} = \frac{(\text{Grand total})^2}{N}$$

Total Sum of Square = Sum square of each treatment – C.F

$$\text{Treatment Sum of Square} = \frac{\text{Sum of treatment square}}{\text{Number of Replication}} - C.F$$

$$\text{Replication mean of Square} = \frac{\text{Sum of replication square}}{\text{Treatment Number}} - C.F$$

Error Sum of Square = Total Sum of Square – (Treatment Sum of Square+ Replication Sum of Square)

Mean sums of squares were obtained by dividing the sum of squares with respective degree of freedom.

$$\text{'F' Variance ratio} = \frac{\text{Treatment Mean Sum of square}}{\text{Error Mean Sum of Square}}$$

The significance of treatment was tested by 'F' test by comparing the calculated 'F' value with the tabulated 'F' value at 5% level of significance for the corresponding degree of freedom. (Box, 1954). The analysis of variance was set up as follows:

Table 3.5: Analysis of variance for experimental design

Source	Degree of freedom	Mean sum of square	Expected mean square
Replications (r)	(r-1)	M_r	$\sigma^2_e + g \sigma^2_r$
Genotypes (g)	(g-1)	M_g	$\sigma^2_e + r \sigma^2_g$
Error	(r-1) (g-1)	M_e	σ^2_e
Total	(rg-1)		

Where,

r = Number of replications

g = Number of genotypes

M_r = Mean sum of square due to replications

M_g = Mean sum of square due to genotypes

M_e = Mean sum of square due to error

There, 'F' test was observed to be significant comparison was further extended by testing difference of any 2 treatment means against critical difference (CD) at 5% level of significance.

$$\text{Standard error of mean (S.E.m.)} = \sqrt{\frac{\sigma_e^2}{r}}$$

Where, σ_e^2 = Error mean square

r = Number of replications

Critical difference (CD) = S.E.m. $\times \sqrt{2}$ $\times t$ at error d.f (P= 0.05)

$$\text{Coefficient of variation (CV \%)} = \frac{\sqrt{\sigma_e^2}}{\bar{x}} \times 100$$

Where, σ_e^2 = Error mean square

$\bar{x}$ = Mean of character

3.7.2 Genetic parameters

3.7.2.1 Mean

This mean is the arithmetic average and is obtained when the sum of the values of individuals in the data is divided by the number of individuals in the data.

$$\bar{X} = \Sigma X / N$$

Where,

ΣX is the summation of the variables

N is the total number of observations.

3.7.2.2 Range

The range of distribution is the difference between the largest and the smallest of observations and gives some idea of the amount of variability present.

3.7.2.3 Standard error

S.E. of the mean was calculated with the help of error mean squares from ANOVA.

$$\text{S.E. (Mean)} = \frac{\sqrt{\frac{\sigma^2 e}{r}}}{\text{or } \sqrt{\frac{\text{Variance due to error}}{\text{Number of replication}}}}$$

3.7.3 Variability

Genotypic and Phenotypic variances were calculated as suggested by Johnson *et al.* (1955).

(a) Genotypic variance (σ^2_g) = $(M_g - M_e)/r$

(b) Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

However, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in percentage were calculated according to Burton and De Vane (1953).

3.7.3.1 Genotypic and Phenotypic coefficient of variation

(a) Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

(b) Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where, σ^2_p = Phenotypic variance

σ^2_g = Genotypic variance

$\bar{x}$ = General mean of the character under study

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were classified as suggested by Shivasubramanian and Menon (1973) as follows:

0-10 % = Low

10-20 % = Moderate

20 % and above = High

3.7.4 Heritability in broad sense (h^2_b)

It is the proportion of phenotypic variability that is due to genetic reasons. It was computed in per cent using the formula given by Allard (1960).

$$h^2_b(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Heritability percentage was categorized as demonstrated by Hanson *et al.* (1956).

0-30 % = Low

30-60 % = Moderate

> 60 % = High

3.7.5 Genetic advance

Genetic advance was estimated by using the method suggested by Johnson *et al.* (1955) and the formula is:

$$GA = K \times \frac{\sigma_g^2}{\sigma_p^2} \times \sigma_p$$

Where,

GA = Genetic advance,

K = Selection intensity (at 5% is 2.06),

h_b^2 = Heritability estimate,

σ_p = Phenotypic standard deviation.

The GA was categorized according to Johnson *et al.* (1955),

>50.1% = High,

20.1 - 50% = Moderate, and

< 20% = Low.

3.7.6 Genetic advance as per cent of mean

Genetic advance as a percentage of mean was calculated from the following formula as proposed by Johnson *et al.* (1955)

$$\text{Genetic advance over mean (\%)} = \frac{G.A}{\bar{X}} \times 100$$

3.7.7 Correlation and Path analysis

3.7.7.1. Analysis of covariance

The analysis of covariance was done adopting the formula at both genotypic and phenotypic co-variance were calculated as given below.

$$\text{Genotypic Covariance } xy = \frac{\text{TMP.XY} - \text{EMPXY}}{r}$$

$$\text{Error Covariance} = \text{EMPXY}$$

$$\text{Phenotypic Covariance XY} = \text{Genotypic Covariance XY} + \text{Error Covariance XY}$$

Where, TMP = Treatment mean sum of products

EMP = Error mean sum of products

R = No. of replication on XY being the two variables

3.7.7.2 Correlation coefficient

a. Genotypic correlation coefficient (r_{gij})

The genotypic correlation is chiefly caused by pleiotropy and the linkage action of gene and r_{gij} was estimated as suggested by Hazel *et al.* (1943).

$$r_{gij} = \frac{\sigma_{gij}}{\sqrt{\sigma_{gi}^2 \times \sigma_{gj}^2}}$$

Where,

r_{gij} = Genotypic correlation coefficient between i^{th} and j^{th} characters

σ_{gi}^2 = Genotypic variances of i^{th} character

σ_{gj}^2 = Genotypic variances of j^{th} character

σ_{gij} = Genotypic covariance between i^{th} and j^{th} character

b. Phenotypic correlation coefficient (r_{pipj})

The genetic and environmental causes of correlation combined together gives phenotypic correlation coefficient (r_{pipj}) and were estimated with help of following formula.

$$r_{pipj} = \frac{\sigma_{pipj}}{\sqrt{\sigma_{pi}^2 \times \sigma_{pj}^2}}$$

Where, r_{pipj} = Phenotypic correlation coefficient between i^{th} and j^{th} characters

σ_{pi}^2 = Phenotypic variances of i^{th} character

σ_{pj}^2 = Phenotypic variances of j^{th} character

σ_{pipj} = Phenotypic covariance between i^{th} and j^{th} character

The genotypic and phenotypic correlation coefficients were worked out for all possible pairs and were tested against standardized tabulated significant values of r with $(g-2)$ and $(rg-2)$ degree of freedom as per the procedure suggested by Fisher and Yates (1963).

3.7.8 Path coefficient analysis

The cause and effect, interrelationship between two variables cannot be estimated from the simple correlation coefficient analysis. Therefore, the path coefficient analysis was carried out according to the method suggested by Wright (1921) and used in plants by Dewey and Lu (1959). Genotypic correlation coefficients were used to estimate the path coefficients for the direct effects of various independent characters on fruit yield per plant.

The path coefficients were obtained by solving simultaneous equations which represent the basic relationship between correlation and path coefficient.

$$r_{ny} = P_{ny} + r_{n2}P_{2y} + r_{n3}P_{3y} + \dots + r_{nx}P_{xy}$$

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{bmatrix} = \begin{bmatrix} 1 & r_{12} & \dots & r_{1n} \\ r_{21} & 1 & \dots & r_{2n} \\ r_{n1} & r_{n2} & \dots & 1 \end{bmatrix} \begin{bmatrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{bmatrix}$$

[A] [B] [C]

Where, [A] = Correlation matrix between yield and biometrical characters

[B] = Correlation matrix between different biometrical characters

[C] = Path coefficient matrix where $P_{1y}, P_{2y}, \dots, P_{ny}$

The value of [C] matrix can be obtained as under,

$$[A] = [B] [C]$$

Thus,

$$[B]^{-1} [A] = [C]$$

The path value means the direct effects were calculated as follows,

$$P_{iy} = \sum c_i l_{riy}$$

The indirect effects of a particular character through other characters were obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

$$\text{Indirect effect} = r_{ij} \times p_{ij}$$

Where, i and j = 1 to n

The residual effect is a composite variable that includes all other unaccounted factors affecting fruit yield per plant in this study and is assumed to be independent of the remaining variables. It was calculated as under.

$$\text{Residual effect (x)} = (1-R^2)^{0.5}$$

Where,

$$R^2 = p_{1y}r_{1y} + p_{2y}r_{2y} + \dots + p_{ny}r_{ny}$$

Path coefficient analysis was categorized as suggested by Lenka and Mishra (1973).

0.00 to 0.09 = Negligible

0.10 to 0.19 = Low

0.20 to 0.29 = Moderate

0.30 to 0.99 = High

More than 1.00 = Very high

3.7.9 Genetic divergence through D^2 analysis

Morphological diversity analysis of all the sixteen characters under study was made on the basis of mean values. The data recorded for various characters were subjected to analysis of variance and Mahalanobis D^2 statistics for estimation of morphological diversity with the help of Spar 1 software.

3.7.9.1 Mahalanobis D^2 statistics

Rao (1952) described the multivariate analysis of genetic divergence using Mahalanobis D^2 Statistics. Transformation of the original mean of various characters

(X_1 's) to uncorrelated variable (Y_1 's) was carried out by computer. This made D^2 value as a simple sum of squares of differences in transformed values for various characters. The generalized distance between any two populations is defined as under

$$pD^2 = b_1d_1 + b_2d_2 + b_3d_3 + \dots + b_p d_p$$

Where,

$X_1, X_2, X_3, \dots, X_p$ as a multiple measurements available on each individual
 $d_1, d_2, d_3, \dots, d_p$ as $X_1^{-1} - X_1^{-2}, X_2^{-1} - X_2^{-2}, \dots, X_p^{-1} - X_p^{-2}$, respectively, being the difference in the mean values of two population.

In terms of variance and covariance, the D^2 value is obtained as follows:

$$PD^2 = W_{ij} (X_i^{-1} - X_i^{-2}) (X_j^{-1} - X_j^{-2})$$

Where, W_{ij} is the inverse estimate variance covariance matrix.

3.7.9.2 Group constellation based on D^2 values

Grouping of the genotypes in different cluster was done by using Tocher's method (Rao, 1952). The criterion used in clustering in this method is that any two genotypes belonging to the same cluster should on an average show a smaller D^2 values than those belonging to different clusters. To start with, two genotypes having the lowest D^2 values between them were considered, to which a third genotype having next the smallest D^2 value from these genotypes was added. Next, the nearest fourth genotype was considered and so on. At a certain stage, when it was felt that the inclusion

of a genotype results in an abrupt increase in the average D^2 value of the genotypes (for that cluster), that genotype was not included in the cluster. In a similar way the other clusters were formed. This procedure was continued till all the genotypes were included in one cluster or the other. After the formation of the clusters, average intra-cluster distance (D) was calculated by using the formula

$$D = \Sigma D_i^2 / N$$

Where, ΣD_i^2 = Sum of distance between all possible combination of the populations included in the cluster

N = Number of populations in the cluster

The intra-cluster distance was calculated by measuring the distance between cluster I and cluster II, between cluster II and cluster III and so on. Likewise, one by one cluster was taken and their distances from other clusters were calculated.

3.7.9.3 Estimation of intra-cluster and inter-cluster variances for different characters

Unweighted analysis of variance using the mean values of different characters was carried out. The format of analysis of variance is given below.

Source of variation	Degree of freedom	Mean sum of square	Expected mean square
Between cluster	$K - 1$	M1	$\sigma^2_w + \sigma^2_b$
Within cluster	$\Sigma n_i - k$	M2	σ^2_w

Where, K = Number of clusters

n_i = Number of genotypes in i^{th} cluster and

$$M = \Sigma n_i - (\Sigma n_i^2 / \Sigma n_i) / K - 1$$

Using the mean square estimates of intra-cluster and inter-cluster variance i.e., σ^2_w and σ^2_b were obtained for each of the clusters.

In addition to this, the ratio of the inter cluster variance to the total variance was obtained as under.

$R^2 = \sigma^2_b / (\sigma^2_w + \sigma^2_b)$ Where, σ^2_b = Variance between clusters

σ^2_w = Variance within cluster

And, inter-cluster coefficient of variation was calculated as

$$CV_b = \frac{\sqrt{\sigma^2_b}}{\bar{X}} \times 100$$

Where, $\bar{X}$ = General mean for the character

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EXPERIMENTAL FINDINGS

The experimentation results of the research are presented in the following tables and illustration. The data recorded for the fourteen characters for fifteen genotypes of the brinjal which were tested statistically. The result is presented under the following heads.

4.1 Analysis of variance

The analysis of variance for RBD in respect to sixteen characters (Table 4.1) which shows highly significant results for characters viz., plant height, plant spreading (both direction), number of primary branches, fruit length, fruit width, number of fruits per plant, average fruit weight, fruit yield per plant, fruit yield per hectare at one percent level of significance which indicated the existence of variability in the experimental material.

4.2 Mean performance

The mean values of all characters for seventeen genotypes as follows and depicted in table from 4.2 to 4.8

4.2.1 Plant height (cm)

Growth and vigour of plant is determined by its height. The maximum value of plant height was found in genotype Arka Keshav (96.36) followed by JB 9 (95.72) and the minimum value was found in genotype IVB-2 (58.72). The grand mean value was 82.87 and coefficient of variance was 1.62.

4.2.2 Number of primary branches per plant

The number of primary branches per plant also have some effect on yield trait. The highest number of primary branches per plant was observed in variety Sobha (10.03) followed by IVB-2 (9.40), whereas lowest number of branches per plant was recorded in variety HABR-4 (4.60). The value of grand mean was 8.15 and coefficient of variance value was 9.27.

Table 4.1: ANOVA table for various characters in brinjal genotypes

Sl.No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	14	28
1	Plant height (cm)	5.6050	417.863**	1.793
2	Plant spread (East-West) (cm)	4.0310	204.879**	4.721
3	Plant spread (North-South) (cm)	3.710	218.445**	5.57
4	No. of primary branches per plant	0.6690	5.19**	0.572
5	Fruit length (cm)	0.1350	20.499**	0.366
6	Fruit width (cm)	0.3640	6.796**	0.251
7	Average fruit weight (g)	131.8250	2933.663**	70.507
8	No. of fruits per plant	8.1170	158.987**	2.754
9	Chlorophyll content	1.3830	787.668**	6.025
10	Total soluble solids (°Brix)	0.150	0.476**	0.091
11	Ascorbic acid content (mg/100gm)	1.1670	281.242**	1.248
12	No. of seeds per fruit	1357.6350	618695.945**	8739.522
13	Test weight (g)	0.0110	4.591**	0.14
14	Fruit yield/plant (kg)	0.0010	1.247**	0.029
15	Fruit yield (q/ha)	34.1870	22749.105**	490.534
16	pH	0.0470	0.412**	0.031

**** Significant at 1 per cent probability level**

4.2.3 Plant spread (East-West) (cm)

Highest plant spread in the direction of East-West was found in variety NBH-1156 (89.47) followed by UR-11 (84.66) and minimum was observed in genotype IVB-2 (61.85). The grand mean and coefficient of variance was 73.67 and 2.95 respectively.

4.2.4 Plant spread (North-South) (cm)

Highest plant spread in the direction of North-South was found in variety UR-11 (83.23) followed by HABR-4 (79.62) and minimum was observed in genotype IVB-2 (50.63). The grand mean and coefficient of variance was 68.28 and 3.46 respectively.

4.2.5 Fruit length (cm)

The length of fruit also determines the yield. The maximum value was recorded in genotype HABR-4 (14.20) followed by Green Long (13.54). The minimum value was recorded variety IVB-2 (5.94) and KS-331 (6.76). The value of grand mean and coefficient of variance was 10.64 and 5.68 respectively.

4.2.6 Fruit width (cm)

The highest value for this trait was recorded in genotype KS-331 (8.08) followed by NBH-1156 (7.33), whereas the lowest value of fruit width was found in variety PPL-Nepal (2.39). The grand mean value in this character was 4.64 and coefficient of variance was 10.78.

4.2.7 Average fruit weight (g)

Average fruit is an important component of good yield. The genotype NBH-1156 (166.16) had the highest fruit weight, followed by KS-331 (165.03). The genotype annamalai had the lowest fruit weight (61.39). The coefficient of variance was 7.54 and the grand mean was 111.32.

4.2.8 Number of fruits per plant

The number of fruits also determine the total yield of crop. The high value was obtained in genotype Arka Keshav (38.77) followed by Green Long (31.27), whereas lowest values found in variety KS 331 (11.53). The grand mean and coefficient of variance was 22.01 and 7.54 respectively.

Table 4.2: Mean performances for plant height and number of primary branches per plant of fifteen genotypes of brinjal

Sl. No.	Genotype	Plant height (cm)	Number of primary branches per plant
1	HABR 4	82.18	4.60
2	JB 9	95.72	8.40
3	UR 11	85.88	8.33
4	JBL 03 04	94.62	8.20
5	Green Long	92.18	8.00
6	Sobha	71.32	10.03
7	SEP 034	86.63	8.33
8	Arka Keshav	96.36	8.47
9	NBJ 19	79.74	7.07
10	NBH 1156	81.29	9.67
11	Punjab Nagina	93.56	7.73
12	PPL-Nepal	62.09	9.33
13	Annamalai	87.57	7.40
14	IVB 2	58.72	9.40
15	KS 331	75.27	7.33
	Mean	82.87	8.15
	CV	1.62	9.27
	SEm $\pm$	0.77	0.44
	CD at 5%	2.24	1.26
	CD at 1%	3.02	1.71

Table 4.3: Mean performances for plant spread in both direction of fifteen genotypes of brinjal

Sl. No.	Genotype	Plant Spread (East-West) (cm)	Plant Spread (North-South) (cm)
1	HABR 4	80.69	79.62
2	JB 9	65.99	59.54
3	UR 11	84.66	83.23
4	JBL 03 04	69.73	64.39
5	Green Long	78.51	74.48
6	Sobha	72.37	72.38
7	SEP 034	83.19	75.69
8	Arka Keshav	74.59	66.40
9	NBJ 19	73.08	63.11
10	NBH 1156	89.47	73.78
11	Punjab Nagina	65.70	63.68
12	PPL-Nepal	75.72	70.54
13	Annamalai	64.43	60.28
14	IVB 2	61.85	50.63
15	KS 331	66.45	66.43
	Mean	73.76	68.28
	CV	2.95	3.46
	SEm±	1.25	1.36
	CD at 5%	3.63	3.95
	CD at 1%	4.9	5.32

Table 4.4: Mean performances for fruit length and fruit width of fifteen genotypes of brinjal

Sl. No.	Genotype	Fruit length (cm)	Fruit width (cm)
1	HABR 4	14.20	4.73
2	JB 9	11.16	4.07
3	UR 11	13.71	4.69
4	JBL 03 04	12.25	4.32
5	Green Long	13.54	3.95
6	Sobha	8.47	5.57
7	SEP 034	12.32	4.16
8	Arka Keshav	12.95	3.71
9	NBJ 19	9.50	5.09
10	NBH 1156	8.26	7.33
11	Punjab Nagina	11.98	4.60
12	PPL-Nepal	9.34	2.39
13	Annamalai	9.28	2.52
14	IVB 2	5.94	4.45
15	KS 331	6.76	8.08
	Mean	10.64	4.64
	CV	5.68	10.78
	SEm $\pm$	0.35	0.29
	CD at 5%	1.01	0.84
	CD at 1%	1.36	1.13

Table 4.5: Mean performances for average fruit weight and number of fruits per plant of fifteen genotypes of brinjal

Sl. No.	Genotype	Average fruit weight (g)	Number of fruits per plant
1	HABR 4	128.03	16.50
2	JB 9	114.44	26.43
3	UR 11	122.61	17.80
4	JBL 03 04	127.89	24.07
5	Green Long	79.59	31.27
6	Sobha	113.36	26.20
7	SEP 034	83.19	24.73
8	Arka Keshav	111.16	38.77
9	NBJ 19	131.20	18.67
10	NBH 1156	166.17	15.13
11	Punjab Nagina	101.47	16.93
12	PPL-Nepal	64.59	20.67
13	Annamalai	61.39	27.00
14	IVB 2	99.68	14.40
15	KS 331	165.03	11.53
	Mean	111.32	22.01
	CV	7.54	7.54
	SEm±	4.85	0.96
	CD at 5%	14.04	2.78
	CD at 1%	18.94	3.74

4.2.9 Chlorophyll content

The maximum value of chlorophyll content was found in genotype Sobha (99.19 spad meter), followed by Green Long (97.99 spad meter), while the lowest value was reported in JBL 03 04 (45.17 spad meter). This character's grand mean value was 82.02 and its coefficient of variance was 2.99.

4.2.10 Total soluble solid (°Brix)

The highest value for this trait was observed in genotype Punjab Nagina (6.03) followed by PPL-Nepal (5.40). The lowest value of total soluble solids recorded in variety Arka Keshav (4.40). The grand mean was 5.09 and coefficient of variance was 5.92.

4.2.11 Ascorbic acid content (mg/100g)

The highest ascorbic acid content was found in genotype JBL 03 04 (46.91) followed by Green Long (45.48), while the lowest was found in PPL-Nepal (11.37). The grand mean and coefficient of variance was 30.29 and 3.69 respectively.

4.2.12 pH

The genotype HABR-4 (7.62) had the highest pH value, followed by KS-331 (7.47), while NBJ-19 had the lowest pH value (6.50). 6.85 and 2.55, respectively were the grand mean and coefficient of variance for this trait.

4.2.13 Number of seeds per fruit

The highest number of seeds per fruit was observed in genotype Punjab Nagina (1833.20) followed by KS 331 (1738.10). The lowest value was observed in variety Green Long (348.21). The grand mean value was 1034.29 and coefficient of variance was 9.04 for this trait.

4.2.14 Test weight (g)

The highest value for this trait was recorded in genotype Annamalai (6.47) followed by IVB-2 (6.37). The lowest value was observed in genotype PPL-Nepal (3.17). The grand mean and coefficient of variance was 4.70 and 7.96, respectively for test weight.

Table 4.6: Mean performance for chlorophyll content and total soluble solids in fifteen genotypes of brinjal

Sl. No.	Genotype	Chlorophyll Content	Total soluble solids (°Brix)
1	HABR 4	95.15	4.87
2	JB 9	96.58	5.07
3	UR 11	83.96	4.83
4	JBL 03 04	45.17	4.60
5	Green Long	97.99	4.67
6	Sobha	99.19	5.27
7	SEP 034	97.32	5.20
8	Arka Keshav	83.33	4.40
9	NBJ 19	66.59	5.23
10	NBH 1156	95.46	5.33
11	Punjab Nagina	71.92	6.03
12	PPL-Nepal	83.85	5.40
13	Annamalai	69.52	4.90
14	IVB 2	60.57	5.30
15	KS 331	83.68	5.23
	Mean	82.02	5.09
	CV	2.99	5.92
	SEm±	1.42	0.17
	CD at 5%	4.11	0.5
	CD at 1%	5.54	0.68

Table 4.7: Mean performance of ascorbic acid and pH of fifteen genotypes of brinjal

Sl. No.	Genotype	Ascorbic acid (mg/100g)	pH
1	HABR 4	23.36	7.62
2	JB 9	35.72	6.83
3	UR 11	23.64	6.80
4	JBL 03 04	46.91	6.53
5	Green Long	45.48	6.50
6	Sobha	35.80	6.60
7	SEP 034	23.53	6.68
8	Arka Keshav	34.26	6.65
9	NBJ 19	35.72	6.50
10	NBH 1156	22.82	7.16
11	Punjab Nagina	22.97	7.07
12	PPL-Nepal	11.37	6.58
13	Annamalai	34.82	6.52
14	IVB 2	23.01	7.21
15	KS 331	34.92	7.47
	Mean	30.29	6.85
	CV	3.69	2.55
	SEm±	0.64	0.1
	CD at 5%	1.87	0.29
	CD at 1%	2.52	0.39

Table 4.8 Mean performance for number of seeds per fruit and test weight in fifteen genotypes in brinjal

Sl. No.	Genotype	Number of seeds per fruit	Test weight (g)
1	HABR 4	1107.30	6.23
2	JB 9	1669.73	3.37
3	UR 11	1249.65	4.27
4	JBL 03 04	643.35	5.29
5	Green Long	348.21	3.43
6	Sobha	677.15	6.17
7	SEP 034	1028.88	3.97
8	Arka Keshav	970.39	3.23
9	NBJ 19	1073.39	4.40
10	NBH 1156	972.93	5.80
11	Punjab Nagina	1832.53	3.87
12	PPL-Nepal	1141.43	3.17
13	Annamalai	625.75	6.47
14	IVB 2	434.90	6.37
15	KS 331	1738.10	4.43
	Mean	1034.29	4.7
	CV	9.04	7.96
	SEm±	53.97	0.22
	CD at 5%	156.36	0.63
	CD at 1%	210.92	0.84

Table 4.9 Mean performance for fruit yield per plant and fruit yield (q/ha) in fifteen genotypes of brinjal

Sl. No.	Genotype	Fruit yield per plant (kg)	Fruit yield (q/ha)
1	HABR 4	2.12	286.52
2	JB 9	2.90	391.54
3	UR 11	2.22	299.84
4	JBL 03 04	3.09	416.80
5	Green Long	2.52	340.14
6	Sobha	1.89	255.19
7	SEP 034	1.97	265.74
8	Arka Keshav	3.22	434.89
9	NBJ 19	2.44	332.42
10	NBH 1156	1.14	153.84
11	Punjab Nagina	1.66	224.18
12	PPL-Nepal	1.25	168.88
13	Annamalai	1.73	233.89
14	IVB 2	1.37	184.26
15	KS 331	1.86	251.21
	Mean	2.09	282.62
	CV	8.18	7.84
	SEm $\pm$	0.1	12.79
	CD at 5%	0.29	37.04
	CD at 1%	0.39	49.97

4.2.15 Fruit yield per plant (kg)

Effective crop improvement programme helps to increase the yield. High yield leads to increase the income of the grower. The highest fruit yield was recorded in genotype Arka Keshav (3.22 kg) followed by JBL-03-04 (3.09 kg), while the lowest value was found in NBH 1156 (1.14 kg). The grand mean and coefficient of variance was 2.09 and 8.18, respectively for this trait.

4.2.16 Fruit yield (q/ha)

Productivity of a crop is determined by its yield in per unit area. The highest fruit yield was recorded in genotype Arka Keshav (434.89 q/ha) followed by JB-9 (391.54 q/ha), while the lowest value was found in NBH 1156 (153.84 q/ha). The grand mean and coefficient of variance was 282.62 and 7.84, respectively for this trait.

Fig 4.1: Variability in fifteen genotypes of brinjal fruits



HABR-4



JB 9



UR 11



JBL 03 04



Green Long



Sobha



NBH 1156



SEP 034



Arka Keshav



NBJ 19



Punjab Nagina



PPL Nepal



Annamalai



IVB 2



KS 331

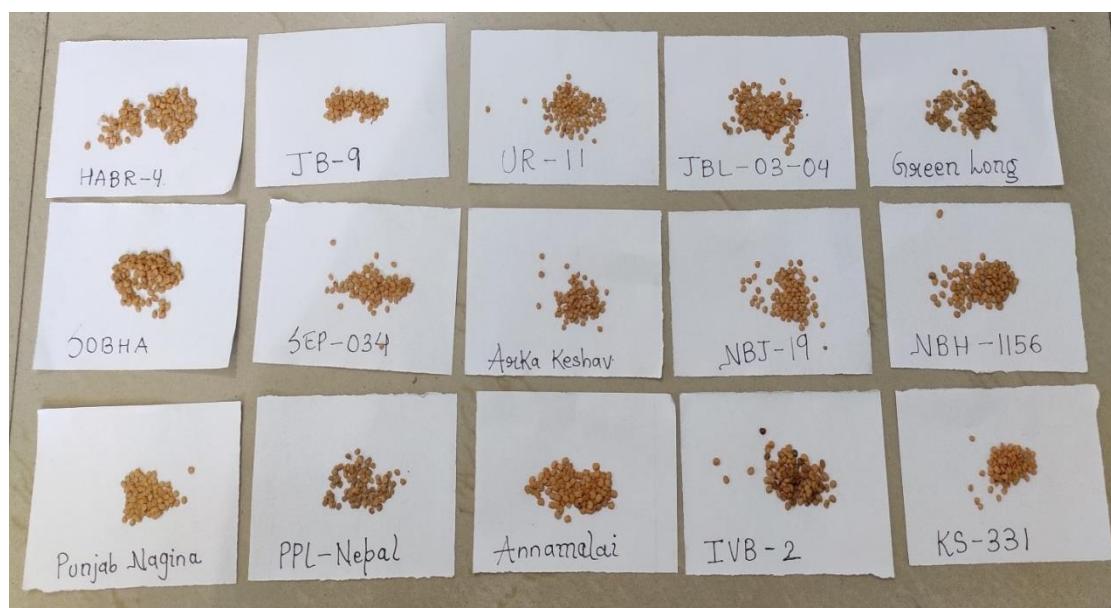


Figure 4.2: 100 seed of fifteen genotypes of brinjal

4.3 Variability

From variance components and mean values, range, the variability parameters heritability in the broad sense (h^2_b), genotypic coefficient of variation (GCV percent), phenotypic coefficient of variation (PCV percent) and genetic progress as a percent of mean were calculated. Table 4.10 summarises all of these estimations.

4.3.1 Range

The fifteen brinjal genotypes tested for sixteen traits showed a wide range of variance. The genotypes performance demonstrated that, the range for plant height varied from 58.72 (IVB-2) to 96.36 (Arka Keshav). The range of plant spread (East-West) varied from 61.85 (IVB-2) to 89.47 (NBH-1156) while the plant spread (North-South) varied from 50.63 (IVB-2) to 89.47 (UR-11). In case of number of primary branches per plant ranged from 4.60 (HABR-4) to 10.03 (Sobha). The range of fruit length varied from 5.94 (IVB-2) to 14.20 (HABR-4) while the fruit width varied from 2.39 (PPL-Nepal) to 8.08 (KS-331). The range of average fruit weight varied from 61.39 (Annamalai) to 166.16 (NBH-1156). Range of number of fruits per plant varied from 11.53 (KS-331) to 38.77 (Green long). The range of variation in chlorophyll content varied from 45.17 (JBL-03-04) to 99.19 (Sobha). The range for total soluble solids varied from 4.40 (Arka Keshav) to 6.03 (Punjab Nagina). The range for ascorbic acid content varied from 11.37 (PPL-Nepal) to 46.91 (JBL-03-04). The range of pH

varied from 6.50 (NBJ-19) to 7.62 (HABR-4). In case of number of seeds per fruit, the range varied from 348.21 (Green long) to 1833.20 (Punjab Nagina). The range of test weight varied from 3.17 (PPL-Nepal) to 6.47 (Annamalai). The range for fruit yield per plant varied from 1.14 (NBH-1156) to 3.22 (Arka Keshav) while fruit yield per hectare showed variation from 153.84 (NBH-1156) to 434.89 (Arka Keshav).

4.3.2 Genotypic coefficient of variation

The genotypic coefficient of variation for various traits varied from 43.60% (number of seeds per fruit) to 5.21% (pH). High genotypic coefficient of variation was observed for number of seeds per fruit (43.60) followed by number of fruits per plant (32.79), ascorbic acid content (31.90), fruit width (31.81), fruit yield (q/ha) (30.48), fruit yield per plant (30.47), average fruit weight (27.75), test weight (25.93) and fruit length (24.34). On the other hand, low genotypic coefficient of variation was observed for pH (5.21) and total soluble solids (7.04). The traits chlorophyll content (19.68), number of primary branches per plant (15.22), plant height (14.21), plant spread (North-West) (12.34) and plant spread (East-West) (11.07) exhibited moderate values of genotypic coefficient of variation which means that the extent of genetic variation observed was somewhat less for these characters among genotypes studied.

4.3.3 Phenotypic coefficient of variation

Number of seeds per fruit (44.52) had the highest phenotypic coefficient of variation, followed by number of fruits per plant (33.65), fruit width (33.58), ascorbic acid content (32.11), fruit yield per plant (31.55), fruit yield (q/ha) (31.47), average fruit weight (28.76), test weight (27.13) and fruit length (24.99). The genotypic coefficient of variation for the traits like chlorophyll content (19.91), number of primary branches per plant (17.82), plant height (14.30), plant spread (North-South) (12.81) and plant spread (East-West) (11.46) were moderate, whereas on the other hand, pH (5.80) and total soluble solids (9.20) had a lowest genotypic coefficient of variation.

For all of the characters, the PCV was larger than the equivalent GCV, which might be owing to some genotype-environment interaction or a greater effect of environmental influences on the expression of these features.

4.3.4 Heritability

The experiment showed a wide range of heritability for different characters. The highest heritability was observed in plant height (98.72) followed by ascorbic acid content (98.68), chlorophyll content (97.74), number of seeds per fruit (95.88), number of fruits per plant (94.98), fruit length (94.83), fruit yield (q/ha) (93.80), plant spread (East-West) (93.39), fruit yield per plant (93.28), average fruit weight (93.12), plant spread (North-South) (92.72), test weight (91.38), fruit width (89.70), pH (80.62) and number of primary branches per plant (72.93), whereas moderate heritability was seen in total soluble solids (58.61).

4.3.5 Genetic advance

In case of genetic advance, wide range was being observed for all characters varied from 0.57 to 909.53. The high value was recorded in number of seeds per fruit (909.53) followed by fruit yield (171.85) and average fruit weight (61.41), while the moderate value was observed in chlorophyll content (32.87) followed by plant height (24.11) and the lowest value was recorded in total soluble solids (0.57).

4.3.6 Genetic advance expressed as percentage of mean

The predicted genetic advance with regard to sixteen characteristics was estimated at a selection intensity of 5%, but the expected genetic advance expressed as a percentage of mean for all traits was also calculated and provided in Table 4.10 for comparison. Genetic advance expressed as percentage of mean ranged from 9.63 (pH) to 87.94 (number of seed per fruit). These values were found higher in magnitude for number of seeds per fruit (87.94) followed by number of fruits per plant (65.83), ascorbic acid content (65.27), fruit width (62.06), fruit yield (60.81), fruit yield per plant (60.62), average fruit weight (55.17), test weight (51.07), fruit length (48.83), chlorophyll content (40.08), plant height (29.09), number of primary branches (26.77), plant spread (North-South) (24.47) and plant spread (East-West) (22.05) while moderate value showed in total soluble solids (11.11). Whereas, pH (9.63) exhibited lowest genetic advance expressed as percentage of mean.

Table 4.10: Estimate of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic gain for 15 different genotypes of brinjal

Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic gain (%)
Plant height (cm)	58.72-96.36	82.87	14.21	14.30	98.72	24.11	29.09
Plant spread (East-West) (cm)	61.85-89.47	73.76	11.07	11.46	93.39	16.26	22.05
Plant spread (North-South) (cm)	50.63-83.23	68.28	12.34	12.81	92.72	16.71	24.47
No. of primary branches per plant	4.60-10.03	10.64	15.22	17.82	72.93	2.18	26.77
Fruit length (cm)	5.94-14.20	10.64	24.34	24.99	94.83	5.20	48.83
Fruit width (cm)	2.39-8.08	4.64	31.81	33.58	89.70	2.88	62.06
Average fruit weight (g)	61.39-166.17	111.32	27.75	28.76	93.12	61.41	55.17
No. of fruits per plant	11.53-38.77	22.01	32.79	33.65	94.98	14.49	65.83
Chlorophyll content	45.17-99.19	82.02	19.68	19.91	97.74	32.87	40.08
Total soluble solids (°Brix)	4.40-6.03	5.09	7.04	9.20	58.61	0.57	11.11
Ascorbic acid content (mg/100gm)	11.37-46.91	34.92	31.90	32.11	98.68	19.77	65.27
No. of seeds/fruit	348.21-1833.20	1034.29	43.60	44.52	95.88	909.53	87.94
Test weight (g)	3.17-6.47	4.70	25.93	27.13	91.38	2.40	51.07
Fruit yield per plant (kg)	1.14-3.22	2.09	30.47	31.55	93.28	1.27	60.62
Fruit yield (q/ha)	153.84-434.89	282.62	30.48	31.47	93.80	171.85	60.81
pH	6.50-7.62	6.85	5.21	5.80	80.62	0.66	9.63

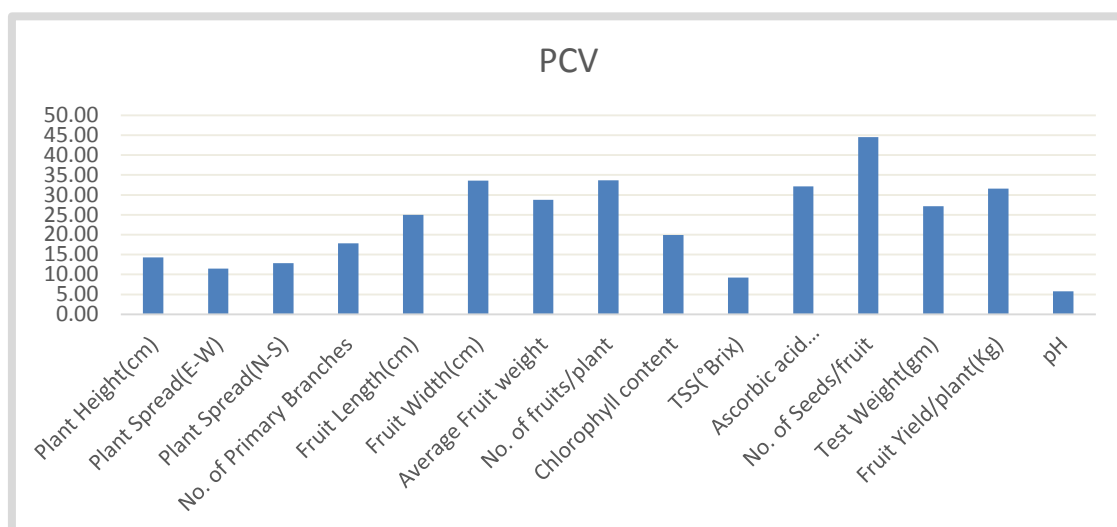


Figure 4.3: Graphical representation of phenotypic coefficient of variation

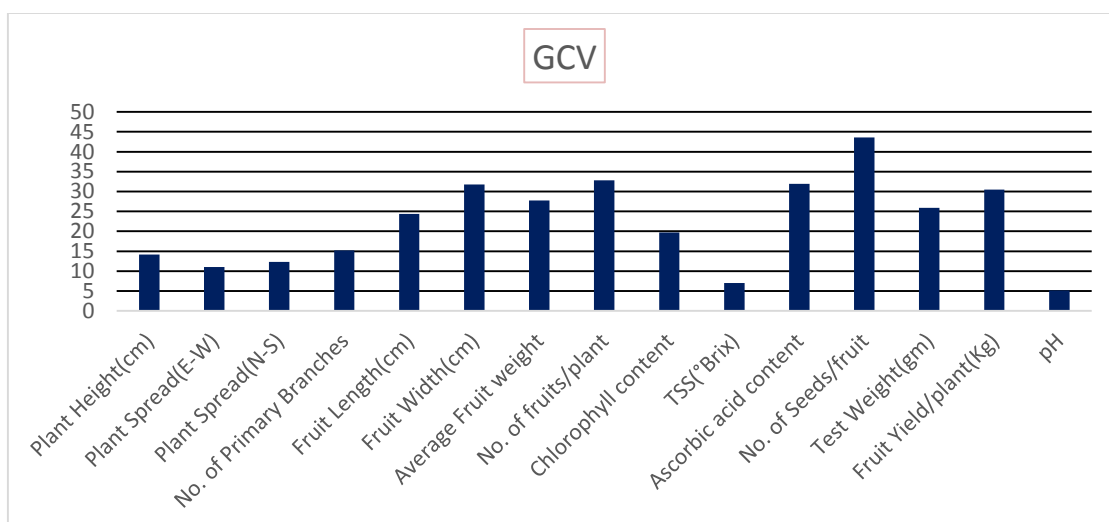


Figure 4.4: Graphical representation of genotypic coefficient of variation

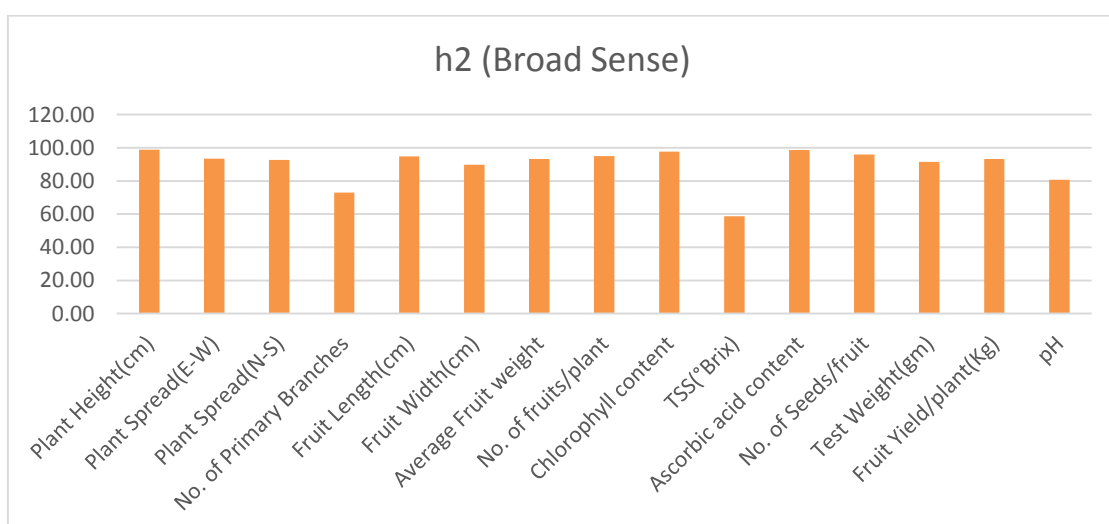


Figure 4.5: Graphical representation of broad sense heritability

4.4 Correlation coefficient analysis

In a breeding programme, association analysis is a critical component. It defines the component traits, on which selection may be utilised for genetic improvement in fruit production, and it offers an understanding of the kind and size of association among the various features. The efficacy of the selecting process is influenced by the degree of association.

The phenotypic correlation is the relationship between the features that may be seen directly. The ability to understand the phenotypic link between yield contributing features aids in the development of a crop selection programme. The genotypic correlation is useful in the design of selection indices since it allows for the prediction of correlated responses as well as the evaluation of the relative effect of one character on the other.

To determine the relationship between fruit production per plant and other yield contributing factors, phenotypic and genotypic correlation coefficients (Table 4.11 and Table 4.12) were calculated for sixteen characters using fifteen brinjal genotypes.

4.4.1 Genotypic correlation coefficient

The data on genotypic correlation coefficient for different fifteen characters of brinjal genotypes are presented in Table 4.11.

Plant height exhibited positive and significant correlation with fruit length (0.719), fruit yield per plant (0.709), number of fruits per plant (0.527) and ascorbic acid content (0.519). It had negative and significant correlation with total soluble solids (-0.437), test weight (-0.355) and number of primary branches per plant (-0.325),

It was reported that plant spread (East-West) was positively and significantly correlated with plant spread (North-South) (0.867), chlorophyll content (0.551) and fruit length (0.435). Plant spread (North-South) had positive and significant correlation with plant spread (East-West) (0.867), chlorophyll content (0.608) and fruit length (0.579).

Negative and significant correlation of number of primary branches per plant was observed with fruit length (-0.468), pH (-0.441) and plant height (-0.325).

Fruit length showed positive and significant correlation with plant height (0.719), fruit yield per plant (q/ha) (0.594), plant spread (North-South) (0.579), number of fruits per plant (0.455) and plant spread (East-West) (0.435). It had negative and significant correlation with total soluble solids (-0.487), number of primary branches per plant (-0.468), test weight (-0.403) and fruit width (-0.388).

A positive and significant correlation for fruit width was observed for average fruit weight (0.920), pH (0.612) and number of seeds per fruit (0.319). It showed negative and significant correlation for number of fruits per plant (-0.580) and fruit length (-0.388).

Average fruit weight was positively and significantly correlated with fruit width (0.920), pH (0.587) and number of seeds per fruit (0.356). It had a negative and significant correlation with number of fruits per plant (-0.580).

The number of fruits per plant was positively and significantly correlated with fruit yield (q/ha) (0.647), plant height (0.527), ascorbic acid content (0.471) and fruit length (0.455). It had negative and significant correlation with pH (-0.711), total soluble solids (-0.684), fruit width (-0.580), average fruit weight (-0.476) and number of seeds per fruit (-0.372), test weight (-0.369).

Positive and significant correlation of chlorophyll content was observed with plant spread (North-South) (0.608) and plant spread (East-West) (0.551).

Total soluble solids were positively and significantly correlated with number of seeds per fruit (0.533) and pH (0.306). It showed negative and significant correlation with fruit yield (-0.789), number of fruits per plant (-0.684), ascorbic acid content (-0.605), fruit length (-0.487) and plant height (-0.437).

Fruit yield (q/ha) (0.718), plant height (0.519) and number of fruits per plant (0.471) all showed a positive and significant association with ascorbic acid. At the genotypic level, ascorbic acid had a negative and significant correlation with total soluble solids (-0.684), pH (-0.390) and number of seeds per fruit (-0.309).

Number of seeds per fruit revealed positive and significant correlation with total soluble solids (0.533) and fruit width (0.319) and it showed a negative and significant correlation with test weight (-0.447), pH (-0.444), number of fruits per plant (-0.372) and ascorbic acid content (-0.309).

Table 4.11 Genotypic correlation of various character of brinjal

Genotypical Correlation Matrix															
	Plant height (cm)	Plant spread (East-West) (cm)	Plant spread (North-South) (cm)	No. of primary branches per plant	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits per plant	Chlorophyll content	Total soluble solids (°Brix)	Ascorbic acid content (mg/100g)	No. of seeds per fruit	Test weight (g)	pH	Fruit yield per plant (kg)
Plant height (cm)	1.0000	0.1047	0.1513	-0.325*	0.719**	-0.1410	0.0364	0.527**	0.0402	-0.437*	0.519**	0.1959	-0.355*	-0.2540	0.709**
Plant spread (East-West) (cm)		1.0000	0.867**	0.0189	0.435*	0.1871	0.2188	0.0121	0.551**	-0.1956	-0.2859	-0.0905	-0.1165	0.0080	-0.0824
Plant spread (North-South) (cm)			1.0000	-0.1920	0.579**	0.1605	0.1414	0.0116	0.608**	-0.2288	-0.1982	0.0665	-0.1361	0.0563	-0.0060
No. of primary branches per plant				1.0000	-0.468*	0.0354	-0.1029	0.1739	0.0394	0.1686	-0.1211	-0.2553	-0.0776	-0.441*	-0.2662
Fruit length(cm)					1.0000	-0.388*	-0.1874	0.455*	0.2099	-0.487**	0.1501	0.0540	-0.403*	-0.2013	0.594**
Fruit width(cm)						1.0000	0.920**	-0.580**	0.1887	0.2695	0.0885	0.319*	0.2387	0.612**	-0.1922
Average fruit weight (g)							1.0000	-0.476**	0.0223	0.0247	0.1405	0.356*	0.1960	0.587**	0.0746
No. of fruits per plant								1.0000	0.1756	-0.684**	0.471*	-0.372*	-0.369*	-0.711**	0.647**
Chlorophyll content									1.0000	0.0076	-0.2009	0.1750	-0.2274	0.1586	-0.1243
Total soluble solids (°Brix)										1.0000	-0.605**	0.533**	0.0379	0.306*	-0.789**
Ascorbic acid content (mg/100g)											1.0000	-0.309*	0.0164	-0.390*	0.718**
No. of seeds per fruit												1.0000	-0.447*	0.444*	-0.0297
Test weight (g)													1.0000	0.332*	-0.381*
pH														1.0000	-0.355*
Fruit yield per plant (kg)															1.0000

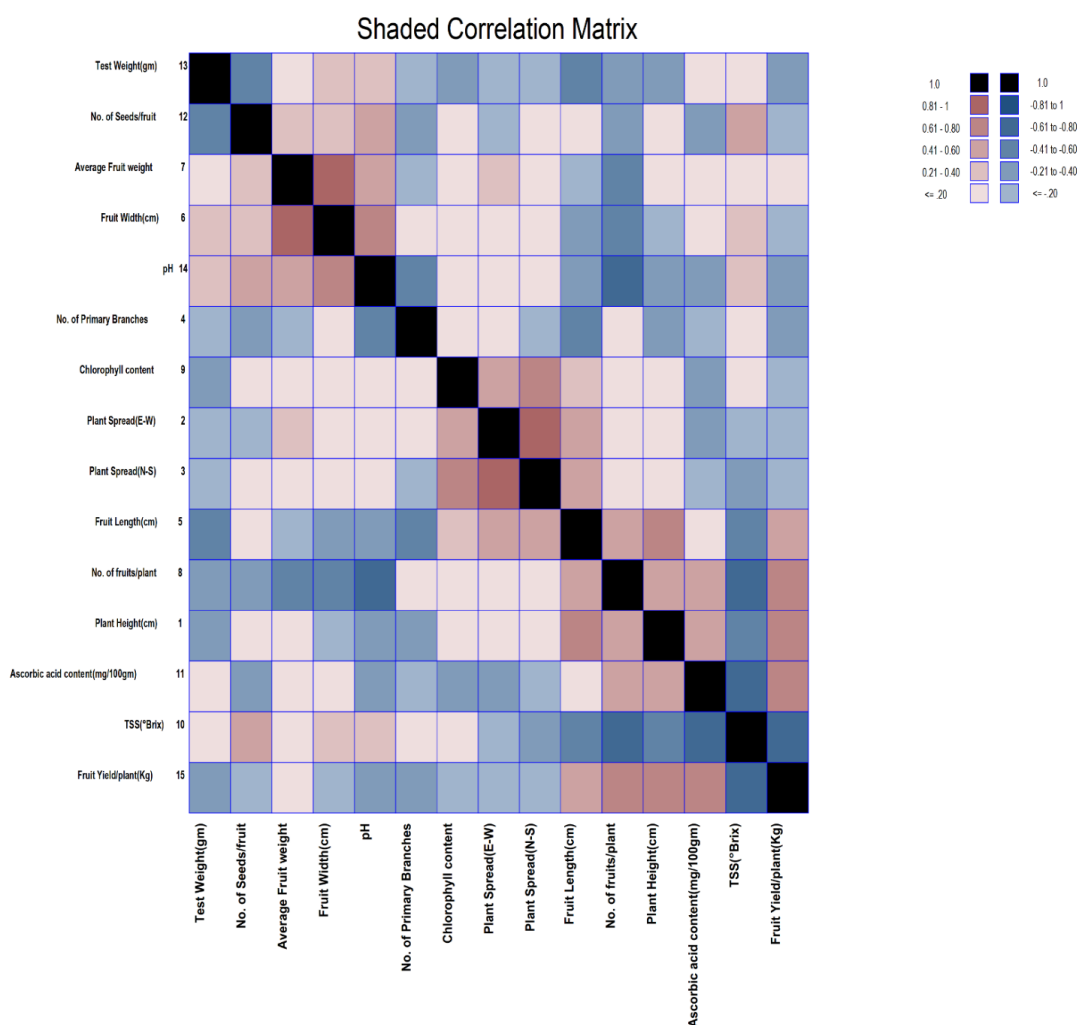


Figure 4.6: Shaded genotypic correlation matrix

The test weight exhibited a positive and significant relationship with pH (0.322), but number of seeds per fruit (-0.447), fruit length (-0.403), fruit yield (-0.381), number of fruits per plant (-0.369) and plant height (-0.355) had negative and significant relationships.

The pH was found to have a positive and significant correlation with fruit width (0.612), average fruit weight (0.587), number of seeds per fruit (0.444) and test weight (0.332), but a negative and significant correlation with number of primary branches per plant (-0.441), number of fruits per plant (-0.711), ascorbic acid (-0.390) and fruit yield (-0.355).

Fruit yield per plant exhibited positive and significant correlation with ascorbic acid content (0.718), plant height (0.709), number of fruits per plant (0.647) and fruit length (0.594), whereas it had showed negative and significant correlation with total soluble solids (-0.789), test weight (-0.381) and pH (-0.355).

4.4.2 Phenotypic correlation coefficient

The data on phenotypic correlation coefficient for different fifteen characters of brinjal genotypes are presented in Table 4.12.

Fruit length (0.698), fruit yield per plant (0.676), number of fruits per plant (0.512), ascorbic acid content (0.514) and were all positively and significantly associated with plant height. Test weight (-0.343) and total soluble solids (-0.331) were found to be negatively and significantly correlated.

Plant spread (East-West) was shown to have a positive and significant relationship with plant spread (North-South) (0.842), chlorophyll content (0.518) and fruit length (0.412). Plant spread (North-South) had positive and significant correlation with plant spread (east-west) (0.842), chlorophyll content (0.575) and fruit length (0.547). Number of primary branches had revealed negative and significant correlation with fruit length (-0.413) and pH (-0.312).

Plant height (0.698), fruit yield per plant (0.561), plant spread (North-South) (0.547), number of fruits per plant (0.431) and plant spread (East-West) (0.412) all demonstrated positive and significant relationships with fruit length. The number of

primary branches per plant (-0.413), total soluble solids (-0.405), test weight (-0.369) and fruit width (-0.364) all revealed negative and significant correlation.

Fruit width was found to have a positive and significant correlation with average fruit weight (0.837) and pH (0.520), whereas number of fruits per plant (-0.510) and fruit length (-0.364) were found to have a negative and significant relationship.

Average fruit weight was positively and significantly correlated to fruit width (0.837), pH (0.483) and number of seeds per fruit (0.347), whereas it showed negative and significant correlation with number of fruits per plant (-0.470).

The number of fruits per plant manifested positive and significant correlation with fruit yield per plant (0.600), plant height (0.512), ascorbic acid content (0.461) and fruit length (0.431). It showed negative and significant correlation with pH (-0.615), fruit width (-0.510), total soluble solids (-0.504), average fruit weight (-0.470), number of seeds per fruit (-0.358) and test weight (-0.330). Chlorophyll content showed positive and significant correlation with plant spread (North-South) (0.575) and plant spread (East-West) (0.518).

Total soluble solids depicted positive and significant correlation with number of seeds per fruit (0.400), whereas it showed negative and significant correlation with fruit yield per plant (-0.587), number of fruits per plant (-0.504), ascorbic acid content (-0.469), fruit length (-0.405) and plant height (-0.331).

Fruit yield (q/ha) (0.675), plant height (0.514) and number of fruits per plant (0.461) were found to have positive and significant correlations with ascorbic acid concentration, whereas total soluble solids (-0.469), pH (-0.346) and number of seeds per fruit (-0.310) were found to have negative and significant correlations.

Number of seeds per fruit was found positive and significant association with total soluble solids (0.400), pH (0.364) and average fruit weight (0.347), whereas it showed negative and significant association with test weight (-0.418), number of fruits per plant (-0.358) and ascorbic acid content (-0.310).

Test weight positively and significantly correlated with pH (0.299), whereas it showed negative and significant correlation with number of seeds per fruit (-0.418),

fruit length (-0.369), fruit yield (q/ha) (-0.359), plant height (-0.343) and number of fruits per plant (-0.330).

pH revealed positive and significant correlation with fruit width (0.520), average fruit weight (0.483), number of seeds per fruit (0.364) and test weight (0.299). It showed negative and significant correlation with number of fruits per plant (-0.615), fruit yield per plant (-0.352), ascorbic acid content (-0.346) and number of primary branches (-0.312).

Plant height (0.676), ascorbic acid content (0.675), number of fruits per plant (0.600) and fruit length (0.561) had positive and significant correlations with fruit yield per plant, whereas total soluble solids (-0.587), test weight (-0.359) and pH (-0.352) had negative and significant correlation with fruit yield per plant.

Table 4.12 Phenotypic correlation of various characters of brinjal

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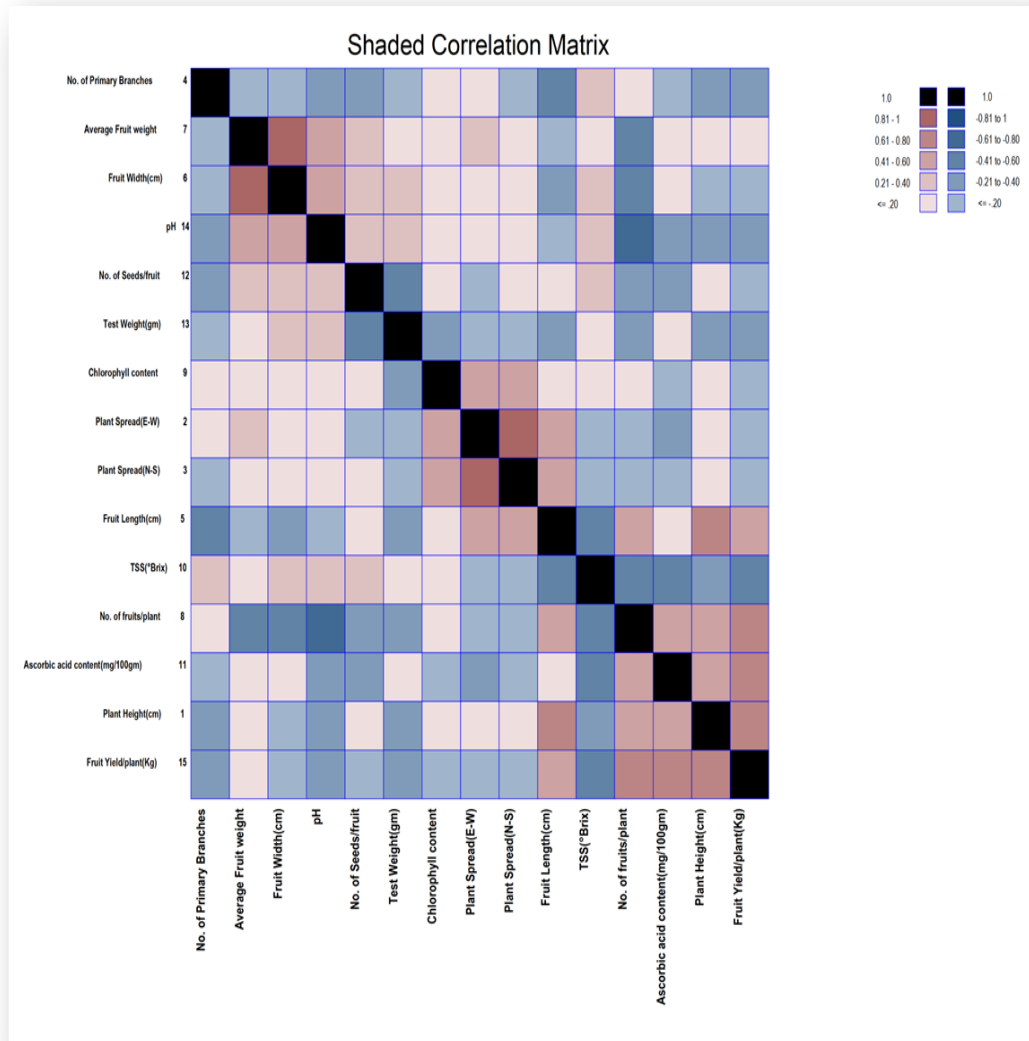


Figure 4.7: Shaded phenotypic correlation matrix

4.5 Path coefficient analysis

Path coefficient analysis deconstructs the relationship between qualities into their direct and indirect impacts on the economic product, allowing for a rigorous study of each individual trait's contribution to the total effect. It also aids in determining the relative significance of each attribute. The estimations of genotypic and phenotypic coefficients were used in this study to perform path analysis. The correlation coefficient analysis, together with information on the path coefficient, aids in the discovery of relevant characters for optimal weighting of each characteristic during selection. An examination of the genotypes and phenotypes under investigation yielded a clear indication of the attribute that may lead to enhanced fruit yield, as well as prospective future avenues for improving these features.

The estimates of direct and indirect effects of various traits on fruit yield per plant were presented in table given below.

4.5.1 Genotypic path coefficient effects

The effect of genotypic path coefficient on various characters can be divided into two categories: direct and indirect effects.

4.5.1.1 Direct effects

The genotypic path coefficient analysis showed that the highest positive direct effect with regard to fruit yield was found for average fruit weight (0.7140) followed by ascorbic acid content (0.6517), fruit length (0.4981), chlorophyll content (0.2891), number of primary branches (0.1842) and number of seeds per fruit (0.1835). The highest negative direct effect towards fruit yield was observed in fruit width (-0.8160) and total soluble solids (-0.2831).

4.5.1.2 Indirect effects

1. Plant height (cm)

Total soluble solids (0.0946) had the highest positive indirect effect on fruit yield for plant height, followed by test weight (0.0767), while number of fruits per plant had the highest negative effect (-0.1141).

2. Plant spread (East-West) (cm)

Ascorbic acid content (0.0505) had the highest positive indirect effect on fruit yield for plant spread (East-West), followed by total soluble solids (0.0346), whereas plant spread (North-South) had the highest negative indirect effect (-0.1532).

3. Plant spread (North-South) (cm)

Total soluble solids (0.0422) had the highest positive indirect effect on fruit yield for plant spread (North-South), followed by ascorbic acid content (0.0366), while plant spread (East-West) had the highest negative indirect effect (-0.1599).

4. Number of primary branches per plant

Number of fruits per plant (0.0320) had the highest positive indirect effect on fruit yield for number of primary branches per plant followed by total soluble solids (0.0311), while pH had the highest negative indirect effect (-0.0812).

5. Fruit length (cm)

Plant height (0.3579) had the greatest positive indirect effect on fruit yield for fruit length, followed by plant spread (North-South) (0.2884), while total soluble solids had the greatest negative indirect effect (-0.2426).

6. Fruit width (cm)

The number of fruits per plant (0.6750) had the greatest positive indirect effect on fruit yield, followed by fruit length (0.4520), while the average fruit weight had the greatest negative indirect effect (-0.7210).

7. Average fruit weight (g)

The pH (0.6687) had the highest positive indirect effect on fruit yield for average fruit weight, followed by fruit width (0.6240), while the number of fruits per plant had the highest negative indirect effect (-0.5427).

8. Number of fruits per plant

The pH (0.1421) had the highest positive indirect effect on fruit yield for number of fruits per plant, followed by total soluble solids (0.1367), while plant height had the highest negative indirect effect (-0.1055).

9. Chlorophyll content

Plant spread (North-South) (0.1757) had the greatest positive indirect effect on fruit yield for chlorophyll content, followed by plant spread (East-West) (0.1593), while test weight had the greatest negative indirect effect (-0.0657).

10. Total soluble solids (° Brix)

The number of fruits per plant (0.1935) had the highest positive indirect effect on fruit yield, followed by ascorbic acid content (0.1712). The number of seeds per fruit had the highest negative indirect effect on fruit yield (-0.1509).

11. Ascorbic acid content (mg/100g)

Plant height (0.3380) had the highest positive indirect effect on fruit yield for ascorbic acid content, followed by number of fruits per plant (0.3072), while total soluble solids had the highest negative indirect effect (-0.3942).

12. Number of seeds per fruit

Total soluble solids (0.0979) had the highest positive indirect effect on fruit yield for number of seeds per fruit, followed by pH (0.0814), while test weight had the highest negative indirect effect (-0.0820).

13. Test weight (g)

Number of seed per fruit (0.0631) had the highest positive indirect effect on fruit yield for test weight, followed by number of fruits per plant (0.0521), while pH had the highest negative indirect effect (-0.0469).

14. pH

Number of fruits per plant (0.0393) had the highest positive indirect effect on fruit yield for pH, followed by number of primary branches per plant (0.0243), while fruit width had the highest negative indirect effect (-0.0338).

4.5.1.3 Residual effects

The genotypic residual impact of 0.254 shows that the study effort covers all of the proportions necessary to support the objectives, but certain components must still be incorporated in order to acquire more accurate results.

Table 4.13: Genotypic path coefficient effect of various character of brinjal on fruit yield

PATH matrix of Fruit Yield/plant(Kg)															
	Plant height (cm)	Plant spread (East-West) (cm)	Plant spread (North-South) (cm)	No. of primary branches per plant	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits per plant	Chlorophyll content	Total soluble solids (°Brix)	Ascorbic acid content (mg/100g)	No. of seeds per fruit	Test weight (g)	pH	Fruit yield per plant (kg)
Plant height (cm)	-0.2164	-0.0227	-0.0328	0.0704	-0.1555	0.0305	-0.0079	-0.1141	-0.0087	0.0946	-0.1122	-0.0424	0.0767	0.0550	0.709**
Plant spread (East-West) (cm)	-0.0185	-0.1767	-0.1532	-0.0033	-0.0769	-0.0331	-0.0387	-0.0021	-0.0974	0.0346	0.0505	0.0160	0.0206	-0.0014	-0.0824
Plant spread (North-South) (cm)	-0.0279	-0.1599	-0.1845	0.0354	-0.1068	-0.0296	-0.0261	-0.0021	-0.1121	0.0422	0.0366	-0.0123	0.0251	-0.0104	-0.0060
No. of primary branches per plant	-0.0599	0.0035	-0.0354	0.1842	-0.0861	0.0065	-0.0190	0.0320	0.0073	0.0311	-0.0223	-0.0470	-0.0143	-0.0812	-0.2662
Fruit length(cm)	0.3579	0.2167	0.2884	-0.2328	0.4981	-0.1932	-0.0933	0.2266	0.1046	-0.2426	0.0747	0.0269	-0.2005	-0.1003	0.594**
Fruit width(cm)	0.1643	-0.2180	-0.1870	-0.0413	0.4520	-0.8160	-0.7210	0.6750	-0.2198	-0.3139	-0.1030	-0.3714	-0.2781	-0.7124	-0.1922
Average fruit weight (g)	0.0415	0.2494	0.1611	-0.1173	-0.2136	0.6240	0.7140	-0.5427	0.0255	0.0282	0.1601	0.4053	0.2234	0.6687	0.0746
No. of fruits per plant	-0.1055	-0.0024	-0.0023	-0.0348	-0.0910	0.1159	0.0952	-0.2000	-0.0351	0.1367	-0.0943	0.0744	0.0738	0.1421	0.647**
Chlorophyll content	0.0116	0.1593	0.1757	0.0114	0.0607	0.0546	0.0065	0.0508	0.2891	0.0022	-0.0581	0.0506	-0.0657	0.0458	-0.1243
Total soluble solids (°Brix)	0.1237	0.0554	0.0648	-0.0477	0.1379	-0.0763	-0.0070	0.1935	-0.0022	-0.2831	0.1712	-0.1509	-0.0107	-0.0865	-0.789**
Ascorbic acid content (mg/100g)	0.3380	-0.1863	-0.1291	-0.0789	0.0978	0.0576	0.0916	0.3072	-0.1309	-0.3942	0.6517	-0.2010	0.0107	-0.2540	0.718**
No. of seeds per fruit	0.0360	-0.0166	0.0122	-0.0469	0.0099	0.0585	0.0653	-0.0683	0.0321	0.0979	-0.0566	0.1835	-0.0820	0.0814	-0.0297
Test weight (g)	0.0501	0.0165	0.0192	0.0110	0.0569	-0.0337	-0.0277	0.0521	0.0321	-0.0054	-0.0023	0.0631	-0.1413	-0.0469	-0.381*
pH	0.0140	-0.0004	-0.0031	0.0243	0.0111	-0.0338	-0.0324	0.0393	-0.0088	-0.0169	0.0215	-0.0245	-0.0183	-0.0552	-0.355*
Fruit yield per plant (kg)	0.709**	-0.0824	-0.0060	-0.2662	0.594**	-0.1922	0.0746	0.647**	-0.1243	-0.789**	0.718**	-0.0297	-0.381*	-0.355*	1.0000

Residual= 0.254 Diagonal and bold underline figures shows direct effect on fruit yield per plant (kg)

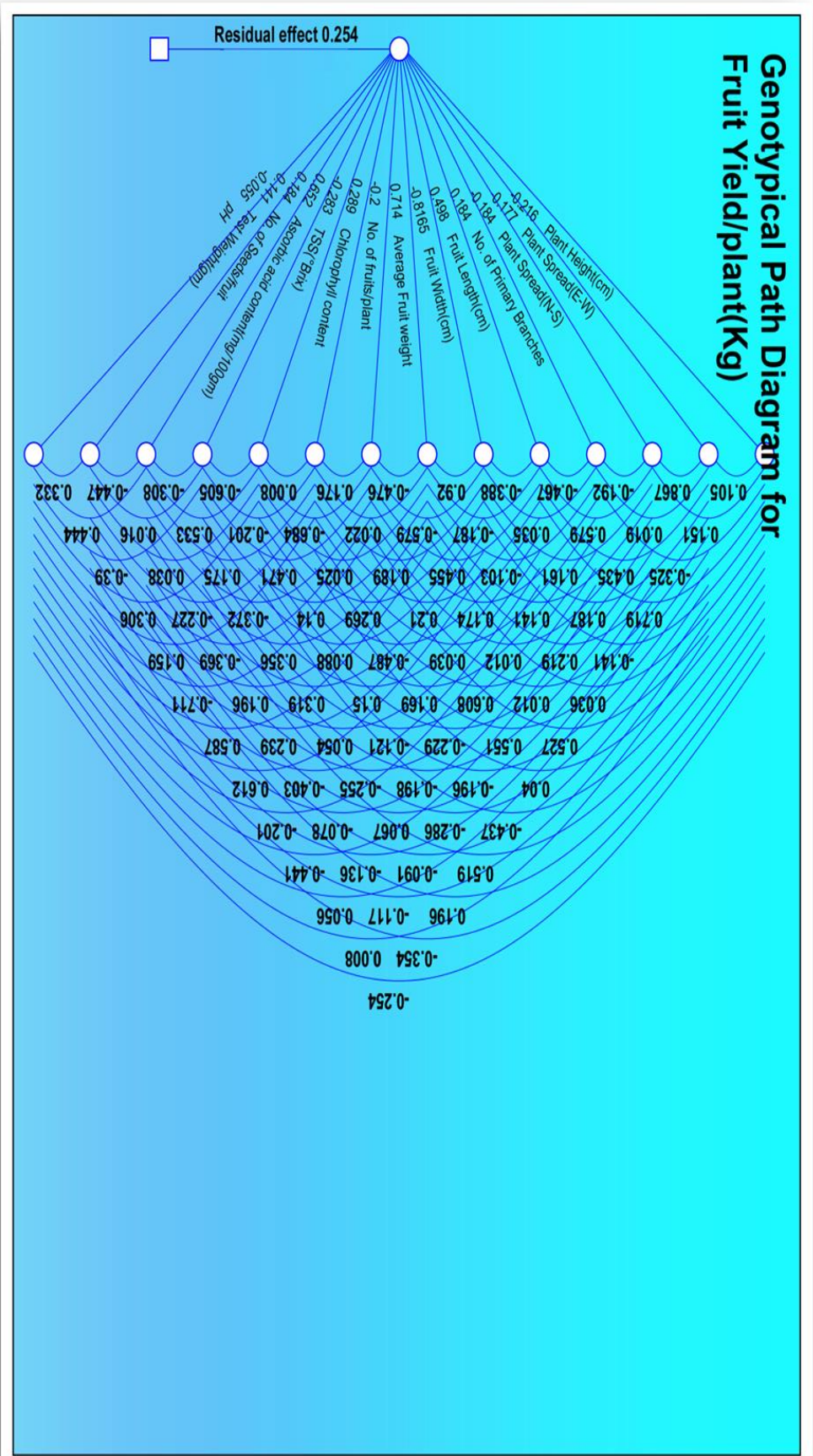


Figure 4.8: Genotypic path coefficient diagram of various character of brinjal

4.5.2 Phenotypic path coefficient effects

The direct and indirect effect of yield contributing traits on fruit yield at phenotypic level mentioned in Table 4.14

4.5.2.1 Direct effect

The phenotypic path coefficient analysis showed that the highest positive direct effect with regard to fruit yield was found for fruit length (0.6656), followed by average fruit weight (0.6653), ascorbic acid content (0.3815), number of fruits per plant (0.3238), number of seeds per fruit (0.1155) and chlorophyll content (0.0238). The highest negative direct effect towards fruit yield was observed in plant height (-0.2943) and fruit width (-0.2674).

4.5.2.2 Indirect effect

1. Plant height (cm)

The highest positive indirect effect towards fruit yield for plant height was observed with test weight (0.1009), followed by total soluble solids (0.0975) while highest negative indirect effect was observed with fruit length (-0.2052).

2. Plant spread (East-West) (cm)

The highest positive indirect effect towards fruit yield for plant spread (East-West) was observed with ascorbic acid content (0.0460) followed by total soluble solids (0.0339), whereas highest negative indirect effect was recorded with plant spread (North-South) (-0.1433).

3. Plant spread (North-South) (cm)

The highest positive indirect effect towards fruit yield for plant spread (North-South) was recorded with ascorbic acid content (0.0421), followed by total soluble solids (0.0360), whereas highest negative indirect effect was observed with plant spread (East-West) (-0.1875).

4. Number of primary branches per plant

The highest positive indirect effect on fruit yield per plant exhibited *viz.*, fruit length (0.0099) followed by pH (0.0075), whereas highest negative indirect effect was observed with number of fruits per plant (-0.0032).

5. Fruit length (cm)

Fruit length showed highest positive indirect effects on fruit yield per plant through plant height (0.4642) followed by plant spread (North-South) (0.3638). The highest negative indirect effects of fruit length exerted *viz.*, number of primary branches per plant (-0.2747).

6. Fruit width (cm)

The highest positive indirect effects of number of fruits per plant (0.1364), followed by fruit length (0.0974) depicted on fruit yield per plant. Fruit width exerted highest negative indirect effect on average fruit weight (-0.2239).

7. Average fruit weight (g)

The highest positive indirect effect towards average fruit weight for fruit yield was observed with fruit width (0.5571), followed by pH (0.3213), whereas highest negative indirect effect was observed with number of fruits per plant (-0.3125).

8. Number of fruits per plant

Number of fruits per plant showed highest positive and indirect effect through plant height (0.1657), followed by ascorbic acid content (0.1492) on fruit yield per plant. The highest negative indirect effects of number of fruits per plant *via* characters pH (-0.1992) on fruit yield per plant.

9. Chlorophyll content

Chlorophyll content exerted highest positive indirect effect *via* plant spread (North-South) (0.0137), followed by plant spread (East-West) (0.0123) on fruit yield per plant. Whereas, highest negative indirect effect manifested *via* test weight (-0.0053) on fruit yield per plant.

10. Total soluble solids (°Brix)

The highest positive indirect effect toward fruit yield for total soluble solids was recorded with number of fruits per plant (0.0488), followed by ascorbic acid content (0.0454), whereas highest negative indirect effect was observed with number of seeds per fruit (-0.0387).

11. Ascorbic acid content (mg/100g)

Plant height (0.1960), followed by number of fruits per plant (0.1757) had highest positive indirect effect on fruit yield per plant, whereas highest negative indirect effect was observed with total soluble solids (-0.1787).

12. Number of seeds per fruit

The maximum positive indirect effect towards fruit yield for number of seeds per fruit was recorded with total soluble solids (0.0461) followed by pH (0.0421), whereas negative indirect effect was observed with test weight (-0.0483).

13. Test weight (g)

The highest positive indirect effect towards fruit yield per plant for test weight was observed with number of seeds per fruit (0.0510) followed by fruit length (0.0451), while highest negative indirect effect was observed with pH (-0.0365).

14. pH

The highest positive indirect effect towards fruit yield per plant for pH was observed with number of fruits per plant (0.0893) followed by ascorbic acid content (0.0501), whereas highest negative indirect effect was observed with fruit width (-0.0754).

4.5.2.3 Residual effects

The phenotypic residual impact of 0.291 suggests that the study work covers all of the proportions necessary to support the aim, but that certain components must still be incorporated to achieve more specific findings.

Table 4.14 Phenotypic path coefficient effect of various traits of brinjal on fruit yield

PATH matrix of Fruit Yield/plant(Kg)															
	Plant height (cm)	Plant spread (East-West) (cm)	Plant spread (North-South) (cm)	No. of primary branches per plant	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	No. of fruits per plant	Chlorophyll content	Total soluble solids (°Brix)	Ascorbic acid content (mg/100g)	No. of seeds per fruit	Test weight (g)	pH	Fruit yield per plant (kg)
Plant height (cm)	-0.2943	-0.0274	-0.0402	0.0827	-0.2052	0.0353	-0.0103	-0.1506	-0.0108	0.0975	-0.1512	-0.0557	0.1009	0.0648	0.676**
Plant spread (East-West) (cm)	-0.0159	-0.1701	-0.1433	-0.0013	-0.0701	-0.0300	-0.0352	0.0015	-0.0882	0.0339	0.0460	0.0157	0.0157	-0.0005	-0.0945
Plant spread (North-South) (cm)	-0.0304	-0.1875	-0.2226	0.0359	-0.1217	-0.0305	-0.0291	0.0014	-0.1279	0.0360	0.0421	-0.0070	0.0271	-0.0120	-0.0220
No. of primary branches per plant	0.0068	-0.0002	0.0039	-0.0240	0.0099	0.0003	0.0029	-0.0032	-0.0013	-0.0052	0.0020	0.0054	0.0024	0.0075	-0.2345
Fruit length (cm)	0.4642	0.2743	0.3638	-0.2747	0.6656	-0.2425	-0.1225	0.2869	0.1246	-0.2696	0.0878	0.0389	-0.2459	-0.1016	0.561**
Fruit width (cm)	0.0321	-0.0471	-0.0366	0.0030	0.0974	-0.2674	-0.2239	0.1364	-0.0480	-0.0539	-0.0226	-0.0779	-0.0568	-0.1390	-0.1935
Average fruit weight (g)	0.0232	0.1376	0.0871	-0.0794	-0.1225	0.5571	0.6653	-0.3125	0.0212	0.0056	0.0873	0.2305	0.1183	0.3213	0.0933
No. of fruits per plant	0.1657	-0.0028	-0.0021	0.0437	0.1396	-0.1651	-0.1521	0.3238	0.0528	-0.1631	0.1492	-0.1160	-0.1069	-0.1992	0.600**
Chlorophyll content	0.0009	0.0123	0.0137	0.0013	0.0045	0.0043	0.0008	0.0039	0.0238	0.0008	-0.0046	0.0039	-0.0053	0.0035	-0.1062
Total soluble solids (°Brix)	0.0321	0.0193	0.0157	-0.0210	0.0392	-0.0195	-0.0008	0.0488	-0.0031	-0.0969	0.0454	-0.0387	-0.0008	-0.0254	-0.587**
Ascorbic acid content (mg/100g)	0.1960	-0.1032	-0.0722	-0.0325	0.0503	0.0323	0.0501	0.1757	-0.0741	-0.1787	0.3815	-0.1183	0.0059	-0.1318	0.675**
No. of seeds per fruit	0.0219	-0.0107	0.0036	-0.0258	0.0068	0.0337	0.0400	-0.0414	0.0189	0.0461	-0.0358	0.1155	-0.0483	0.0421	-0.0055
Test weight (g)	0.0419	0.0113	0.0148	0.0123	0.0451	-0.0260	-0.0217	0.0403	0.0271	-0.0010	-0.0019	0.0510	-0.1222	-0.0365	-0.339*
pH	0.0319	-0.0004	-0.0078	0.0453	0.0221	-0.0754	-0.0701	0.0893	-0.0214	-0.0380	0.0501	-0.0528	-0.0434	-0.1451	-0.352*
Fruit yield per plant (kg)	0.676**	-0.0945	-0.0220	-0.2345	0.561**	-0.1935	0.0933	0.600**	-0.1062	-0.587**	0.675**	-0.0055	-0.359*	-0.352*	1.0000

Residual= 0.291 Diagonal and bold underline figures shows direct effect on fruit yield per plant (kg)

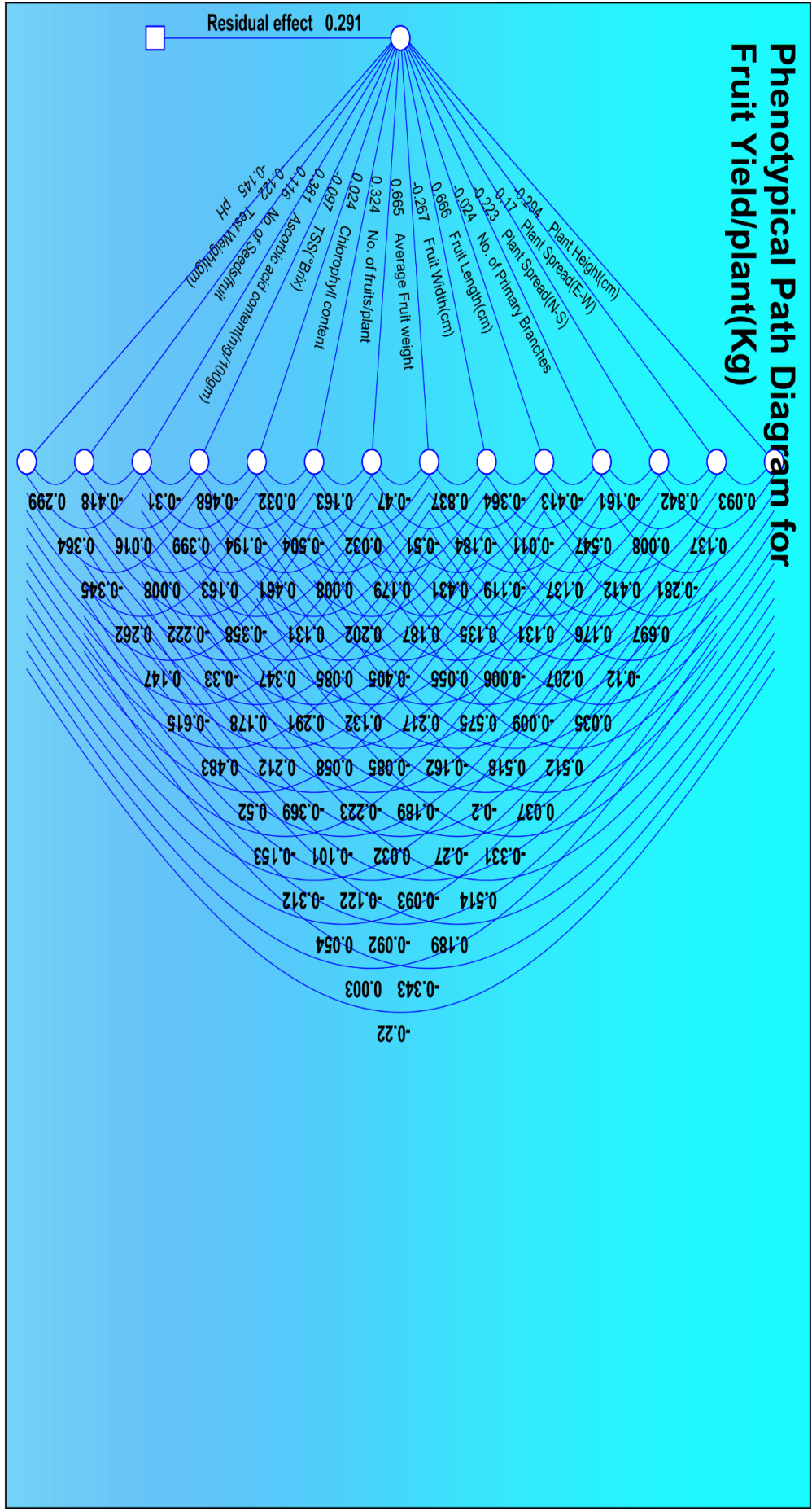


Figure 4.9: Phenotypic path coefficient diagram of various character of brinjal

4.6 Genetic Divergence

The study of genetic divergence among the 15 genotypes of brinjal was carried out using Mahalanobis D^2 statistics.

4.6.1 Grouping of eggplant genotypes

The 15 genotypes were grouped into six different non overlapping clusters (Table 4.15). The dendrogram revealed that cluster I has maximum genotypes i.e., seven genotypes followed by cluster II which has four genotypes and remaining clusters entailed with single genotype. The tendency of genotypes from different centers to group together in one cluster might be due to similarity in requirements and selection of different approach followed under domestication.

4.6.2 Intra and Inter cluster distance

Table 4.16 shows the estimations of inter and intra cluster distances represented by D^2 values.

Intra cluster D^2 values ranged from 0.00 to 348.16. Out of seven clusters, cluster II with four genotypes showed maximum intra cluster distance ($D^2 = 348.16$) followed by cluster I with seven genotypes had intra-cluster distance ($D^2 = 264.50$). The clusters III, VI, V and VI had no intra-cluster distance ($D^2 = 0.00$) as they possessed single genotype in each cluster.

Maximum inter-cluster distance was observed between cluster IV and cluster V (2740.09) which suggested that members of these two clusters were genetically very diverse to each other. The inter cluster value between cluster I and cluster VI (2403.42), cluster III to cluster V (2259.34), cluster III to cluster VI (1740.57), cluster I to cluster V (1704.73), cluster IV to VI (1570.53), cluster V to cluster VI (1424.66), cluster II to cluster IV (941.59) were very high.

The minimum inter-cluster D^2 values was recorded in case of cluster III to cluster IV (266.01) followed by cluster I to cluster III (479.14). The higher the inter cluster distance, the more genetic divergence there was between the genotypes of these clusters and the shorter the inter cluster distance, the less genetic diversity there was between the genotypes of these clusters.

4.6.3 Mean performance for all the characters in different clusters

The cluster mean for twenty-three genotypes are tabulated in Table 4.17.

The highest cluster mean for plant height was observed in cluster V (94.62 cm) followed by cluster I (90.36 cm) and the lowest cluster mean was observed in cluster IV (62.10 cm). The highest cluster mean for plant spread (East-West) was recorded in cluster III (89.47 cm) followed by cluster I (76.19 cm), whereas lowest cluster mean was recorded in cluster II (69.09 cm).

The highest cluster mean for plant spread (North-South) was depicted in cluster III (73.78 cm) followed by cluster I (71.81 cm) and the lowest cluster mean was observed in cluster VI (50.63 cm). The highest cluster mean for number of primary branches was recorded in cluster III (9.67) followed by cluster VI (9.40) and the lowest cluster mean was observed in cluster I (7.70).

The highest cluster mean for fruit length was showed in cluster I (12.84 cm) followed by cluster V (12.25 cm), whereas lowest cluster mean was observed in cluster VI (5.94 cm). The maximum cluster mean for fruit width was observed in cluster III (7.33 cm) followed by cluster II (5.31 cm) and lowest cluster mean observed in cluster IV (2.39 cm).

The highest cluster mean for average fruit weight was recorded in cluster III (166.17g) followed by cluster V (127.89g) and the lowest cluster mean was recorded in cluster IV (64.59g). The highest cluster mean for number of fruits per plant was observed in cluster I (24.63) followed by cluster V (24.07) and the lowest cluster mean was recorded in cluster VI (14.40).

The highest cluster mean for chlorophyll content was found in cluster III (95.46) followed by cluster I (89.47) and the least cluster mean was observed in cluster V (45.17). The maximum cluster mean for total soluble solids was observed in cluster IV (5.40) followed by cluster III (5.33) and lowest mean was observed in cluster V (4.60).

The highest cluster mean for ascorbic acid content was observed in cluster V (46.91) followed by cluster II (35.32) and the lowest cluster mean was observed in cluster IV (11.37). The highest cluster mean for pH was observed in cluster VI (7.21)

followed by cluster III (7.16) and the lowest cluster mean was observed in cluster V (6.53).

The highest cluster mean for number of seeds per fruit was observed in cluster I (1172.48) followed by cluster IV (1141.43) and the lowest cluster mean was observed in cluster VI (434.90). The highest cluster mean for test weight was observed in cluster VI (6.37 g) followed by cluster III (5.80 g) and the lowest cluster mean was observed in cluster IV (3.17g).

The highest cluster mean for fruit yield per plant was recorded in cluster V (3.09 kg) followed by cluster I (2.37 kg), whereas lowest mean was recorded in cluster III (1.14 kg). The highest cluster mean for fruit yield per plant was observed in cluster V (416.80 q/ha) followed by cluster I (320.41 q/ha) while the lowest cluster mean was observed in cluster III (153.84 q/ha).

4.6.4 Per cent contribution of different traits towards total divergence

The relative contribution of different traits for genetic divergence (D^2) from the characters viz., plant height, plant spread (East-West), plant spread (North-south), number of primary branches per plant, fruit length, fruit width, average fruit weight, number of fruits per plant, chlorophyll content, total soluble solids, ascorbic acid content, pH, number of seeds per fruit, test weight, fruit yield per plant and fruit yield(q/ha) is given in table 4.17.

Average fruit weight (17.62) contributed maximum towards genetic divergence among 15 genotypes of brinjal followed by fruit yield (q/ha) (17.24%), fruit yield per plant (15.24%), chlorophyll content (9%), fruit length (7%), number of primary branches (5%), number of fruits per plant (4.76%), total soluble solids (4.76%), whereas fruit width (0.95%) followed by pH (1.90%) contributed very low towards the divergence.

Table 4.15 Distribution of 15 genotypes of brinjal to different clusters on the basis of D²-statistics

Cluster Group	No. of genotype	List of genotypes
Cluster I	7	HABR 4, UR 11, Punjab Nagina, JB 9, SEP 034, Arka Keshav & Green Long
Cluster II	4	Sobha, Annamalai, NBJ 19 & KS 331
Cluster III	1	NBH 1156
Cluster IV	1	PPL Nepal
Cluster V	1	JBL 03 04
Cluster VI	1	IVB 2

Table 4.16 Average intra-cluster and inter-cluster value for 15 genotypes of brinjal

Cluster Distances						
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	264.50	651.89	479.14	774.20	1704.73	2403.42
Cluster II		348.16	704.88	941.59	834.93	1080.68
Cluster III			0.00	266.01	2259.34	1740.57
Cluster IV				0.00	2740.09	1570.53
Cluster V					0.00	1424.66
Cluster VI						0.00

Table 4.17 percentage contribution by different trait of brinjal on genetic divergence

Source	Contribution %	Times ranked 1st
Plant Height (cm)	2.53	3
Plant Spread (East-West) (cm)	2	2
Plant Spread (North-South) (cm)	3	3
No. of Primary Branches per plant	5	5
Fruit Length (cm)	7	7
Fruit Width (cm)	0.95	1
Average Fruit weight (g)	17.62	19
No. of fruits/plant	4.76	5
Chlorophyll content	9	9
Total soluble solids (°Brix)	4.76	5
Ascorbic acid content (mg/100gm)	3	3
No. of Seeds/fruit	2	2
Test Weight (g)	4	4
Fruit Yield/plant (kg)	15.24	16
Fruit Yield (q/ha)	17.24	18
pH	1.9	2

Per cent contribution towards Divergence

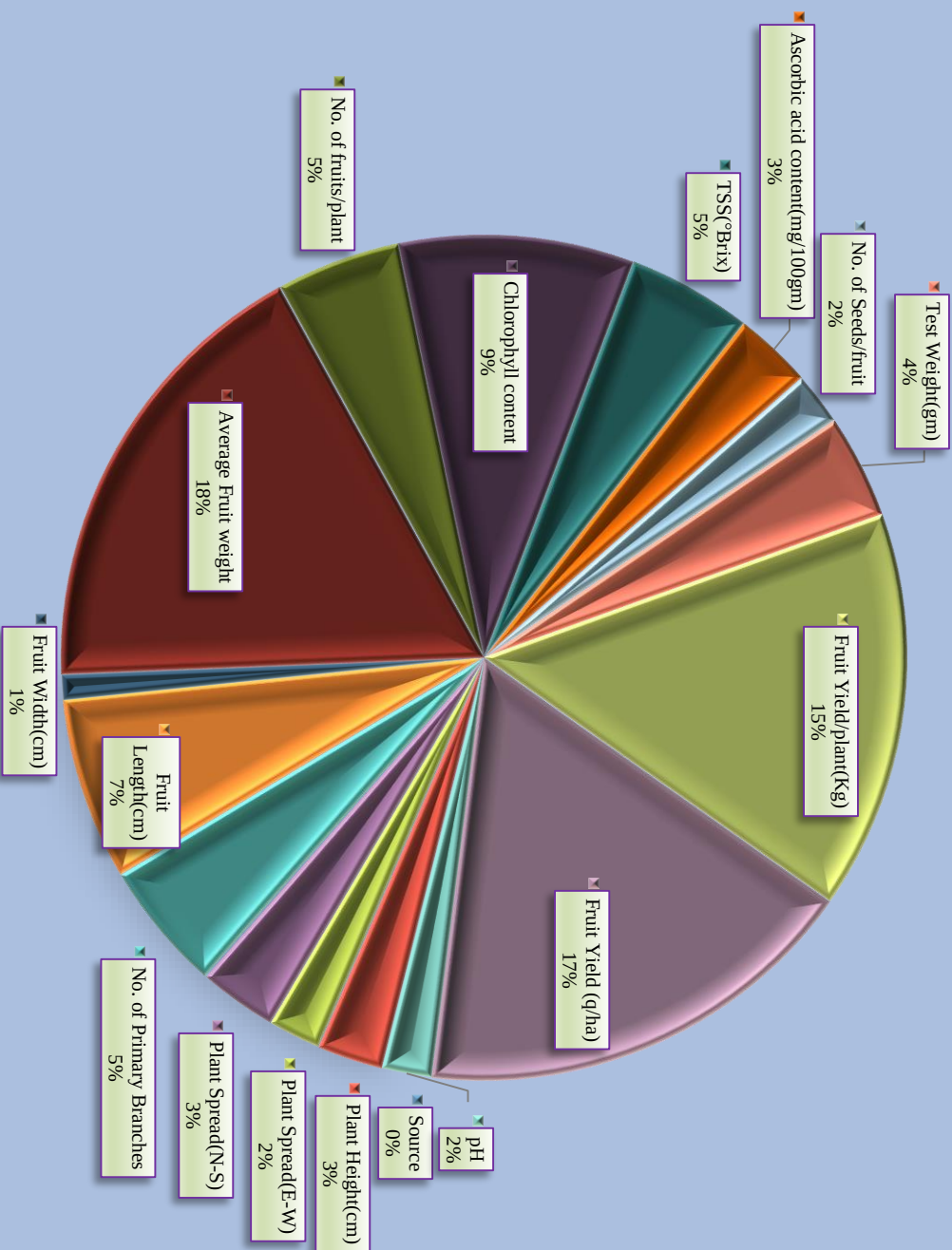


Table 4.18: Clusters means of different characters in brinjal

Cluster Means : Tocher Method																
	Plant Height(c m)	Plant Spread(E-W)	Plant Spread(N-S)	No. of Primary Branches	Fruit Length(cm)	Fruit Width(c m)	Average Fruit weight	No. of fruits/pl ant	Chlorop hyll content	TSS(°Br ix)	Ascorbi c acid content(mg/100g m)	No. of Seeds/fr uit	Test Weight(gm)	Fruit Yield/pl ant(Kg)	Fruit Yield (q/ha)	pH
Cluster 1	90.36	76.19	71.81	7.70	12.84	4.27	105.79	24.63	89.47	5.01	29.85	1172.48	4.05	2.37	320.41	6.88
Cluster 2	78.47	69.09	65.55	7.96	8.50	5.31	117.75	20.85	79.75	5.16	35.32	1028.60	5.37	1.98	268.18	6.77
Cluster 3	81.29	89.47	73.78	9.67	8.26	7.33	166.17	15.13	95.46	5.33	22.82	972.93	5.80	1.14	153.84	7.16
Cluster 4	62.10	75.72	70.54	9.33	9.34	2.39	64.59	20.67	83.85	5.40	11.37	1141.43	3.17	1.25	168.88	6.58
Cluster 5	94.62	69.73	64.39	8.20	12.25	4.32	127.89	24.07	45.17	4.60	46.91	643.35	5.29	3.09	416.80	6.53
Cluster 6	58.72	61.85	50.63	9.40	5.94	4.45	99.68	14.40	60.57	5.30	23.01	434.90	6.37	1.37	184.26	7.21

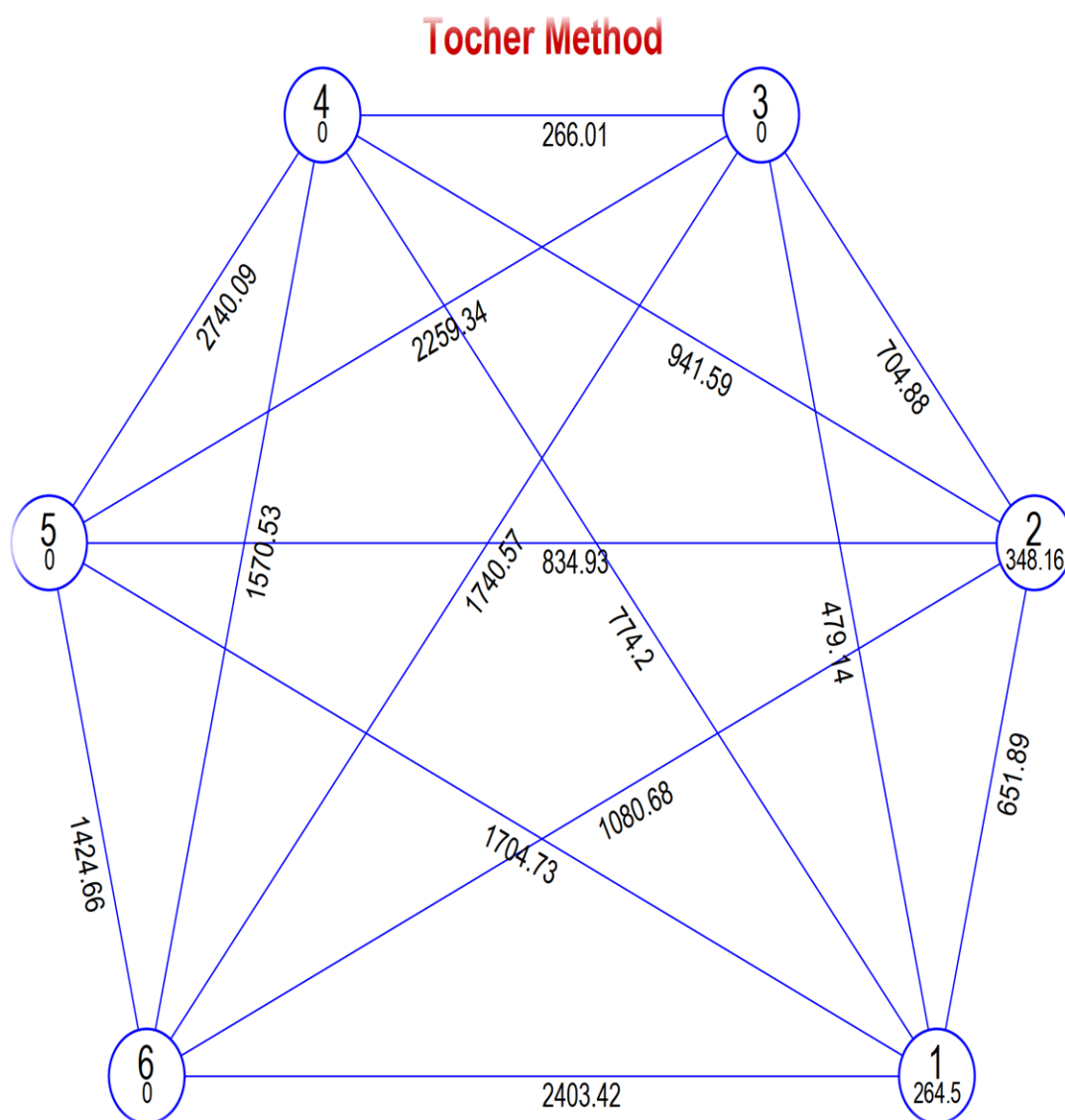


Figure 4.10: Clustering pattern of different group with inter cluster and intra cluster distance among the brinjal genotypes

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DISCUSSION

Brinjal (*Solanum melongena* L.) is a prized solanaceous vegetable. The demand for eggplant has been steadily increasing in recent years because to its numerous health advantages, which include anti-oxidant, anti-diabetic, hypotensive, cardio-protective, and hepato-protective properties. However, in vegetables, notably eggplant, the production of cultivars with increased fruit quality and high phytochemical qualities, with an urgent demand for greater market value, has gotten relatively little attention via breeding.

The quantity of genetic diversity present in the population influences the planning and execution of a breeding programme for improving different quantitative and qualitative features. As a result, investigations on genetic variability, using appropriate biometrical methods such as the coefficient of variation, heritability and genetic advance, have become essential in crop improvement programmes for achieving practical outcomes. The relationship of various yield and contributing qualities that may be attributable to linkage is referred to as correlation. Correlation studies are useful in determining the relationship between various qualities, which aids in the selection of a more effective combination of traits.

Some specific facts based on the results are discussed here under the heads of:

5.1 Analysis of variance

5.2 Mean

5.3 Variability, Heritability and Genetic Advance

5.4 Correlation coefficient

5.5 Path coefficient

5.6 Genetic divergence

5.1 Analysis of variance

The genotype-based mean squares were extremely significant for all 16 characters studied in this study, as well as for all of the attributes. In other words, the genotypes' performance on these qualities differed statistically, indicating that brinjal has a lot of scope for improvement in a variety of areas.

5.2 Mean

According to mean performance, plant height was highest in genotype Arka Keshav and JB-9, and lowest in IVB-2. The genotype NBH-1156 and UR-11 had the largest plant spread (East-West), while IVB-2 had the smallest. The genotype HABR-4 and SEP 034 had the greatest plant spread (North-South), while IVB-2 had the smallest. The variety Sobha and NBH-1156 both had the most primary branches per plant, whereas HABR-4 had the fewest. The genotype HABR-4 and UR-11 produced the longest fruits, whereas IVB-2 produced the shortest. The genotype PPL-Nepal had the shortest fruit width, while KS-331 and NBH-1156 had the widest. The genotype NBH-1156 and KS-331 had the highest average fruit weight, whereas Annamalai has the lowest. The variety Arka Keshav and Green Long had the most fruits per plant, whereas lowest number in KS-331. The genotype Sobha and Green Long had the maximum chlorophyll content, while JBL-03-04 had the lowest. The variety Punjab Nagina and PPL-Nepal had the greatest total soluble solids values, while SEP 034 had the lowest. The variety JBL-03-04 and Green Long had the most ascorbic acid, whereas PPL-Nepal had the least. The genotype Green Long and NBJ-19 had the greatest pH, whereas HABR-4 and KS 331 had the lowest. The variety Punjab Nagina and KS-331 had the maximum seeds per fruit, whereas Green Long had the least. The genotype PPL-Nepal had the greatest test weight and Annamalai, and IVB-2 had the lowest. The variety Arka Keshav and JBL-03-04 produced the maximum fruit yield per plant and fruit yield (q/ha), respectively, whereas NBH-1156 had the lowest.

Similar findings for quantitative traits were also reported by Kumar *et al.*, (2010); Singh *et al.*, (2011); Vidhya and Kumar., (2015); Saikia *et al.*, (2021) and Sharma *et al.*, (2022). Some biochemical traits such as total soluble solids and ascorbic acid content have also been reported by Parvati *et al.*, (2018) and Nazir *et al.*, (2019).

Ahmed *et al.*, (2006); Singh *et al.*, (2011) and Singh *et al.*, (2011) also found similar findings for similar parameters having different genotypes or treatments.

5.3 Genetic variability, Heritability and Genetic advance

The most important thing for a breeder to understand about any population with which he is working is to account for sufficient genotypic variation, without which there would be no response to selection. Hybridization, mutation and other approaches to produce variety are used in modern breeding practises. It must be stated that a proper and complete assessment of the naturally occurring diversity in the collections should be conducted with the goal of finding high yielding genotypes that may be released for commercial cultivation. This will also aid in the identification of donors who excel in one or a few yield contributing characteristics and such genotypes may be employed effectively in combination breeding to boost yield.

GCV and PCV give information about the relative amount of variation in distinct features by measuring the degree of variability. The estimates of PCV for all of the characteristics in this investigation were somewhat higher than the estimates of GCV, which might be related to genotype-environment interactions (Sharma *et al.*, 2022 and Saha *et al.*, 2019).

Number of seeds per fruit, number of fruits per plant, fruit width, ascorbic acid content, fruit yield per plant, fruit yield (q/ha), average fruit weight, fruit length and test weight all had high phenotypic and genotypic coefficients of variation. Patel *et al.*, (2004); Singh and Kumar (2005); Tripathi *et al.*, (2009); Kumar *et al.*, (2010); Dhaka and Soni (2012); Kumar *et al.*, (2013); Lokesh *et al.*, (2013); Mili *et al.*, (2014); Gavade and Ghadage (2015); Vidhya and Kumar (2015); Koundinya *et al.*, (2017); Rani *et al.*, (2017); Sujin *et al.*, (2017); Kumar *et al.*, (2018); Banerjee *et al.*, (2018); Bajpai *et al.*, (2020); Sakriya *et al.*, (2020); and Anbarasi and Haripriya (2021) all found similar findings.

The given heritability estimates were made in a broad sense only, therefore the overall genetic variance may contain dominance and epistatic components that are not selectable. Because heredity is a single numerical expression based on the ratio of two variances, selection based only on heritability estimates may not lead to success. As a

result, high heritability in combination with a strong genetic progress as a percentage of the mean was more useful in forecasting the effect of selection.

Among the characters studied, highest heritability estimate was recorded for plant height (98.72%), ascorbic acid content (98.68%), Chlorophyll Content (97.74%), number of seeds per fruit (95.88%), number of fruit per plant (94.98%), fruit length (94.83%), fruit yield (q/ha) (93.80%), fruit yield per plant (93.28%), plant spread (East-West) (93.39%), plant spread (North-South) (92.72%), test weight (91.38%) and similar kind of result obtained by Naik *et al.*, (2009); Tripathi *et al.*, (2009); Kumar *et al.*, (2010); Dhaka and Soni (2012); Singh *et al.*, (2013); Koundinya *et al.*, (2017); Banerjee *et al.*, (2018); Kumar *et al.*, (2018); Sakriya *et al.*, (2020) and Anbarasi and Haripriya (2021).

In case of genetic advance wide range for all characters was being observed from 0.565 to 909.53. The high value was recorded for number of seeds per fruit (909.53%) followed by fruit yield (q/ha) (171.85%) and average fruit weight (61.41%). The genetic advance as a percent of mean (genetic gain) ranges from 9.63% to 65.83%. The high value was recorded in number of seeds per fruit (87.94%) followed by number of fruits per plant (65.83%) and ascorbic acid content (65.27%).

Similar results were in agreement with Singh and Kumar (2005); Naik *et al.*, (2009); Tripathi *et al.*, (2009); Dhaka and Soni (2012); Singh *et al.*, (2013); Lokesh *et al.*, (2013); Kumar *et al.*, (2013); Singh *et al.*, (2013); Lokesh *et al.*, (2013); Mili *et al.*, (2014); Vidhya and Kumar (2015); Patel *et al.*, (2015); Senapati *et al.*, (2016); Koundiya *et al.*, (2017); Rani *et al.*, (2017); Kumar *et al.*, (2018); Saha *et al.*, (2019); Kumar *et al.*, (2020); Konyak *et al.*, (2020); Anbarasi and Haripriya (2021) for the character viz. number of fruits per plant, average fruit weight, fruit yield per plant and fruit width whereas for number of seed per fruit was reported by Anbarasi and Haripriya (2021).

5.4 Correlation coefficient analysis

Correlation research reveals the type and size of the relationship between distinct component features and fruit production. It also assists us in comprehending the nature of inter-relationships among the component features. In the end, this type of

study might aid the breeder in developing selection techniques to increase pod production. Both genotypic and phenotypic correlations for yield and its contributing features were determined in this study.

Fruit yield per plant showed positive and significant correlation ascorbic acid content, plant height, number of fruits per plant and fruit length and show negative and significant correlation with total soluble solids, test weight and pH at genotypic level, whereas fruit yield per plant showed positive and significant correlation with plant height, ascorbic acid content, number of fruits per plant and fruit length, while negative and significant association with total soluble solids, test weight and pH at phenotypic level.

Similar findings were found in agreement with Bansal and Mehta (2008); Senapati *et al.*, (2009); Nayak and Nagare (2013); Patel *et al.*, (2015); Sujin *et al.*, (2017); Saha *et al.*, (2019); Tiwari *et al.*, (2019); Gurve *et al.*, (2020); Kumar *et al.*, (2020); Chithra *et al.*, (2020); Kumar *et al.*, (2020); Nikitha *et al.*, (2020); Rameshkumar *et al.*, (2021) for plant height, number of fruits per plant and fruit length. Thangawani and Jansirani (2012) showed same result for ascorbic acid and Pandey *et al.*, (2016) and Koundinya *et al.*, (2017) also show similar negative correlation for total soluble solids.

5.5 Path coefficient analysis

The path-coefficient analysis is a proven statistical approach that uses correlation estimations to evaluate the interrelationships of various components and their direct and indirect impacts on fruit output. The goal of this research was to determine traits, their relationships, and direct and indirect impacts on fruit yield in brinjal genotypes.

Average fruit weight was found to have the highest positive direct effect on fruit yield, followed by ascorbic acid content, fruit length, chlorophyll content, number of primary branches and number of seeds per fruit in genotypic path coefficient analysis. However, phenotypic path coefficient analysis revealed that fruit length, average fruit weight, ascorbic acid content, number of fruits and number of primary branches had the highest direct positive effect on fruit yield.

Similar result regarding positive and direct effect of average fruit weight reported by Sharma and Swaroop (2008); Saha *et al.*, (2019); Konyak *et al.*, (2020); Pal *et al.*, (2021); Dhaka and Soni (2022). Positive and direct effect of number of fruit per plant was also reported by Reena and Mehta (2007); Sharma and Swaroop (2008); Patel *et al.*, (2015); Senapati *et al.*, (2016); Koundinya *et al.*, (2017); Sujin *et al.*, (2017); Bende *et al.*, (2019); Nikitha *et al.*, (2020); Gurve *et al.*, (2020); Kumar *et al.*, (2020); Pal *et al.*, (2021); Dhaka and Soni (2022), whereas positive and direct effect of fruit length was reported by Reena and Mehta (2007); Thangawani and Jansirani (2012); Saha *et al.*, (2019); Sakriya *et al.*, (2022). Positive direct effect on seed per fruit was showed the same result by Reena and Mehta (2007) and number of primary branches reported by Reena and Mehta (2007); Thangawani and Jansirani (2012); Tirkey *et al.*, (2018); Nikitha *et al.*, (2020); Gurve *et al.*, (2020).

The residual effect at the genotypic (0.254) and phenotypic (0.291) levels indicates that the research work completed covers all of the proportions required to justify the goal, but that some portions must still be included in order to obtain more specific results. Other features, environmental conditions, or sampling error may have contributed to the residual effect on fruit yield in this study

5.6 Genetic divergence

The D^2 statistics of Mahalanobis are used to measure genetic diversity and are important in selecting acceptable parental lines for heterosis breeding as well as selecting parents for hybridization programmes to recover superior transgressive segregates. The clusters were created using Tocher's approach, which was also used to determine the distance between and within the clusters.

The clustering based on D^2 statistics divided genotypes into six groups, indicating that the genotypes under investigation have a wide range of genetic diversity. Cluster 1 has seven genotypes, followed by cluster II, which has four genotypes and clusters III, VI, V and VI, which each have one genotype. Geographic diversity did not appear to have a direct relationship with genetic diversity, according to the clustering pattern obtained in this study.

Cluster II has the largest intra cluster distance, followed by Cluster I. Intra cluster values are lower than inter cluster values, indicating that genotypes within and between clusters are homogeneous and heterogeneous. Cluster IV and cluster V had the greatest inter-cluster distance, followed by cluster III and cluster IV, indicating a large genetic difference between them. Genotypes from clusters with the greatest inter-cluster distance have the most genetic variety and hybridization between genotypes from different clusters is likely to yield a wide range of segregants. Cluster III and IV had the shortest inter-cluster distance, indicating the least degree of divergence and close genetic composition of the genotypes in these clusters.

Cluster means were compared and significant discrepancies between clusters of distinct characters were discovered. Fruit length, number of fruits per plant, and number of seeds per fruit were all the greatest in Cluster I. Plant spread (East-West), plant spread (North-South), number of primary branches, fruit breadth, average fruit weight and chlorophyll content all indicated the greatest cluster mean value in Cluster III. Total soluble solids and ascorbic acid levels were greatest in Cluster IV. Plant height, fruit production per plant and fruit yield had the greatest cluster mean in Cluster V, whereas test weight and pH had the highest cluster mean in Cluster VI.

Similar findings were also be obtained by Singh *et al.*, (2006); Kumar *et al.*, (2007); Quamruzzaman *et al.*, (2009); Rath *et al.*, (2011); Tripathi *et al.*, (2011); Shinde *et al.*, (2012); Sadarunnisa *et al.*, (2015); Yadav *et al.*, (2017); Arti *et al.*, (2018); Gurve *et al.*, (2019); Dash *et al.*, (2020); Mohanty *et al.*, (2021); Anbarasi and Haripriya (2021) and Verma *et al.*, (2021).

The maximum contribution towards genetic divergence was contributed by average fruit weight followed by fruit yield (q/ha), fruit yield per plant, chlorophyll content, fruit length, number of primary branches, number of fruits per plant, total soluble solids, test weight, plant spread (North-South), ascorbic acid content, plant height, plant spread (East-West), number of seeds per fruit, pH and fruit width. Singh *et al.*, (2006); Kumar *et al.*, (2007); and Verma *et al.*, (2021) for fruit yield per plant and Sadarunnisa *et al.*, (2015) for average fruit weight, each indicated a similar contribution to divergence.

SUMMARY AND CONCLUSION

During Rabi 2020-21, at the Vegetable Research Farm of the Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, an attempt was made to assess genetic variability, heritability, path analysis, genetic advance, and genetic diversity for various quantitative and qualitative characters in brinjal.

The experimental material consisted of fifteen brinjal genotypes that were cultivated in a randomized block design (RBD) with three replication and observations were recorded for plant height, plant spread (East-West) (cm), plant spread (North-South) (cm), number of primary branches per plant, fruit length (cm), fruit width (cm), average fruit weight (g), number of fruits per plant, chlorophyll content, total soluble solids, ascorbic acid content, pH, number of seeds per fruit, test weight (g), fruit yield per plant and fruit yield (q/ha). The mean data were analysed using standard statistical techniques with the goal of determining the genetic variability of the genotypes, the relationship between characters and the direct and indirect effects of various component characters on fruit yield, as well as the nature and magnitude of genetic diversity available in the genotypes, in order to recommend the best methodology for brinjal improvement.

The analysis of variance revealed significant differences among genotypes for all the characters under investigation which indicated that the experimental material had sufficient genetic variability for different traits. High GCV and PCV were observed for number of seeds per fruit, number of fruits per plant, ascorbic acid content, fruit width, fruit yield indicating high variability available in the genotypes for these characters for further improvement. Whereas, moderate was found in chlorophyll content, number of primary branches and plant height. The estimates of GCV and PCV were low for pH which suggested existence of poor variability among the genotypes studied for this character. The differences between PCV and GCV values were minimal, genotype variance accounted for a significant portion of the total variance for all of the characters, implying that the observed variability was primarily due to genotypes, with little influence from the environment and that these characters could be improved by phenotypic selection.

High value of heritability was observed in plant height, ascorbic acid content, chlorophyll content, number of seed per fruit, number of fruits per plant, fruit length, fruit yield, plant spread (East-West), fruit yield per plant, average fruit weight, plant spread (North-South), test weight, fruit width, pH and number of primary branches, whereas moderate heritability seen in total soluble solids. Out of these number of seeds per fruit and fruit yield (q/ha) exhibited high genetic advance. The genetic advance as a percent of mean (genetic gain) exhibited high value in number of fruits per plant and ascorbic acid content.

In the current study, a little difference was identified between genotypic and phenotypic correlation coefficients for several qualities, indicating a lower effect of the environment on the expression of these traits and the presence of a strong intrinsic link among the traits. At both the phenotypic and genotypic levels, plant height and ascorbic acid showed a positive and highly significant relationship with fruit yield per plant, indicating the importance of these traits in yield selection and identifying them as yield attributing characters on which selection can be relied for genetic improvement of brinjal yield.

The average fruit weight had the greatest positive direct influence on fruit yield, followed by ascorbic acid content, fruit length, chlorophyll content, number of primary branches per plant and number of seeds per fruit, according to the genotypic path coefficient analysis. Fruit width had the strongest negative direct influence on fruit yield, whereas fruit width had the strongest positive indirect effect via number of fruits per plant. Fruit length had the greatest positive direct influence on fruit yield, followed by average fruit weight, ascorbic acid content, number of fruits per plant, chlorophyll content and number of seeds per fruit, according to phenotypic path analysis. Plant height had the greatest negative direct impact on fruit yield, followed by fruit width and highest positive indirect effect was observed in average fruit weight via. fruit width. The high positive direct effect of traits appeared to be the main factor for their strong association with fruit yield per plant. Hence, direct selection for these traits would be effective.

The fifteen genotypes were grouped into six clusters based on Mahalanobis D^2 statistic. Cluster I has maximum genotypes i.e., seven genotypes followed by cluster II

has four genotypes and cluster III, IV and V are solitary entailed with single genotype. Among the six clusters, cluster II with four genotypes showed maximum intra-cluster diversity ($D^2 = 348.16$) and cluster III, IV and V had no intra-cluster distance as they possessed single genotype in each cluster. Based on distance between clusters, the maximum inter-cluster distance of ($D^2 = 2740.09$) was observed between cluster IV and cluster V followed by cluster III and cluster V ($D^2 = 2259.34$) which comprehend that the genotypes in these clusters can be utilized as a parent in the hybridization programme to get higher heterotic hybrids. The lowest inter-cluster distance was observed between cluster I and cluster III ($D^2 = 479.14$). Maximum inter cluster distance depicts that genotype in cluster IV and IV are highly diverse. Average fruit weight (17.62 %) contributed maximum to the total genetic diversity among fifteen genotypes followed by fruit yield (q/ha) (17.24 %), fruit yield per plant (15.24 %). However, traits like plant height, plant spread (East-West), plant spread (North-South), number of primary branches, fruit length, fruit width, number of fruits per plant, chlorophyll content, total soluble solids, ascorbic acid content, pH, number of seeds per fruit, test weight had no substantial contribution to total divergence.

Conclusion

- The best genotypes are identified in present study based on the mean yield performance under field condition are Arka Keshav, JBL-03-04 and JB-9.
- In the current study, moderate to high heritability with high genetic advance over mean was observed for traits like plant height, ascorbic acid content, chlorophyll content, number of seed per fruit, number of fruits per plant, fruit length, fruit yield, plant spread (East-West), fruit yield per plant, average fruit weight, plant spread (North-South), test weight, fruit width, pH and number of primary branches and total soluble solids under field condition. As a result, harnessing these traits to create superior genotypes has a lot of potential.
- The association of fruit yield per plant was positive and significant with plant height, ascorbic acid content, number of fruits per plant and fruit length at both genotypic and phenotypic levels. These traits were crucial in predicting fruit yield, and they should be given more attention during the selection process.

- In the present study found that the traits like average fruit weight, ascorbic acid and fruit length had shown maximum positive direct effect on fruit yield per plant. Thus, these characters accounted to have for improvement in increased fruit yield.
- Divergence study revealed that the maximum inter-cluster distance was observed between cluster IV and cluster V followed by cluster III and cluster V and maximum intra-cluster recorded in II succeeded by III. The crosses between the genotypes of these clusters can be utilized for improvement in brinjal for improving fruit yield.



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