GENETIC DIVERGENCE STUDIES IN SPINE GOURD

(*Momordica dioica* Roxb.)

BY

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PARBHANI - 431402 (M.S.), INDIA
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THESIS

Submitted to the
Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani
in partial fulfilment of the
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MASTER OF SCIENCE
(Horticulture)
IN
VEGETABLE SCIENCE

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2019

CANDIDATE'S DECLARATION

I, hereby declare that, the entire work embodied

in this dissertation or part thereof,

has not been previously submitted

by me for a degree of

any University or

Institution.

Place : Parbhani
Date: 31/05/2019

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CERTIFICATE – I

This is to certify that the dissertation entitled **"GENETIC DIVERGENCE STUDIES IN SPINE GOURD (*Momordica dioica* Roxb.)"** "submitted by, **Miss. PATIL SAMIKSHA JAGDISH** to the Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (Horticulture)** in the subject of **VEGETABLE SCIENCE** is record of original and bonafide research work carried out by her under my guidance and supervision. It is of sufficiently high standard to warrant its presentation for the award of the said degree.

I also certify that the dissertation or part thereof has not been previously submitted by her for a degree of any university.

Place: Parbhani
Date: 31/05/2019

Dr. V. S. Khandare
Research Guide

CERTIFICATE-II

This is to certify that the dissertation entitled **"GENETIC DIVERGENCE STUDIES IN SPINE GOURD (*Momordica dioica* Roxb.)"** submitted by **MISS. PATIL SAMIKSHA JAGDISH** (Reg. No. 2017HT/15M) to the V**asantrao Naik Marathwada Krishi Vidyapeeth, Parbhani** in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (Horticulture)** in the subject of **VEGETABLE SCIENCE** has been approved by the student's advisory committee after viva voce examination in collaboration with the external examiner

( ) **Dr.V. S. Khandare**

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> ***We must stand on our own feets and fight as best as we can for our rights, so carry on your agitation and organize your forces power and prestige will come to you through struggle.***
>
> ***DR. B.R.AMBEDKAR***

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Place : PARBHANI
Date : 31/05/2019 **(*Samiksha Patil*)**

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ABBREVIATIONS

@ - at the rate
% - per cent

/ - per

CD - Critical difference

cm - Centimeter

CV - Coefficient of variance

DF - Degrees of freedom

e.g. - Exampli gratia (for example)

et al. - Et alia (and associates)

etc. - Et cetera

Fig. - Figure

g - Grams

G - Genotypic

GA - Genetic advance

GCV - Genotypic coefficient of variation

ha - Hectare

i.e. - That is

kg - Kilogram (s)

m - Meter

MPA - Meta phosphoric acid

MSS - Mean sum of squares

No. - Number

P - Phenotypic

PCV - Phenotypic coefficient of variation

q - Quintal

r - Correlation coefficient

SE ± - Standard error

Sig. - Significant

TSS - Total soluble solid

Viz. - Videlicet (namely)

Thesis Abstract

ABSTRACT

GENETIC DIVERGENCE STUDIES IN SPINE GOURD

[*Momordica dioica Roxb.*]

By

PATIL SAMIKSHA JAGDISH

A candidate for the degree

Of

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2019

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The present investigation was undertaken to estimate the genetic divergence in spine gourd genotypes and to carry out yield component analysis through correlation and path analysis. Twenty genotypes were sown in a randomized block design with three replications, during *kharif* 2018-2019 at Horticulture Research Scheme, (Vegetable) VNMKV, Parbhani , Maharashtra.

The D^2 analysis was carried out for twenty characters which partitioned the twenty genotypes into four clusters. The result revealed that, the maximum genetic divergence was observed between clusters I and III. The maximum intra cluster distance was shown by cluster I. The characters *viz.* fruit yield per plant, acidity, number of fruit per plant, fruit yield per hectare, node number at first female flower appearance and plant height contributed greatly towards diversity.

The analysis of variance revealed significant difference for twenty characters wide range of variability was observed for plant height, fruit yield per plant, fruit yield

per plot, fruit yield per hectare, plant height, number of fruits per plant, average fruit weight and single fruit weight.

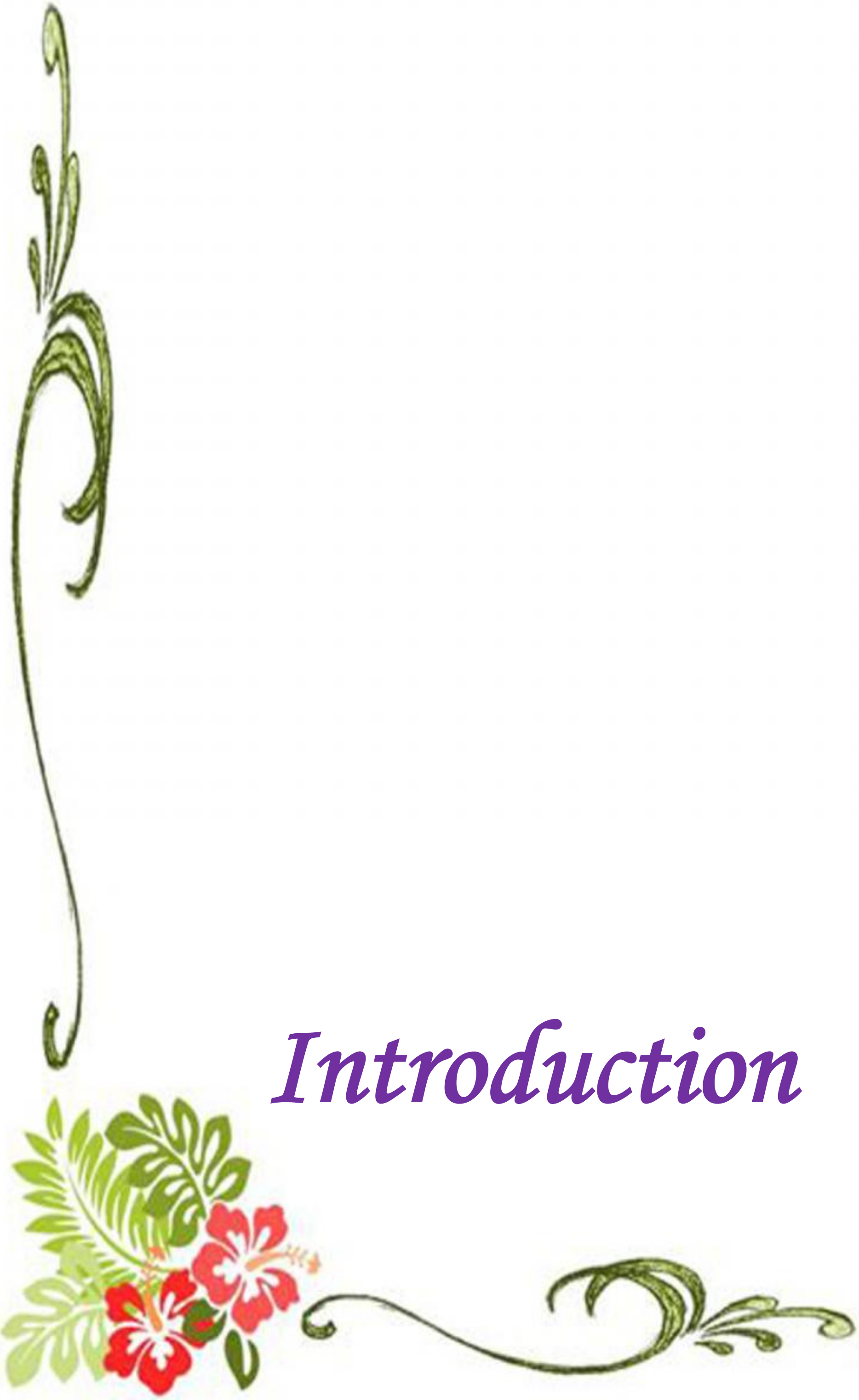
In a true agreement with the GCV and PCV values in the present investigation for the twenty characters was noticed and indicated additive genetic variance governing the high heritability with genetic advance as percent of mean.

Correlation studies revealed that, fruit yield per plant has exhibited highly significant positive association with plant height, number of branches per plant, days to last harvest , number of fruit plant , fruit length, fruit diameter, ascorbic acid , TSS and fruit yield per hectare at both phenotypic and genotypic level.

Path analysis revealed that maximum positive direct effect on fruit yield per plant was exhibited with node number of first female flower appearance , days to last harvest , number of fruit per plant, fruit pedicel length, ascorbic acid ,total soluble solid , Acidity , fruit yield per hectare at both phenotypic and genotypic level .

On the basis of the mean performance of the genotypes as MDH-1, GPR-1, GPR-5, MOD 10, MOD-11 , MOD-13, MOD-15, MDH- 3, MDH-4 were identified as promising lines for further crop improvement in spine gourd .

Introduction



CHAPTER-I

INTRODUCTION

Spine gourd (*Momordica dioica* Roxb.) is a cucurbitaceous crop, belongs to the family cucurbitaceae with chromosome number 2n=28, under the genus Momordica (Raj *et al*. 1993). It is an underutilized, dioecious and perennial crop known by various names like Kakrol, Kartoli, Kankad, Teasel gourd or Bhat kerala. As many of the species of this genus have been found to grow wide in India, Bangladesh, Sri Lanka, Myanmar and Malay etc. (Hooker, 1879) indicated that this region might be the origin of spine gourd. Kartoli mainly grown in Orisa, Bihar and West Bengal as a crop and kitchen garden plant but occurs as wild in Punjab, Uttar Pradesh, Rajasthan, Madhya Pradesh, Kerala and Maharashtra.

It is widely distributed in tropical and sub-tropical parts of India. For cultivation it requires a warm and humid climate with temperature ranging from 25-35°C and average rainfall of 1500-2500 mm. Commercial propagation of spine gourd is largely depending on tuberous roots, followed by stem cuttings and seeds. Planting is usually done during the summer months at the onset of monsoon. Spine gourd thrives well under warm humid climate. It can be grown in areas where temperature ranges between 25-40 ^{0}C with annual rain fall of 150-200 cm. Flowering usually starts in May to July and fruiting are available from July to September in most of areas. This popular vegetable has high demand in market but still remains as under utilized and under exploited due to vegetative mode of propagation and dioecious nature. In severe winter, underground tubers undergo dormancy but after harvesting of crop, the vine cuttings of that crop having 2-3 node from basal vine can be taken for planting before severe winter.

Spine gourd leaves are simple membranous, broadly ovate in outline, variable in length, cordate at the base, deeply lobed in 3-5 triangular lobes, distinctly denticulate. Petiole 1.3-4.5 cm long channelled above, pubescent and glandular. Stem is slender, branched, furrowed, glabrous and shining. Tendrils are elongated, simple, striate and glabrous. Roots are tuberous, used as planting material. Male flower is solitary, slender usually pubescent near the top, bract cuculate, strongly nerved, Calyx lobed distinct, linear lanceolate, petals are wholly yellow.

Female flowers peduncle nearly as long as male, with small bract below the middle of the peduncle, ovary clothed with long soft papillate. Fruit is shortly beaked, obtuse with inner red kernel, densely echinate with soft spines, green and yellow at maturity. Seeds are rounded broadly ellipsoid, slightly compressed, slightly and irregularly corrugated enclosed in red pulp.

The delicious young tender fruits are used as vegetable. Spine gourd fruit, per 100 g edible part, contains moisture 84.1g, fat 1.0 g, fiber 3.0 g, carbohydrates 7.7 g, carotene 162 mg, protein 3.1 g, calcium 33 mg, phosphorus 42 mg, iron 4-6 mg, thiamin 0.05 mg, riboflavin 0.18 mg and niacin 0.06 mg (Ram *et al.*,2004). Spine gourd root contains aliphatic compounds. It possesses several medicinal and curative properties against many ailments. Fruit are diuretic, alexiteric stomachic laxative and have antivenum property. It is also used to cure asthma, leprosy, excessive salivation, prevent the inflammation caused by lizard, snake bite, elephantiasis, fever, mental disorders, digestive disorders and troubles of heart and to treat discharge from mucous membrane. Fresh fruit juice is prescribed for hypertension. Spine gourd fruit is cooked in a small amount of oil and consumed for treating diabetes. Tender fruits are rubbed on skin for pimples. Seeds are roasted and taken for eczema and other skin problems. It is also used to cure fever, jaundice, asthma, bronchitis, piles, hepatic damages, bleeding piles bowel afflictions and urinary complaints. Leaf paste is applied externally to skin and orally two or three times daily for skin disease. Juice of root is stimulant, astringent, antiseptic. The mucilaginous tubers are antihelmintic, spermicidal, antifertility abortificant, used in case of bleeding piles, similar bowel afflictions and urinary complaints. Powder of root is applied to skin to make it soft and to reduce perspiration. The toasted root is used to stop bleeding from piles and also in bowel complaints (Baratakke, *et al.*2013). This popular vegetable has high demand in market because of good nutritional, medicinal value, high keeping quality, ability to withstand long distance transportation, high market price and good export potential.

Commercial cultivation of spine gourd has a number of problems including low yield, Fruits become inedible at maturity owing to the presence of large number of hard seeds. Low rate of tuber production (10-20 tuberous pieces per year), germination of seeds is very low or impossible due to hard seed coat , non-availability of improved varieties, difficulties in propagation by seed due to dormancy, dormancy of tubers and unpredictable sex ratio in seedling progeny (Ali, *et al.*1991). Overcoming all problems Genetic divergence has been considered as an important factor in discriminating the genetically diverse parents for successful hybridization programme in order to get potential transgressive segregants. Selecting genetically diverse parents for a successful hybridization programme helps in quantification of genetic diversity .

Correlation analysis is a biometrical technique to find out the nature and degree of associations among various traits. Therefore, information on variability of plant characters and association among yield and quality characters are of vital importance in plant breeding programme. The multivariate analysis, and in particular, the principal component and cluster analysis have been utilized for the evaluation of germplasm when studying various traits .Evaluation of germplasm is useful not only in selection of core collection but also its utilization in breeding programmes. Various numerical taxonomic techniques have been successfully used to classify and measure the pattern of genetic diversity in germplasm. In order to develop high yielding cultivars resistant to various stresses, exploitation of the gene poolis of paramount importance. A large number of variables are often measured by plant breeders, some of this may not be sufficient discriminatory power of germplasm evaluation, characterization, and management. In such case, principal component analysis (PCA) may be used to reveal patterns and eliminate redundancy in data sets (Adams, 1995).

There is need to improve its yield potential make its more acceptable among the indigenous populace. An assessment has been made to identify the differences among the genotypes and major variable which, leads to the identification of possible groups and relationships among genotypes.

Improvement in any crop depends upon the genetic variability available in the germplasm. High values of heritability estimates indicate the potential for substantial improvement using standard selection procedures. Heritability estimates in conjunction with estimates of genetic advance, are more useful in selecting superior genotypes. Knowledge of the association between yield and its contributing traits will be of great value in planning a breeding programme. (Lerner, 1958) stressed the importance of correlation of the various characters with yield. The phenotypic correlation indicates the extent of the observed relationship between characters, while genotypic correlation provides an estimate of inherent association between genes controlling any two characters. Path analysis splits the correlation coefficients into direct and indirect effects of a set of dependent variables on the independent variable thereby aids in the selection of elite genotype. All the above mentioned parameters are the pre-requisites to formulate the sound and successful breeding programme.

Hence an experiment was conducted on “Genetic divergence studies in spine gourd” to study the different genotypes collected from different regions of Maharashtra with the following objectives

OBJECTIVES

1. To assess the genetic divergence among genotypes.
2. To estimate the variability, heritability and genetic advance for yield and other components.

Review of Literature

CHAPTER - II

REVIEW OF LITERATURE

The success of breeding programme depends on the quantum of genetic variability available for exploitation. The information on the type of variation in the available genetic material and the part played by the environment on the expression of plant characters is of prime importance for the appraisal of rate and magnitude of possible improvement. A brief review of information available on the above aspects under study "**Genetic divergence studies in spine gourd (*Momordica dioica* Roxb.)** Since available relevant literature on spine gourd to the various aspects of present study is less, so some other cucurbits has also been reviewed briefly under the following heads

2.1 Genetic divergence
2.2 Genetic variability
2.3 Correlation studies
2.4 Path coefficient analysis

2.1 Genetic divergence

Study of genetic divergence among genotypes gives the relationship of one character with the other. Yield, itself is not a unitary character but the end product of various component characters either jointly or singly. Therefore, knowledge of divergence in genetic association of yield and various component characters are of economic worth in formulating and executing the breeding programme. Hence, the prime requirement is to have precise and clear-cut information on the strength and direction of association of these traits with any worth character and also inter relation among themselves. The selection efficiency is improved by making judicious combinations of the characters. The degree of associations between any character and its contributors can be estimated by correlation coefficient at genotypic and phenotypic levels. Correlation coefficient measure the genetic divergence among the genotypes. The literature available on correlation studies in spine gourd is reviewed as follows:

Parhi *et al.* (1993) grouped 13 varieties of bitter gourd into 6 clusters based on similarities of D^2 values. The most divergent clusters were III and V followed by III and IV. It was found that 100 seed weight contributed maximum to divergence followed by number of seeds per fruit and fruit length

Dora *et al*. (2001) collected eleven genotypes of *Trichosanthes dioica* for genetic divergence study in yield and yield attributing components. The genotypes were grouped into four clusters based on Mahalanobis D2 statistics, with the clustering pattern not reflecting a significant association between geographical distribution and genetic diversity. Inter-cluster distances were greater than intra-cluster distances, suggesting considerable genetic diversity among genotypes. The highest D2 value was recorded between cluster II (BPS-5, BPS-2, BPS-6 and BPS-7) and cluster IV (BPS-11). The genotypes included in these two clusters may give useful transgressive segregants in segregating generations.

Rasul and Okubo (2002) studied the genetic divergence among 30 M.dioica and one M.cochinchinesis clones and grouped them into 7 clusters. The wild relative of teasle gourd, Cl 31 was clustered as single group in cluster I. The maximum inter cluster distance was observed between the cluster I and V. Characters like chlorophyll content, fruit shape and pedicel length contribute considerably to the total divergence.

Hazra *et al.* (2003) grouped 167 accessions of pointed gourd into eight non overlapping clusters, with cluster IV comprising the highest number of accessions (37 accessions) whereas cluster VI comprising of the lowest number of genotypes (6 accessions). Intra-cluster distance ranged from 1.25 in cluster I to 1.65 in cluster VII. Cluster VII and V were the most diverse as indicated by the maximum inter-cluster distance between them (6.04).

Kutty and Dharmatti (2005) studied Genetic divergence among forty genotypes of Bittergourd (*Momordica charantia* L.) of different ecogeographic origin was assessed using Mahalanobis D2 statistics. The total genotypes were grouped into 10 clusters on similarities of D2 values. Most of the genotypes were grouped in cluster I (16), II (11), and IV (4), respectively. The genotypes falling in cluster II had the maximum divergence, followed by the cluster IV and I. The maximum inter cluster distance was between cluster VI and IX followed by cluster VII and IX. The characters like number of leaves at 50% flowering and productive length of vine contributed maximum to divergence.

Bharathi *et al.* (2005) grouped 32 genotypes into 7 clusters. Inter cluster distance were greater than intra cluster distance, revealing considerable amount of diversity among the genotypes. The maximum inter cluster distance was recorded between cluster VI and VII. They found that considerable diversity was due to yield per plant, number of fruits and fruit weight.

Dey *et al.* (2007) grouped 38 bitter gourd genotypes including two promising gynoecious lines into 6 clusters. The maximum inter cluster distance was obtained between cluster II and IV. Gynoecious lines were grouped into cluster IV. Cluster IV followed by cluster III showed superiority for yield and other desirable traits indicating their potentiality for providing basic material for future breeding programmes.

Tomar *et al.* (2008) studied genetic distance and cluster analysis among fifty diverse musk melon genotypes. The maximum genetic distance was observed between clusters II and V followed by Cluster IV and V, cluster I and II and cluster V and VI. However, cluster III and VII displayed lowest degree of divergence. The mean value of most of characters was highest in cluster III, while cluster II and VI showed highest values for two characters. Cluster II showed lowest mean values for maximum characters. Total soluble sugars followed by fruit yield per plant and total soluble solids contributed maximum towards genetic divergence.

Sundaram (2008) formed 6 clusters from 22 genotypes of bitter gourd. Among the six clusters, maximum number of genotypes was found in cluster I and the cluster V and VI were found to be mono genotypic. He observed that fruit weight contributed maximum to the divergence followed by yield of fruits per vine and length of fruit.

Kabir *et al.* (2009) estimated the genetic diversity among twenty four genotypes of pointed gourd by using D2 statistical for nine characters. The genotypes were grouped into five clusters. The cluster I and III consisted of highest number of genotypes and it was six. The cluster IV contained the lowest number of 23 genotypes and it was three. The inter cluster distance were larger than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups. The highest intra cluster distance was computed for cluster IV (35.80) and the minimum intra cluster distance was found in cluster III (18.37).

Bharathi *et al*. (2010) studied genetic diversity among the 26 accessions of spine gourd collected from eastern India and grouped them into 3 clusters following Ward's clustering technique. The maximum inter-cluster distance was observed between clusters I and III. Cluster I was characterized with genotypes early in flowering (except CHSG 119), more number of fruits per plant (> 100), number of seeds per fruit (> 10) and greater yield per plant (> 1.8 kg/plant). Cluster II comprised the accessions having high individual fruit weight and 100-seed weight. The accessions grouped in cluster III recorded lower values for most of the traits studied.

Rahman *et al*. (2011) grouped 11 genotypes of sweet gourd into 3 clusters. They found the maximum inter cluster distance between the cluster II and III. Cluster II had highest mean values for node to which first female flower appears, fruit weight, fruit length, fruit diameter, fruit girth, days taken from fruit set to edible maturity and fruit yield per vine.

Rabbani *et al*. (2012) collected sixty genotypes of ridge gourd (*Luffa acutangula* Roxb.) and studied their variability, character association and genetic diversity. Based on Mahalanobis D2 statistics, the sixty genotypes were grouped into four different clusters. The average inter-cluster distances were always higher than the average intra-cluster distances indicating wider genetic diversity among the genotypes among the clusters. Custer-III had the maximum intra-cluster distance (97.9).

Kundu *et al.* (2012) assessed genetic divergence among 36 genotypes of bitter gourd (*Momordica charantia* L.) Through multivariate analysis based on 22 characters 36 genotypes were grouped into six distant clusters. Cluster VI includes maximum genotypes (12) followed by cluster I (6) and cluster II (6). Cluster V, cluster III and cluster I comprised 5, 4 and 3 genotypes respectively. The inter-cluster distances were higher than the intra-cluster distances. The inter-cluster distance was maximum between cluster III and IV (28.71) followed by the distance between cluster I and cluster IV (23.61). The intra-cluster distances in all the 6 clusters were more or less low indicating the closeness of genotypes within the same cluster. The highest intra-cluster distance was observed for cluster III (1.84) followed by the cluster I (1.38).

Pandit *et al* .(2012) collected thirty one diverse genotypes of snake gourd were grouped into six clusters with cluster 1 having the highest number of genotypes (13) followed by cluster 2, 10 genotypes; cluster 3 contained 5 and clusters 4, 5 and 6, one genotype each. Such a clustering pattern shows wide range of diversity among the genotypes. The intra-cluster distance was low, indicating homogeneity in the genotypes in a particular cluster. The maximum inter-cluster distance was recorded between cluster 3 and 5 (18.003).

Yadav *et al*. (2013) evaluated thirteen diverse genotypes of bitter gourd to study the extent of genetic variability. The analysis of variance showed significant difference among all the genotypes for yield and its attributing traits. The highest range of variation was recorded for yield/ha, followed by fruit weight, number of nodes per vine, days to first appearance of female flower, days to first appearance of male flower, fruit length and minimum variation was observed for the trait yield per vine.

Gautam (2013) worked on 42 diverse genotypes of ridge gourd collected from different indigenous sources planted in augmented design-II. The study was undertaken to estimate the genetic diversity by Non-hierarchical euclidean cluster analysis. According to the study 42 diverse genotype of ridge gourd were grouped into three non-overlapping clusters The analysis revealed that the maximum inter-cluster distance (5.684) was found between cluster I and II, while maximum cluster distance was observed in cluster III (3.550).

Kant Visen *et al*. (2015) analysed genetic diversity for yield and its contributing traits in 31 bottle gourd genotypes. The cluster analysis grouped all 31 bottle gourd genotypes into 5 major clusters based on D2 value. Extreme genetic divergence was estimated among clusters. Maximum number of genotypes were grouped into cluster V included ten genotypes, whereas, cluster II included eight genotypes. The cluster I had six genotypes, which is followed by cluster IV and cluster III had only three genotypes in each cluster. Fruit length, fruit girth and average fruit weight contributes maximum towards genetic divergence.

Tyagi *et al.* (2017) Studied the genetic divergence in Bitter Gourd (*Momordica charantia)* genotypes of bitter gourd were grouped by Tocher's method into six distinct clusters. The cluster IV had maximum number of genotypes (7), followed by cluster V. The inter-cluster distances were higher than the intra-cluster distances. The inter-cluster distance was maximum between cluster III and VI (58.37), followed by cluster II and VI which indicating that members of these two clusters are genetically very diverse to each other. The highest intra-cluster distance was observed for cluster I (18.42) followed by the cluster V. The cluster -IV and III and II performed L.) better in most of the biometric characters. Among 12 characters studied, vine length contributed maximum (34.41%) towards genetic divergence followed by fruit diameter and average fruit weight in bitter gourd.

Bhagat *et al.* (2018) studied genetic diversity among spine gourd genotypes was executed through principal component analysis first seven principal component axes accounted for 76.4% variation towards the divergence. Among four clusters cluster III had highest number of genotypes (12) on the other hand cluster I (11) genotypes cluster II (8) and cluster IV contain only two genotypes in PCA and cluster analysis the genotypes grouped into four different clusters based on principal component scores.

2.2: Genetic variability

Genetic variability is of great importance to begin with planning of research programme. The existence of very high to low an moderate genetic variability with respect to yield and yield attributing traits is the basic need in order to select the desirable types. Information on important biometrical techniques such as simple measures of variability, components of variability, association analysis, D2 statistics and discriminant function analysis are essential for the systematic assessment of variability existing in the natural population, selection of elite genotypes and to chalk out an efficient breeding programme for the genetic improvement of yield and its contributing traits. A review of literature on these aspects is presented below.

Baruah *et al*. (1993) carried out genetic variability and association studies involving twenty genotypes of sweet gourd. Characters like number of leaves per plant and thickness of fruit pericarp exhibited the highest estimates of genotypic and phenotypic coefficients of variability.

Bhave *et al.* (2003) reported higher phenotypic coefficient of variation than genotypic coefficient of variation for flowering duration, harvesting span, fruit length, average fruit weight, fruit number per vine and total fruit yield per vine and high genotypic coefficient of variation and phenotypic coefficient of variation for total fruit yield.

Ram *et al*. (2004) evaluated twenty four diverse germplasm of kartoli. The widest range was recorded for days to female flower anthesis. The characters like days to female flower anthesis, fruit set to edible maturity, plant height, fruit diameter, fruit length, number of fruits/plant and yield/plant expressed maximum variability at phenotypic and genotypic level.

Choudhary *et al.* (2008) observed highly significant differences among genotypes were recorded for all the characters in ridge gourd. Maximum range of mean values was obtained for fruit weight followed by yield per plant and fruit length. High degree of variability was observed for fruit weight, yield per plant, fruit length, node at Ist female flowering and fruits per plant. High estimates of heritability in broad sense were observed for fruit weight and fruit length suggesting both these traits are governed by additive gene action.

Rana and Pathak (2011) studied genetic variability, character association and path analysis were studied in 21 genotypes of snake gourd. The genotypic coefficient of variation was high for days to seedling emergence, length of fruit, total number of male flowers, total number of seeds per fruit, total number of fruits per plant and yield of fruit. High to moderate heritability as well as genetic advances were estimated for days to seedling emergence, number of seeds per fruit, days to 50% female flower opening, days to first fruit setting, days to first female flower opening, days to 50% fruit setting and total number of male flowers. Correlation studies revealed that fruit yield had significant positive correlation with total number of fruits, total number of primary branches and total number of nodes.

Naik *et al.* (2012) studied five female clones of Teasle gourd were evaluated to estimate the variability, heritability and genetic advance in randomized complete block design with four replications. Higher phenotypic coefficients of variation were observed for all the characters except fruit length at marketable stage. Total sugar in mesocarp, total sugar in exocarp, reducing sugar in mesocarp, ascorbic acid in exocarp, ascorbic acid in mesocarp, total soluble solids (TSS) in exocarp, b-carotene in exocarp, acidity in mesocarp, b-carotene in mesocarp, TSS in mesocarp, acidity in exocarp showed high heritability coupled with high genetic advance .

Kumar *et al.* (2013) evaluated the performance, genetic variability, heritability, genetic advance, correlation and path analysis for yield and yield contributing characters of 20 sponge gourd genotypes. Significant variations were found for all the characters in all the genotypes used in the experiment. Highest genotypic and phenotypic variations were observed for total yield per vine followed by number of seeds per fruit, average weight of fruit and total soluble solids. Number of seeds per fruit, average weight of fruit and specific gravity showed high heritability with high genetic advance.

Devi and Mariappan (2013) recorded higher values of phenotypic coefficient of variation and genotypic coefficient variation for fruit weight, fruit length and number of fruits per plant in snake gourd. They were also observed high heritability along with high genetic advance for fruit length, fruit yield, fruit girth and number of fruits per plant in snake gourd which is indicative of additive gene action in control of these traits.

Basumatary and Bora (2014) studied analysis of variance revealed significant differences among the genotypes for all the characters studied in 15 local germplasm of spine gourd (*Momordica dioica* Roxb.) High genotypes variance followed by high genotypic coefficient variation was observed for node at which first female flower appears, vine length, 100 seed weight and fruit yield per plant. In general the phenotypic coefficient of variation (PCV) estimates were higher than the genotypic coefficient of variation (GCV) estimates for all the traits. Correlation study revealed highly significant and positive correlation of yield per plant with number of primary branches, internode length, fruits per plant, fruit diameter and single fruit weight.

Pathak *et al*. (2014) studied Variability, correlation and Path coefficient among eight horticultural characters of twenty bitter gourd hybrids. High genotypic (GCV) and phenotypic coefficient of variation (PCV) was observed for number of fruits per plant, fruit weight and fruit length whereas low GCV and PCV was observed for days to first male and female flower anthesis (days after sowing). For most of the parameters under study, PCV was found to be higher than GCV. High heritability with high genetic advance (GA) was observed for fruit weight, fruit length and number of fruits per plant which is an indicative of greater proportion of additive genetic variance and consequence a high genetic gain from selection.

Radha Rani *et al.* (2015) determined the various parameters of genetic variability and nature of interrelationships among traits affecting yield in bitter gourd.

Analysis of variance showed highly significant differences for all the characters studied. High heritability in association with high genetic advance as per cent of mean was observed for yield/vine, number of fruits/vine, average fruit weight, fruit length, vine length and number of laterals/vine. Yield /vine expressed positive and significant genotypic association with number of fruits/vine, average fruit weight, vine length, number of laterals/vine and fruit length whereas significant negative association with sex ratio, days to 1st female flower and node number at 1st female flower appeared.

Mandal *et al* .(2015) evaluated the twenty seven genotypes of bottle gourd , The analysis of variance showed highly significant differences for all the characters studied indicating considerable variability among the genotypes. The highest GCV (34.84%) and PCV (35.14%) were observed for sex ratio. The differences between GCV and PCV were high for fruit number per plant indicating environmental influences. High heritability associates with high estimates of genetic advance in per cent of mean were noted for node number of first female flower, sex ratio, fruit length, fruit girth, number of fruits per plant and fruit yield per plant. Indicated the presence of additive gene effect and selection for these traits would be effective.

Damor *et al.* (2016) studied genetic parameters to elucidate the genetic variability, heritability and genetic advance in forty bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] Analysis of variance revealed presence of considerable variability among the genotypes for all sixteen characters. Phenotypic coefficient of variation (PCV) was somewhat higher than genotypic coefficient of variation (GCV) for all the characters studied. High heritability combined with high genetic advance was observed for the characters first male flowering node number, first female flowering node number, length of pedicel, fruit length, fruit girth, fruit weight, number of fruits per plant, fruit yield per plant, total soluble solids, total sugar content, antioxidant activity and total chlorophyll content indicates the preponderance of additive gene action and better scope for improvement of these characters for effective selection of genotypes.

Pal *et al.* (2016) evaluated 30 genotypes of bitter gourd and estimated the nature and magnitude of genetic variability, heritability and genetic gain for twenty-four important characters. The magnitude of PCV was higher than the corresponding GCV for all the characters studied. These confirm presence of sufficient variability in the germplasm, predominance of additive gene action and high transmissibility of the characters. Therefore, direct selection will be rewarding depending upon these traits. Hence, hybridization followed by selection will be promising for improving these traits.

Khan *et al.* (2016) studied Genetic variability, heritability and path coefficient analysis in 21 genotypes of snake gourd. The phenotypic coefficient of variations was found slightly higher than the genotypic coefficient of variations for all characters studied. The genotypic coefficient of variation was high for the fruit yield, number of fruits per vine, length of fruit and single fruit weight. Correlation studies revealed that the fruit yield had a significant, positive correlation with the number of fruits per vine, length of fruit and single fruit weight. Importantly, more than 90% of the genotypic total variation was contributed by the characters included in the path analysis. The highest direct positive effect was recorded for the number of fruits per vine.

Jena *et al*. (2017) evaluated 22 genotypes of Pointed Gourd (*Trichosanthes dioica* Roxb.) The objective was to estimate the nature and magnitude of genetic variability, heritability and genetic gain for seventeen important characters. Analysis of variance revealed presence of considerable variability among the genotypes for all seventeen characters. The magnitude of PCV was higher than the corresponding GCV for all the characters studied. Among the characters studied, high PCV and GCV were observed for characters like observed fruit weight (g), pulp weight per fruit (g), pulp seed ratio, number of seeds per fruit, seed weight per fruit, internodal length and fruit yield (t/ha) indicating high variability available in the germplasm for these characters for further improvement.

Bhagat *et al* . (2017) Studied with thirty four spine gourd (*Momordica dioica* Roxb.) genotypes for evaluate their performance for various quantitative as well as qualitative characters. All the qualitative characters *viz.* fruit colour, fruit shape, leaf colour, leaf margin, leaf pubescence, stem colour, spine strength, conical spine density, pedicel attachment with the fruit, node colour, collection site showed wide variation.

Singh *et al* . (2017) studied the genetic variability, heritability and genetic advance for eleven yield and its contributing traits in nine bottle gourd genotypes. Highly significant treatment differences for all traits in the three environments *viz.,* E1, E2 and E3 except for fruit circumference in E2 and vine length in E3, represent inherent genetic difference among the genotypes. The field condition revealed that PCV was higher than the GCV in all environments and pooled for most of traits

Rathore *et al.* (2017) showed that, significant effect on the minimum days to germination (3.53 days), days to first appearance of male and female flower (34.07 and 38.30 days), node number at which first male and female flower appear (5.60 and 11.53), sex ratio (34.00), length of main vine (5.30m), minimum days to first harvesting (43.93 days), fruit length (24.27 cm), fruit weight (132.60 gm), fruit diameter (4.75 cm), fruit yield (60.17t/ha), T.S.S. (4.58^0 Brix) and vitamin C (4.59 mg/100gm) was observed maximum in treatment with T6 RIGVAR-6. The treatment T6 (RIGVAR-6) was found to be the best out of 12 genotypes in terms of growth, yield, quality and economic returns.

Rambabu *et al.* (2017) revealed variability with 21 genotypes of bottle gourd,. The results revealed that the greatest diversity was observed in fruit characters especially fruit shape and fruit colour among the genotypes for various characters studied. Analysis of variance revealed significant differences among genotypes for all the characters. In general PCV was marginally higher than the corresponding GCV indicated the less influence of environment in the expression of the characters under study.

Yadagiri *et al.* (2017) evaluated 20 genotypes of bitter gourd for evaluating their performance for various horticultural characters. There was a great deal of significant correlation for all the characters among the genotypes. Correlation analysis revealed that Length of vine (0.640), number of branches per vine (0.577), number of male flowers per vine (0.594), number of female flowers per vine (0.529), number of fruits per vine (0.649), length of fruit (0.724), weight of fruit (0.961), number of seeds fruit (0.360), seed weight per fruit (0.380) had significant positive correlation for yield. Further, path coefficient analysis partitioned the correlation into direct and indirect effects. Yield was found to be directly correlated with crop duration (0.004), length of vine (0.030), number of seeds per fruit.

Usha Rani and Reddy (2017) studied five parents of bottle gourd (*Lagenaria siceraria* (Molina) and their ten F3 crosses derived from 5X5 half diallel set. The characters like fruit length (99.70), days to first female flower opening (98.40), number of branches per vine (98.10) showed high heritability values. Vine length

(60.42) and number of branches per vine (38.01) recorded highest values for genetic advance as per cent of mean offering greater scope for selection. Correlation analysis revealed that number of branches per vine (0.684**), number of fruits per vine (0.898**), fruit length (0.803**), fruit girth(0.588*), number of seeds per fruit(0.539*) showed strong positive correlation with yield and among themselves. Therefore these characters could be used as indices for selection of genotypes with high yielding potential.

Ananthan and Krishnamoorthy (2017) studied the performance of genetic variability, heritability, genetic advance, correlation and path analysis for yield and yield attributing characters namely first female flower node, days taken for first female flowering, number of fruits per plant, fruit length, fruit weight (g), fruit yield per plant (kg) of twenty ridge gourd genotypes .The genotypes exhibited higher percentage of genotypic coefficient variability, phenotypic coefficient variability and genetic advance with fruit yield per plant (31.55, 32.86 and 62.39) respectively and the heritability was high with fruit length (98%).

Karthik *et al.* (2017) revealed that highly significant variation among genotypes for the characters for the viz., characters such as node number for the first female flower appearance, days taken for the first male flower appearance, days taken for the first female flower appearance, vine length, leaf length, fruit length, ovary length, peduncle length, fruit girth, number of fruits per vine, fruit weight, fruit yield/vine and fruit yield/ha. High PCV, GCV, heritability, genetic advance were observed for fruit length (cm), number of fruits per vine, yield per vine (kg) and fruit yield (t/ha).

Prabhakar and Kushwah (2017) screened the Spine gourd (*Momordica dioica Roxb.* ex Willd) germplasm lines for yield and yield attributing traits. A total of ninety germplasm collected from different regions of Madhya Pradesh and was grown in Randamized Block Design during Kharif 2013. The widest range was recorded for fruit yield per plant and number of fruits per plant, while narrowest range was observed for fruit rind thickness. The characters like number of shoot per plant, fruiting period, fruit length and average fruit weight expressed maximum variability.

Maurya *et al* . (2018) reported that analysis of variance genotypes evaluated differed significantly among all the treatment for all the twelve traits. The PCV (phenotypic coefficient of variation) were higher than corresponding GCV (genotypic coefficient of variation), it reveals that variation is due to genotypes as well as environmental factors. The estimates of genotypic as well as phenotypic coefficient of variability were observed higher for no. of fruit per plant followed by fruit yield per plant, vine length and node no. of first staminate flower, fruit length whereas, average fruit weight, node number to anthesis of first pistillate flower, and were moderate coefficient of variability.

Verma *et al* . (2017) determined the magnitude of variability, 35 genotypes of pointed gourd have been evaluated .Through analysis of variance, a high significant difference was found for almost all characters indicating a greater opportunity of exploit variability. PPG-26 has obtained highest mean for fruit length (10.39) and PPG-2 for fruit diameter (4.35) while PPG-31 genotype was resulted as the earliest among all. High GCV along with high PCV was found for the characters like Number of seeds per fruit (33.22 and 33.45), Fruit yield (q/ha) (31.38 and 33.09), Node number to first female flower (29.39 and 30.26) and Number of fruits per plant (29.29 and 29.70). Whereas, high heritability coupled with greater genetic advance was observed for number of fruit per plant and fruit yield per hectare which indicates that these characters are govern with additive gene effect with minimum environment effect for direct selection of pointed gourd genotypes for further improvement.

Chandrashekhar *et al.* (2018) evaluated Thirty two genotypes exhibited significant differences for all the traits under study. A wide range of variability along with high estimates of PCV and GCV was observed for number of nodes per plant, internode length, node at which first female flower appearance, weight of the fruit (g), fruit length (cm), fruit diameter (cm), flesh thickness (mm), rind thickness (mm), yield per plant (kg) and total yield (t ha-1), indicating high variability available among the germplasm for these characters for further improvement.

Tiwari *et al* . (2018) determined genetic variability and heritability in narrow sense involving 9 parental lines of bitter gourd observations were recorded on 13 characters *viz.* node number to first staminate and pistillate flower anthesis, days to first staminate and pistillate flower opening, days to first fruit harvest, number of primary branches per plant, node number of first fruits set, vine length (m), fruit length (cm), fruit diameter (cm), number of fruits per plant, fruits, fruit weight (g), yield per plant (kg). Moderate variability showed in fruit yield per plant Rest of characters showed low coefficient of variability.

Yadav *et al.* (2018) evaluated thirty female clones of spine gourd to estimate the variability, heritability and genetic advance. The phenotypic coefficient of variation was in higher than phenotypic coefficient of variation for all traits. High heritability coupled with high genetic advance as percentage of mean were observed for days to last fruit harvest, internodal length, fruit yield per plant and days to first fruit harvest indicating that these traits were under the additive gene control and simple selection can be used for further improvement in these traits of spine gourd.

Sultanaa *et al. (*2018) studied genetic parameters were studied to elucidate the genetic variability, correlation and path co-efficient analysis in thirty-nine genotypes of bottle gourd .The analysis of variance showed highly significant differences for all the characters studied indicating considerable variability among the genotypes.

2.3 Correlation studies

Dora *et al.* (2003 b) evaluated eleven pointed gourd (*Trichosanthes dioica*) selections which were assessed to estimate genetic variability and correlation for yield and yield attributes. High genetic coefficient of variation (GCV) estimate was observed for the characters such as node at which first female flower appears, number of fruits per plant, number of nodes per plant and length of vine.. The characters having high GCV also exhibited high genetic advance. Yield per plant had a significant positive correlation with number of fruit set, fruits per plant, and fruit retention.

Kutty and Dharmatti (2005 a) observed that days to first female flower opening, node number of first female flowering, number of leaves at 50% flowering, days to first harvest, productive length of vine, number of seeds per fruit, fruit length, number of fruits per plant, total yield per plant, fruit weight, fruit fly infestation and downy mildew incidence. They found that the number of leaves at 50% flowering stage, number of seeds per fruit, fruit length, number of fruits per plant and fruit weight were the most important traits contributing to yield per plant as they showed positive correlation.

Sanwal *et al.* (2007) observed that the phenotypic coefficient of variation (PCV) were relatively higher than their corresponding genotypic coefficient of variation (GCV). High heritability coupled with high genetic advance was observed for number of fruits per plant, fruit yield per plant and days to first flowering. However, high heritability coupled with low genetic advance values were observed for average fruit weight and fruit length in sweet gourd.

Rukam *et al*. (2008) evaluated fifty genotypes of Muskmelon (*Cucumis melo* L.) for variability, correlation and path analysis for yield and its contributing characters. The analysis of variance showed significant variation for all the characters, indicating presence of sufficient variability in the material studied. The moderately high genotypic and phenotypic coefficient of variation was observed for fruit yield per plant followed by acidity percentage, fruit per plant and total soluble sugar. Genotypic correlations were higher than those of their respective phenotypic correlation coefficients in majority of the cases suggesting that genotypic correlations were stronger, reliable and free from the environment factors.

Khan *et.al* (2009) evaluated 24 accessions of pointed gourd for yield and yield components revealed high phenotypic and genotypic coefficients of variation (PCV and GCV, respectively). Wide variations among the accessions in respect of plant, leaf, flower, fruit and seed characters were recorded. The accessions varied significantly for days required to first flowering, number of node at 1st harvest, inter node length at first harvest, vine length at 1st harvest, fruit length, fruit breath, fruit weight, pulp weight per fruit, pulp seed ratio, number of fruits per plant, weight of fruits per plant, number of seeds per fruit, weight of seed per fruit and yield.

Resmi and Sreelathakumary (2012) evaluated twenty five genotypes of ash gourd *Benincasa hispida* (Thunb.) Cogn.] high heritability coupled with high genetic advance was observed for fruits per plant ,average fruit weight ,fruit girth ,fruit length and yield per plant which indicate scope for improvement of these characters through selection.

Husna *et al.* (2011) Variability, correlation and path analysis among different characters of thirty one bottle gourd genotypes were studied. High genotypic co-efficient of variation (GCV) was observed for yield per plant, fruit weight whereas low genotypic co-efficient of variation was observed fruit breadth. In all cases, phenotypic variances were higher than the genotypic variance. Correlation studies revealed that highest significant association of yield per plant with reproductive characters no. of fruit per plant followed by fruit weight at genotypic and phenotypic level.

Devi and Mariappan (2013) recorded higher values of phenotypic coefficient of variation and genotypic coefficient variation for fruit weight ,fruit length ,number of fruits per plant in snake gourd ,they were also observed that high heritability along with high genetic advance for fruit length, fruit length ,fruit yield ,fruit girth, number of fruits per plant in snake gourd which is inadicative of additive gene action in control these traits.

Akter *et al.* (2013) studied variability, correlation coefficient and path analysis for yield and quality related traits of 30 pumpkin genotypes. High genotypic coefficient of variation (GCV) and high heritability coupled with high genetic advance in percent of mean were observed for beta-carotene followed by non-reducing sugar, number of seeds per fruit, yield per plant, dry weight, flesh thickness, number of male flowers per plant and number of female flowers per plant which indicated that these characters were under additive gene control and selection for genetic improvement for these traits might be effective. Correlation co-efficient between yield per plant with number of primary branches, number of fruits per plant and single fruit weight were positive and highly significant.

Pathak *et al*. (2014) studied correlation and Path coefficient among eight horticultural characters of twenty bitter gourd hybrids were studied. High genotypic (GCV) and phenotypic coefficient of variation (PCV) was observed for number of fruits per plant, fruit weight and fruit length whereas low GCV and PCV was observed for days to first male and female flower anthesis (days after sowing). For most of the parameters under study, PCV was found to be higher than GCV.

Aaliya *et al*. (2014) studied Fifty genotypes of spine gourd (*Momordica dioica* Roxb.) Correlation and path coefficient analysis were carried out to study the character association and contribution, respectively for twelve quantitative characters. Correlation and path coefficient analyses revealed that fruiting period and number of fruits per plant not only had positively significant correlation with fruit yield but also had positively high direct effect on it and are regarded as the main determinants of fruit yield. Days to first fruit harvest had positively moderate direct effect on fruit yield and its association was negatively significant, days to last fruit harvest had negatively high direct effect on fruit yield and its association was significant positively, hence restricted simultaneous selection can be made for days to first fruit harvest and days to last fruit harvest.

Singh *et al.* (2014) estimated the nature and magnitude of genetic diversity were estimated in 25 bitter gourd genotypes on ten quantitative traits results indicated that high phenotypic and genotypic coefficients of variation were found for fresh fruit yield per plant followed by fruit length, fruit width and number of fruits per plant, indicating high genetic variability in these traits. High heritability coupled with high genetic advance as percent of mean was observed for fruit length, yield per plant, fruit diameter, fruit weight, branch per plant and seeds per fruit, indicating the possible role of additive gene action.

Islam *et al.* (2014) studied correlation and path coefficient in seven snake gourd genotypes, for yield and eleven yield contributing characters. The corelation studies revealed that yield\plant had positive and highly significant corelation both in phenotypic and genotypic level with fresh weight /fruit, fruit girth, fruits/plants , plant height and fruit length which indicated that yield could be increase by selecting these characters. Direct indirect effect were measured using path coefficeint analysis in order to obtain mechanism of interrelationship between yield /plant.

Jat *et al.* (2014) found that the maximum phenotypic and genotypic coefficient of variation (PCV and GCV) was observed for acidity of fruit followed by weight of fruit, total fruit yield per vine, rind thickness and total soluble solids. High estimates of heritability (broad sense) were observed for days to anthesis of first female flower, weight of fruit and diameter of fruit with high genetic advance. The maximum genetic gain in per cent was observed for acidity of fruit, weight of fruit and total yield per vine in cucumber.

Janaranjani and Kanthaswamy (2015) studied different characters in bottle gourd comprising 36 hybrids obtained by crossing 9 lines and 4 testers by line x testers method to study the correlation and direct and indirect effects of different characters on fruit yield. The overall analysis reveals that fruit yield was positively and significant correlated with fruit flesh thickness, number of fruits per vine and number of fruit pickings. The path analysis indicated that number of fruits per vine, days to first female flower opening, fruit cavity and fruit weight had positive direct effect on fruit yield.

Tiwari and Tigga (2015) analysed variation and best combination for sixteen different characters among twelve Spine gourd genotypes was analyzed wide variations for all the characters indicating sufficient genetic variability to exploit in a breeding programme. The present study revealed that for development of hybrids/varieties with better adaptability, good yield potential and resistance to biotic and abiotic stresses should be undertaken. The yield potential of spine gourd could be increased by adopting improved genotypes and standardized agro- techniques.

Gupta *et al.* (2015) observed correlation of various characters with yield is useful and provides criteria for direct selection of component characters. While selection for yield, improvement of yield contributing characters, which can be better ascertained if the nature and kind of association of such traits with yield is available, must be considered.

Singh *et al* . (2016) revealed that the locally collected genotypes of pointed gourd, correlation coefficient analysis was greater than phenotypic correlation coefficient for most of the characters indicating potential inherent association between the various qualitative traits. The correlation coefficient of yield was found to be positive and significant with length of vine (0.687 and 0.588 cm), number of fruits plant-1 (0.713 and 0.935), and fruit volume (0.643 and 0.808 cc) at both phenotypic and genotypic levels. Average fruit weight (0.718g), number of vine (0.679) and first flower appearance after node (-0.537) at genotypic and fruit diameter (0.583 cm) phenotypic level exhibited significant positive correlation with fruit yield plant.

Bhagat *et al.* (2017) studied 33 genotypes of spine gourd for estimation of genetic parameters, correlation, principal component analysis and cluster analysis. Fruit yield per plant was observed to be positively associated with 43 significant positive correlations between yield and number of first flowering node, ovary length, single fruit weight and number of fruit per plant.

Muralidharan (2017) observed that quantitative and qualitative traits in Bottle gourd all 24 genotypes was used to partition the genotypic correlation into components of direct and indirect effects. The emphasis should be given to improve fruit yield per plant in bottle gourd was found significant and positively correlated with fruit flesh thickness (r = 0.522) and fruit weight (r = 0.644).

Ramesh *et al* . (2018) revealed that fruit yield was positively and significant correlated with fruit percent, number of fruits per plant, fruit length, average fruit weight, fruit diameter, vine length at 90 days, sex ratio and rind thickness while selecting a good hybrid for enhancing the yield of ridge gourd. In ridge gourd 16 important growth, earliness, yield and quality parameters were subjected to Genotypic and Phenotypic path coefficient analysis. Fruit yield per plot had high positive direct effect on yield.

2.4 Path coefficient analysis

Latif (2008) Studied on the variabilities, genetic parameters, character associations and path coefficients between yield and fourteen important characteristics of ten ash gourd genotypes were conducted to determine the critical traits that contribute to yield. The genotypes exhibited a wide range of variability for all the characters studied.. Highest Genetic advance in percentage of Mean (GAPM) were observed in node order of first male and female flower anthesis followed by plant height at first male and female flower anthesis and edible fruit yield per plant and number of plant per hectare.

Rukam *et al.* (2008) revealed that the path analysis based on genotypic associations fruits per plant and moisture percentage were the main yield attributing characters in fruit yield of muskmelon, because of its high positive direct effect and positive correlation with fruit yield per plant. In addition to moisture percentage and fruits per plant, total soluble solids also exhibited positive direct effect on fruit yield per plant.

Hanchinamani and Patil (2009) conducted an experiment to investigate the correlation co-efficient in relation to fruit yield and few other yield attributing characters in cucumber. Data were recorded for 20 characters. Fruit yield had positive and highly significant phenotypically and genotypically association with vine length, inter-nodal length, number of nodes per vine, number of branches per vine, fruit length, fruit diameter, flesh thickness, average fruit weight, dry weight of fruits, number of marketable fruits per vine, number of unmarketable fruits per vine and total number of fruits per vine.

Kumar *et al.* (2011) conducted a study comprising 24 hybrids obtained by crossing 11 parents in bottle gourd. Analysis of variance revealed that adequate variability among the all genotypes (both Parents and Hybrids) for all characters. It was observed that genotypic and phenotypic coefficient of variations was observed high for fruit yield per plant and followed by fruit length and number of seeds per fruit. Heritability was high for fruit yield per plant, number of seeds per fruit and fruit diameter. Genetic advance was high for fruit yield per plant. Hence, there is a scope for these characters that they may be improved through selection.

Khule *et al.* (2011) studied correlation in 30 genotypes of sponge gourd and revealed that marketable fruit yield per plant exhibit significant positive correlation with number of fruit per plant and fruit length. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting that the environmental influence reduces the relationship between yield and yield contributing characters of sponge gourd. Path coefficient analysis showed that number of fruit per plant, days to appear first female flower, fruit length, fruit diameter, number of seeds per fruit and 100-seed weight had direct positive effects on marketable fruit yield per plant. This indicates that this character was the major contributor to fruit yield.

Akter and Rasul (2013) studied variability, correlation coefficient and path analysis for yield and quality related traits of 30 pumpkin genotypes. Path coefficient analysis revealed that the maximum direct contribution towards yield was obtained through number of fruits per plant followed by days to first female flower and single fruit weight indicated that these traits should be considered as primary components of yield. Negative direct effect on yield was exerted by total sugar followed by number of female flowers per plant, reducing sugar and brix content.

Chakraborty *et al.* (2013) found that the maximum direct effect on fruit yield per vine was through traits like number of fruits per vine followed by fruit weight at phenotypic level in bitter gourd.

Kumar and Ameta (2013) studied 20 sponge gourd genotypes performance, genetic variability, heritability, genetic advance, correlation and path analysis for yield and yield contributing characters. Highest genotypic and phenotypic variations were observed for total yield per vine followed by number of seeds per fruit, average weight of fruit and total soluble solids. Number of seeds per fruit, average weight of fruit and specific gravity showed high heritability with high genetic advance. Total yield per vine was found to be positively and significantly correlated with number of fruits per vine, average weight of fruit and number of seeds per fruit. Path coefficient analysis revealed that average diameter of fruit, number of primary branches, number of fruits per vine, average weight of fruit and total soluble solids showed positive direct effects on total yield per vine.

Pathak *et al*. (2014) revealed that number of fruits per plant had significant positive correlation for yield. Further, path coefficient analysis partitioned the correlation into direct and indirect effects. Yield was found to be directly correlated with fruit weight, number of fruits per plant and fruit length, hence selection based on these characters would be more rewarding.

Singh *et al* .(2014) observed path coefficient analysis based on fruit diameter as a dependent variable implicated that plant height had the highest positive direct effect on fruit yield. The emphasis should be given to improve fruit yield per plant in bitter gourd, focus should be given on fruit weight, fruit length, fruit diameter and plant height as it has positive correlation with fruit yield per plant.

Varalakshmi (2015) determined variability, heritability, genetic advance and correlation of fruit yield with 10 yield-contributing traits in ridge gourd. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied, indicating environmental influence on the expression of these traits. However, high heritability (broad-sense), along with high genetic advance, was recorded in node number at which first female-flower appeared, number of branches, fruit length, number of fruits/plant and fruit weight, indicating presence of additive gene effects. Fruit yield/ha was significantly and positively associated with peduncle length, fruit length, number of fruits/plant (at the phenotypic level), fruit weight and fruit yield/plant. Fruit weight had the highest direct effect (0.847) on fruit yield/ha, followed by fruit yield/plant (0.793), fruit number (0.344), peduncle length (0.237) and number of branches (0.216). Therefore, for yield improvement in ridge gourd, emphasis may be laid on indirect selection using fruit parameters like fruit weight, number of fruits/plant and fruit yield/plant.

Thakur *et al.* (2017) studied Correlation and path analysis among different characters of seventy three bottle gourd genotypes were studied. Correlation and path studies revealed that number of fruits per plant and average fruit weight had highest significant positive association with yield q per ha at both phenotypic and genotypic levels and also had significant positive direct effect on fruit yield qtl per ha.

Muralidharan (2017) revealed that the characters like vine length, number of primary branches, number of seeds per fruit and number of pickings were the most important yield determinants, because of their high direct effects and high indirect effects *via.,* many other yield improving characters. This suggests that emphasis must be given on such traits while exercising selection to improve the yield in bottle gourd.

Chetariya *et al.* (2018) evaluated fifty diverse genotypes of bottle gourd were evaluated during summer 2015 for correlation and path analysis. The genotypic path coefficient analysis revealed that ratio of male to female flowers followed by number of female flowers, days to opening of first male flower and average fruit weight exhibited high and positive direct effect on fruit yield per vine and was found to be the most important yield components. The characters fruit length and vine length had moderate and positive direct on fruit yield per plant, while number of fruit per vine, fruit girth and number of node bearing first female flower had low and positive direct effect on fruit yield per vine.

Manju Kumari *et al.* (2018) revealed that Path coefficient analysis proved helpful in partitioning the correlation coefficient into direct and indirect effects also studied the existing genetic variability and to assess interrelationship among sixteen yield and its contributing traits in twenty eight genotypes of bitter gourd. The analysis of variance revealed highly significant differences among the genotypes for all the sixteen characters studied indicating that a significant amount of genetic variability present in the material. Path analysis revealed that ascorbic acid, number of seeds per fruit, vine length, TSS, fruit weight, chlorophyll content, node number at which first female flower appear and days to 50% flowering had a positive direct effect on fruit yield.

Materials and Methods

CHAPTER - III

MATERIAL AND METHODS

The materials used and the methods followed during an experiment on "**Genetic divergence studies in spine gourd**" are briefly described here under.

3.1 Experimental material

For the present investigation twenty genotypes of Spine gourd were collected from different sources. The origin and source of all the genotypes included in the investigation are given in Table 1.

3.2 Location of the experiment

The field experiment was carried out at Horticulture Research Scheme (Vegetable's) and Department of Horticulture, College of Agriculture, VNMKV, Parbhani, during the *kharif* season, 2018-19.

3.3 Weather conditions during the crop period

Parbhani comes under sub-tropical semi-arid region and is situated at 408.50 m above the sea level. Geographically it is situated between 19^0 16'N latitude and 76^0 47' longitude. The weekly mean meteorological data recorded during the crop growth period (June 2018 to November 2018) at meteorological observatory, College of Agriculture, VNMKV, Parbhani, Maharashtra are presented in Appendix-I.

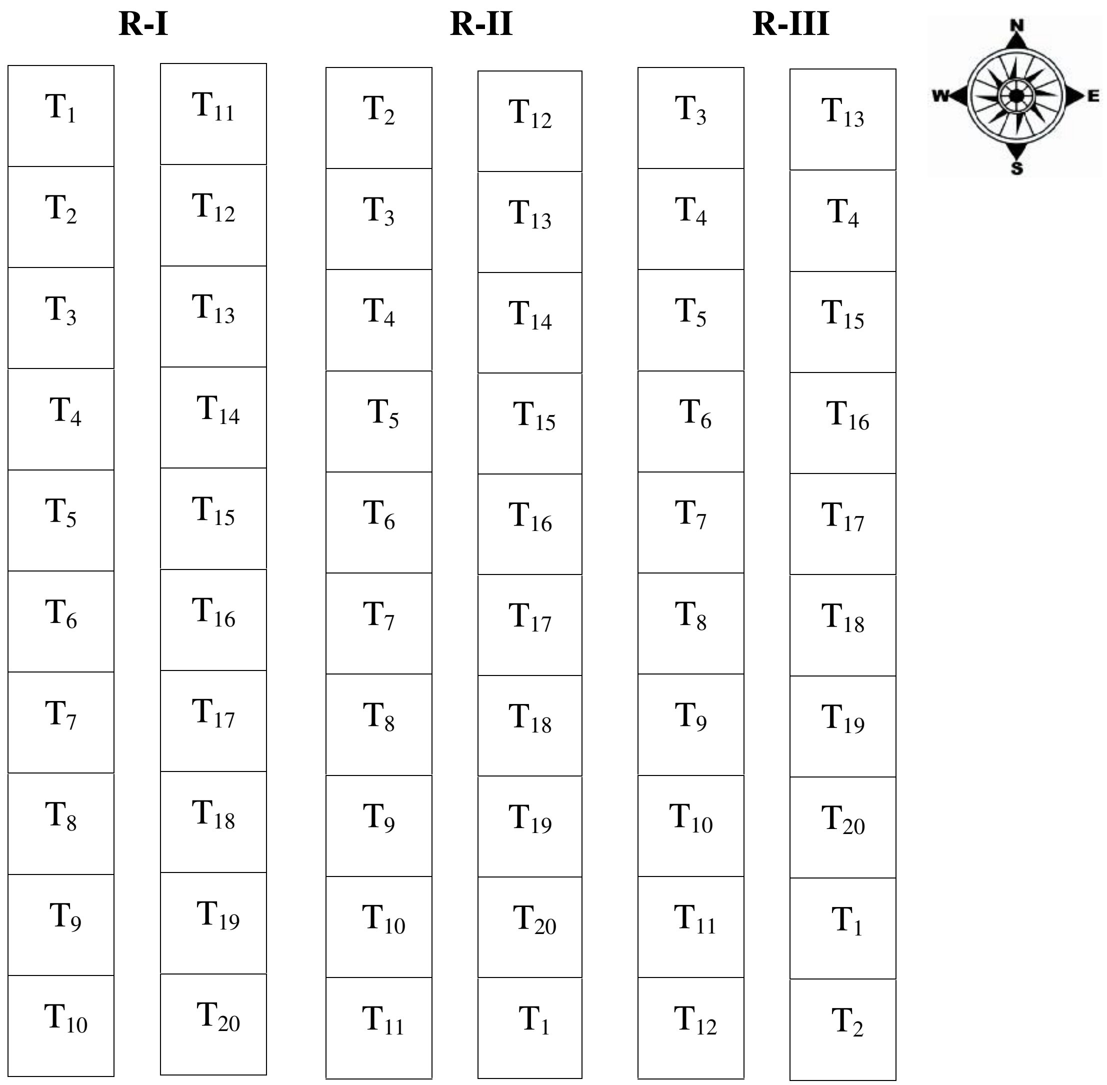
The annual precipitation of Parbhani, which comes under, assured rainfall zone with expected annual rainfall of 800-900 mm. The weekly meteorological data pertaining to rainfall ,temperature and relative humidity prevailed during crop growth period from Jun 2018 to November 2018 were recorded at Central Meteorological Observatory ,VNMKV, Parbhani .The total rainfall received during the complete crop cycle was 615.4 mm. The average maximum temperature of 31.7°C and average minimum temperature of 17.7°C was recorded. Morning and evening mean relative humidity was 79.6% and 45.5%, respectively. The mean maximum BSS during crop growth period was 7.08 hrs. and mean evaporation during crop growth period was 4.71 mm.

3.4 Experimental details

The experiment with 20 genotypes of Spine gourd was laid out in a Randomized Block Design (RBD) with three replications. The plan of layout of experimental plot are presented in Fig 1.

Table 1. Details of genotypes used for genetic diversity study

Sr. No	Treatment symbol	Genotypes	Source
1.	T_1	GPR- 1	Ganeshpur,MH
2.	T_2	GPR-2	Ganeshpur,MH
3.	T_3	GPR-3	Ganeshpur,MH
4.	T_4	GPR-4	Ganeshpur,MH
5.	T_5	GPR-5	Ganeshpur,MH
6.	T_6	MOD-1	Mowad,Nagpur dist,MH
7.	T_7	MOD-2	Mowad,Nagpur dist,MH
8.	T_8	MOD-3	Mowad,Nagpur dist,MH
9.	T_9	MOD-4	Mowad,Nagpur dist,MH
10.	T_{10}	MOD-5	Mowad,Nagpur dist,MH
11.	T_{11}	MOD-7	Mowad,Nagpur dist,MH
12.	T_{12}	MOD-10	Mowad,Nagpur dist,MH
13.	T_{13}	MOD-11	Mowad,Nagpur dist,MH
14.	T_{14}	MOD-12	Mowad,Nagpur dist,MH
15.	T_{15}	MOD-13	Mowad,Nagpur dist,MH
16.	T_{16}	MOD-15	Mowad,Nagpur dist,MH
17.	T_{17}	MDH-1	HRS,VNMKV,Parbhani
18.	T_{18}	MDH-2	HRS,VNMKV,Parbhani
19.	T_{19}	MDH-3	HRS,VNMKV,Parbhani
20.	T_{20}	MDH-3	HRS,VNMKV,Parbhani



Name of the crop: Spine gourd

Design: Randomized Block Design (RBD)

Net plot size: 5.0 × 1.5 m

No. of treatments: 20

Plant spacing: 1 × 0.90 m

No. of replications: 3

Season :*Kharif* (2018-19)

Fig.1: Plan of Layout

3.5 Cultivation details

3.5.1 Field Preparation

The field is prepared by digging pit. The pit is filled with 5kg FYM, 150g SSP and 50g MOP and two time top dressing of Urea @ 80g near the root zone promote plant growth and development.

3.5.2 Soil

Spine gourd grown on sandy loam soil of uniform fertility status ranges from pH 5.5 to 7.0 with well drained and good organic matter .

3.5.3 Planting time

The healthy tubers were transplanted in the experimental plot on June 11, 2018 at the spacing of 1m × 0.90 m between plant to plant and row to row.

3.5.4 Intercultural operations

3.5.4.1 Earthing up

After emergence of sprouts from tuberous roots earthing up was done for the purpose of well development of roots and avoid the damage of roots and vines from over stagnation of water due to high rainfall.

3.5.4.2 Training

Vines were trained along the trellis. These trellis were fitted on the angles with horizontal orientation.

3.5.4.3 Weeding

The experimental plots were kept weed free. To achieve this three hand weedings were done at the interval of one month.

3.5.4 .4 Fertilizer application

Recommended dose of fertilizer @ of 60kg N, 50kg P2O5 and 50kg K2O/ha was applied. One third nitrogen and entire quantity of phosphorus, potassium was applied after emergence of sprouts. Remaining dose of nitrogen was applied in two splits during 30 and 45 days after sprouts emergence.

3.5.4.5 Harvesting

Fruits were harvested at mature green stage. Harvesting of fruits was done on 10-12 days interval in the morning hours.

3.6 Observations recorded

A technique of random sampling was adopted and five plants were selected from each genotypes in all replication for detailed studies on vegetative growth, flowering and yield characters.

3.6.1 Growth attributes

3.6.1.1 Plant height (cm)

Plant height was recorded by measuring the length of main vine from the base of the plant up to the tip at the time of last fruit harvest in centimeters with the help of meter scale.

3.6.1.2 Number of primary branches per plant

The branches arising from the base of plant or from the main stem were considered as primary branches or vines. The number was recorded while measuring the primary branches of vines at the end of flowering.

3.6.1.3 Internodal length (cm)

The length between two inter nodes of sample plants of different treatments at seventy five days after transplanting were measured. The mean was calculated and expressed in cm.

3.6.2 Flowering and fruiting attributes

3.6.2.1 Node at which first female flower appears

The node at which the first female flower appeared was counted from the base of the plant on each plant and average was calculated and the mean value was finally recorded.

3.6.2.2 Days to first flowering

Number of days taken from the day of planting to the anthesis of first flower on any one of the vine in each treatment was recorded.

3.6.2.3 Days to 50% flowering

The number of days taken to 50% of plant population in each genotype for producing the first flower from planting was recorded.

3.6.2.4 Days to first fruit harvest

Days to first fruit harvest was recorded on the basis of number of days taken for the harvest of first fruit from the date of sprouting.

3.6.2.5 Days to last fruit harvest

Days to last fruit harvest was recorded on the basis of number of days taken for the harvest of last fruit from the date of sprouting.

3.6.2.6 Fruit length (cm)

The average length of fruit was calculated from randomly selected five fruits of each genotype from the peduncle end of the fruit to the blossom scar point with help of measuring scale and average value were recorded in centimeter.

3.6.2.7 Fruit diameter (cm)

The average diameter of fruit was calculated from the randomly selected five fruits of each genotype with Vernier Caliper and averaged values were recorded in centimeter.

3.6.2.8 Fruit pedicel length (cm)

The average pedicel length of fruit was calculated from the randomly selected five fruits of each genotype with Vernier Caliper and averaged values were recorded in centimeter.

3.6.2.9 Single fruit weight (g)

The weight of five randomly selected green fruits of each genotype in each replication was recorded and then average fruit weight was calculated in grams.

3.6.3 Fruit morphological characters

3.6.3.1 Fruit colour

It was visually observed and recorded as yellowish (Y), light green (YG)

Green (G), Dark green (DG)

3.6.3.2 Fruit shape:

Fruit shape was observed visually and categorized as cylindrical, spindle, ablon , oval, round.

3.6.3.3. Spine strength

Spine strength of the genotypes was noted through visual observation or by sensory touch as soft, medium, hard.

3.6.4 Quality parameters

3.6.4.1 Ascorbic acid content (mg/100g)

Ten ml of sample was taken and volume made upto 100ml with 3% HPO_3, filtered or centrifuged. Ten ml of the HPO_3 extract of sample was titrated against standard dye up to a pink end point. Titration was done to determine preliminary determination of the titre. In the next determination, most of the dye required was added and then titrated accurately. The aliquot of sample taken should be such that the titre should not exceed 3 to 5 ml.

$$\text{Mg of ascorbic acid per 100ml} = \frac{\text{Tire X Dye factor X Volume made up}}{\text{Aliquot of extract taken for estimation} \ \text{X} \ \text{Volume of sample taken for estimation}} \text{ X } 100$$

3.6.4.2 Total Soluble Solids (TSS)

Total soluble solids (TSS) content of a solution is determined by the index of refraction. TSS of fruits was measured by using hand refractometer. The mean values of Total soluble solids expressed in per cent.

3.6.4.3 Titratable Acidity

The titratable acidity was determined by the procedure given by Ranganna (1991). Total acid content was estimated by titrating 10 g of fruit sample solution against standard solution of 0.1 N NaOH using phenolphthalein as an indicator. The light pink colour appearance denoted the end point.

The titratable acidity is calculated by using following formula and expressed in per cent.

$$\text{Acidity (\%)} = \frac{1 \times \text{Eq. wt. of acid} \times \text{Normality of NaoH} \times \text{titer}}{\begin{array}{c}\text{Aliquot of sample taken}\\ \text{for estimation}\end{array} \times \begin{array}{c}\text{Weight or volume of}\\ \text{sample taken}\end{array} \times 1000} \times 100$$

3.6.5 Yield characters

3.6.5.1 Average fruit weight (g)

Five fruits were randomly taken from each genotype was weighed and the average fruit weight was worked out and expressed in grams.

3.6.5.2 Fruit yield per plant (g)

Fruit yield per plant was recorded from the observational plants under each genotype and the average was worked out.

3.6.5.3 Fruit Yield per plot (kg)

Yield per plot was calculated from yield per plant for each genotype in kilogram.

3.6.5.4 Fruit yield per hectare (q)

Yield of fruits per hectare was calculated in quintal from yield per plot by multiplying with hectare factor. Thus, the yield of fruit in quintal per hectare was calculated.

3.7 Statistical analysis

The mean values of all the traits under consideration were used for statistical analysis. The data were subjected to following statistical analysis.

1. Analysis of variance
2. Estimation of mean and range
3. Genetic divergence analysis
4. Estimation of genetic variability parameters
5. Heritability and genetic advance
6. Correlation
7. Path analysis

3.7.1 Analysis variance

Analysis of variance was performed to test the significance of difference between the lines for all the characterss as per the method described by Panse and Sukhatme (1985). The analysis of variance is set out under ANOVA Table.

$$Y_{ij} = m + G_j + E_{ij}$$

Where,

Y_{ij} = observed value of j^{th} genotype in i^{th} replication.

m = general mean

G_j = effect of j^{th} genotypes

E_{ij} = uncontrolled variation associated with j^{th} genotype in i^{th} replication.

Sr. No.	Source of variation	D.F.	Mean sum of squares		Variance ratio ‘F’ observed	Table ‘F’
			Observed	Expected		
1.	Replication	(r-1)	RMS	$\sigma^2e+ \sigma^2r$		
2.	Treatment	(t-1)	TRMS	$\sigma^2e+ r\sigma^2g$		
3.	Error	(r-1) (t-1)	EMS	σ^2e		
	Total	(rt-1)				

Where,

r = number of replications

t = number of treatments

σ^2e = error variance

σ^2g = genotype variance

σ^2r = replication variance

The mean squares were tested against error variance by usual ‘F’ test. The standard error of difference for comparing any two genotypic means was estimated by formula.

Standard Error (SE) $\pm = \sqrt{EMSS/r}$

Where,

EMSS	=	error mean sum of squares
r	=	number of replications

Critical difference (CD) = SE x $\sqrt{2}$ x t

Where,

t = Table value of‘t’ as error d.f. at 5 or 1 per cent level of significance

3.7.2 Estimation of mean and range

The mean values of all the treatments for the characters under study were worked out by dividing the total by corresponding number of observations.

$$\text{Mean } (\overline{X}) = \frac{1}{n} \sum_{i=1}^{n} Xi$$

Where,

$\overline{X}$ = Mean of character

Xi = i^{th} observation of population

n = Number of observation per replication

Range = The lowest and highest values of mean of each character represented by range.

3.7.3 Genetic divergence analysis

The genetic divergence between genotypes was estimated using Mahalanobis's D^2 statistics (1936). The distance D from the sample was computed using the formula.

$$D^2p = d^1 S^{-1}d$$

Where,

D^2p = Square of distance considering 'p' variables

d = Vector observed differences of the mean values of all the characters (x_{i1}- x_{i2})

S^{-1} = inverse of variance and covariance matrix

3.7.3.1 Clustering of genotypes using D^2 values

All the genotypes used were clustered into different groups following Tocher's method (Rao, 1952). The intra and inter-distance were also computed the criterion used in clustering to the same cluster should at least on the average, show a smaller D^2 values than those belonging to different clusters.

The device suggested by Tocher (Rao, 1952) was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so on. The permissible increase in D^2 value shown by a population to the nearest population. If at any stage increase in average D^2 value exceeded the average of already included, because of the addition of new genotypes, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

3.7.3.2 Intra and inter cluster distances

Based on D^2 values, average intra and inter cluster distances were calculated as per Euclidean method.

3.7.3.3 Intra cluster distance

The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1985).

$$\text{Square of intra cluster distance} = \Sigma Di^2 / n$$

Where,

ΣDi^2 = sum of distance between all possible combinations.

n = Number of all possible combinations

3.7.3.4 Inter cluster distance

The average inter cluster distances were calculated by the formula (Singh and Chaudhary, 1985).

$$\text{Square of inter cluster distance} = \Sigma Di^2 / n_i n_j$$

Where,

ΣDi^2 = sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.7.3.5 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1985). In all the combination, each character is ranked on the basis of di = $y_i^j - y_i^k$ values.

Where,

di = mean deviation

y_i^j = mean value of the jth genotype for the ith character and

y_i^k = mean value of the kth genotype for the ith character.

Rank 'I' is given to the highest mean difference and rank 'p' is given to the lowest mean difference Where, P is the total number of characters.

Finally, number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

3.7.4 Estimation of genetic variability parameters

Various parameters of genetic variability were calculated by using appropriate formulae.

1. Phenotypic and genotypic variances

The genotypic and phenotypic variance were calculated by using the respective mean squares from variance table (Burton 1952).

Genotypic variance ($\sigma^2 g$)

$$\sigma^2 g = \frac{\text{TRMSS - EMSS}}{\text{R}}$$

Error variance = $\sigma^2 e$ – EMSS

Phenotypic variance ($\sigma^2 p$)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

TRMSS = Treatment mean sum of squares

EMSS = Error mean sum of squares

EMSS = Error mean sum of squares

r = Number of replication

2. Phenotypic and genotypic coefficient of variation

The genotypic and phenotypic coefficients of variance (GCV and PCV) were calculated according to method suggested by Burton (1952).

Genotypic coefficient of variation (GCV)

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

Phenotypic coefficient of variation (PCV)

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

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$ = General or grand mean of character

GCV and PCV were classified into 0-10 %: Low, 10-20 %: Moderate, 20 % and above: High as suggested by Siva Subramanian and Menon (1973).

3.7.5 Heritability and genetic advance

1. Heritability (Broad sense) was calculated according to the method suggested by Allard (1960).

$$\text{Heritability } (h^2) \text{ (\%)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Heritability was classified as suggested by Robinson *et al* (1966) and described as 0-30 %: Low, 30 -60 %: Moderate, 60 % and above; High.

2. The genetic advance (at 5 per cent selection intensity) was calculated for each character using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance} = h^2 \text{ x k x } \sqrt{\sigma^2 p}$$

Where,

h^2 = heritability (Broad sense)

K = Selection difference at 5 per cent selection intensity, the value of K = 2.06

σp = Phenotypic standard deviation

3. The expected genetic advance (EGA) in percentage of mean was calculated as

$$\text{EGA} = \frac{\text{GA}}{\bar{x}} \text{ x } 100$$

Where,

GA = Genetic advance

$\bar{x}$ = General or grand mean of character

The genetic advance as percent of mean was categorized into 0-10 %: Low, 10-20 %: Moderate, 20 % and above: High as suggested by Johnson *et al.* (1955).

3.7.6 Correlation

In order to study the extent of association between different traits the genotypic and phenotypic simple correlation coefficient were worked out from the respective variance and covariance's. The formula as suggested by Johnson *et al.* (1955) were used for calculating simple correlation coefficient as given below.

1. Genotypic correlation coefficient (rg_{xy})

$$(rg_{xy}) = \frac{\text{Cov}\ (g_x \text{ x } g_y)}{\sqrt{\sigma g_x \text{ x } \sigma^2 g_y}}$$

Where,

Cov (g_x. g_y) = Genotypic covariance between character x and y

$\sigma^2 g_x$ and $\sigma^2 g_y$ = Genotypic variance of character x and y, respectively.

Similarly,

2. Phenotypic correlation coefficient (rp_{xy})

$$(rp_{xy}) = \frac{\text{Cov}\ (p_x\ .p_y)}{\sqrt{\sigma^2 p_x\ .\ \sigma^2 p_y}}$$

Where,

Cov (p_x .p_y) = Phenotypic covariance between character x and y

$\sigma^2 p_x$ and $\sigma^2 p_y$ = Phenotypic variance of character x and y, respectively

Significance of correlation coefficient was determined from the Fisher and Yates table at 5 and 1 per cent level of significance. The 'r' values were compared against (n-2) degrees of freedom.

3.7.7 Path analysis

The genotypic correlation coefficient between yield and its components were further partitioned into direct and indirect effects with the help of path coefficient analysis originally suggested by Wright (1921) and further outlined by Dewey and Lu (1959).

The first step in path analysis is to prepare the path diagram based on cause and effect relationship in the present study, path diagram was prepared by taking yield as effect i.e. the function of various components like X_1, X_2, X_3 and these components show following type of association with each other (Fig 2).

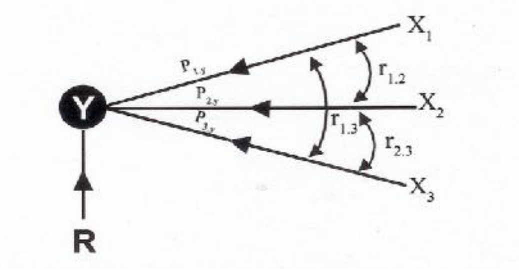


Fig. 2 A path diagram

In path diagram the grain yield is the result of X_1, X_2, X_3 and some other undefined factors designated by R. the double arrowed lines indicates mutual association as measured by correlation coefficient (r_{ij}) and the single arrowed line present direct influence as measured by path coefficient (P_{ij}).

Direct and indirect contribution of eight variable to grain yield were calculated by solving a set of simultaneous equations of the form as per Dewey and Lu (1959).

rny = pny + rn 2p 2y + rn3p3y + ……….Where,

rny = represents correlation coefficient between one component and grain yield

rn2 = represents correlation coefficient between that character and each of other components

pny = represents path coefficient between that characters and grain yield.

Matrix – A Martrix-B

$$\begin{bmatrix} r1,y \\ \\ r2,y \end{bmatrix} \qquad \begin{bmatrix} p_1 \\ \\ p_2 \end{bmatrix} \qquad \begin{bmatrix} r1,1 & r1,2 \ldots..r1,n \\ \\ r2,1 & r2,2 \ldots..r2,n \end{bmatrix}$$

$$\vdots \qquad\qquad \vdots$$

$$rn.y \qquad\qquad p_n \qquad\qquad rn,1 \quad rn,2\ldots\ldots..1$$

The B matrix was inverted (B^{-1}) and path coefficient (p_{ij}) were obtained as

$P_{ij} = A \times B^{-1}$

The coefficient p_1, p_2 …… p_n are estimate of direct effect of character while the indirect effects of ithcharacter on grain yield character through jthcharacter is $r_{ij}p_{ij}$.

The residual factor i.e. variation in yield uncounted by these associations was calculated from the following formula.

Residual factor (Rx) = $\sqrt{1\text{-}R^2}$

Where,

R^2 = (P1y, r1y + p2y, r2y + ……….. + Pny, rny)

Where,

P1y, P2y, ……. Pny, = Path values

r1y, r2y, …… rny, = Correlation coefficient

Results and Discussion

CHAPTER-IV

RESULTS AND DISCUSSION

The present investigation entitled **"Genetic divergence studies in spine gourd (*momordica dioica* Roxb.*)*** subjected to biometrical data analysis and results obtained were presented under the following headings:

4.1 Morphological characters

4.2 Analysis of variance

4.3 Mean performance of genotypes

4.4 Genetic divergence analysis

4.5 Variability, heritability and genetic advance

4.6 Correlation studies

4.7 Path coefficient analysis

4.1 Morphological characters

Morphological characters of twenty spine gourd genotypes are presented in Table 2.

4.2 Analysis of variance

The analysis of variance indicated that highly significant differences among the genotypes for all the characters were studied *viz*., plant height, number of primary branches per plant, internodal length, node number at first female flower appear, days to first flowering, days to 50% flowering , days to first harvest, days to last harvest, average fruit weight, fruit yield per plant, fruit yield per plot, fruit yield per hectare presented in Table 3.

4.3 Mean performance of genotypes

The data for mean performance of the genotypes are presented in Table 4, 5 and 6 and the results of mean performance for twenty spine gourd genotypes are presented below in character wise.

Table 2. Morphological characters of spine gourd genotypes

Genotypes	Fruit shape	Fruit colour	Spine strength
GPR1	Tapering	Yellowish	Medium
GPR2	Tapering	Green	Soft
GPR3	Oval	Dark green	Medium
GPR4	Oval	Green	Medium
GPR5	Oval	Green	Medium
MOD1	Oval	Green	Soft
MOD2	Round	Green	Soft
MOD3	Obovate	Light green	Medium
MOD4	Abovate	Green	Medium
MOD5	Oval	Dark green	Soft
MOD7	Globular	Lark green	Soft
MOD10	Globular	Light green	Medium
MOD11	Globular	Green	Hard
MOD12	Globular	Green	Hard
MOD13	Tapering	Yellowish	Medium
MOD15	Abovate	Light green	Medium
MDH1	Ablong	Dark green	Soft
MDH2	Ablong	Dark green	Soft
MDH3	Globular	Light green	Hard
MDH4	Round	Yellowish	Hard

Table 3. Analysis of variance for twenty characters in spine gourd genotypes

Characters	Replication	Genotypes	Error	SE ±	CD@1%	CD@5%
Plant height (cm)	8.63	10562.12**	10.91	1.90	7.22	5.42
No. of primary branches per plant	0.01	1.31**	0.28	0.30	1.17	0.87
Internodal length (cm)	0.01	2.52**	0.00	0.04	0.17	0.13
Node no. at first female flower appear	0.07	6.01**	0.04	0.12	0.46	0.34
Days to first flowering	2.60	87.77**	2.63	0.93	3.55	2.66
Days to 50% flowering	2.21	33.77**	15.81	2.29	8.70	6.52
Days to first harvest	3.21	69.24**	5.23	1.32	5.00	3.75
Days to last harvest	1.37	250.01**	17.36	2.40	9.11	6.83
Number of fruit per plant	1.51	1433.90**	1.51	0.70	2.69	2.01
Fruit length(cm)	0.07	1.50**	0.01	0.06	0.23	0.17
Fruit diameter (cm)	0.00	28.51**	0.42	0.04	0.16	0.12
Fruit pedicel length(cm)	0.00	0.02**	0.00	0.04	0.17	0.13
Single fruit weight(g)	0.09	61.08**	0.28	0.31	1.17	0.88
Ascorbic acid (mg/100g)	0.27	5.49**	0.26	0.29	1.13	0.84
TSS%	0.04	0.40**	0.01	0.06	0.26	0.19
Acidity%	0.00	0.09**	0.00	0.01	0.04	0.03
Average fruit weight (g)	12.46	1335.18**	10.16	1.84	6.97	5.23
Fruit yield per plant (g)	49.77	464152.61*	32.09	3.27	12.39	9.29
Fruit yield per plot (kg)	0.06	20.15**	0.04	0.12	0.47	0.35
Fruit yield per hectare (q)	0.82	3643.20**	0.72	0.49	1.86	1.39

** Significance at 5% and 1,% levels respectively

4.3.1 Mean performance of spine gourd genotypes for its associated traits

Data on mean performance of associated traits of spine gourd genotypes are presented in Table 4 and 6

4.3.1.1 Plant height

The maximum height was recorded in genotype GPR-1 (349.84 cm) followed by MOD-12 (192.59 cm) and GPR-4 (190.48 cm) while minimum plant height (65.08 cm) was recorded in genotype GPR-2 followed by GPR-5 (66.62 cm) and GPR-3 (74.07cm).While. The overall plant height mean was 171.78 cm. Among twenty genotypes fourteen genotypes were showed more plant height than mean value.

4.3.1.2 Number of primary branches per plant

Number of branches per plant was ranged from 2.37 to 4.60 with a mean of 3.59. The maximum number of branches per plant was recorded in genotype MOD-2 (4.60) followed by in GPR-1 (4.40) while, the minimum number of primary branches per plant was recorded in GPR-3 (2.37) and followed MOD-3 (2.57).

4.3.1.3 Internodal length (cm)

Maximum internodal length was observed in MOD-4 (7.40 cm) followed by GPR-1,2,4 and MOD -10 (5.53 cm) in four genotypes and minimum was recorded in MOD-2 (3.43cm). Inter nodal length ranged from 3.43 cm to 7.40 cm with mean of 3.59 cm.

4.3.1.4 Node number of first female flower appearance

Node number of first female flower appearance was ranged from 4.67 to 10.37. Genotype MDH-2 (4.67) observed lower node for appearance of first female flower followed by MOD-5 (5.80) and MOD-7 (10.37) was recorded for higher node position .Average mean was recorded (7.58).

4.3.1.5 Days to first flowering

Number of days taken for first flowering was ranged from 32.67 to 54.67 days with a mean of 41.50 days. The minimum number of days for first flowering was found in genotype MOD 10 (32.67) followed by MOD-7 (36.00**)**. The maximum number of days for first flowering was observed in GPR-2 (54.67) followed by GPR-3 (53.67).

4.3.1.6 Days to 50% flowering

Number of days taken to 50 % flowering was ranged from 47.33 to 62.67 with a mean of 53.81 days. The minimum number of days for 50 % flowering was found in genotype MOD-10 (47.33) followed by MDH-3 (48.67) and in MOD-7 (51.33) . The maximum number of days for 50 per cent flowering was observed in GPR-2 (62.67) followed by GPR-3 and MDH-2 (57.33) .

4.3.1.7 Days to first harvest

The considerable variation was observed with respect to days to first harvest which was ranged from 60.33 to 77.67 with average mean 70.81. The minimum number of days to first harvest was recorded in genotype MOD-10 (60.33) closely followed by MDH -3 (62.33).whereas, maximum number of days to first harvest was recorded in GPR-2 (77.67) followed by in MDH-4 (77.00) .

4.3.1.8 Days to last harvest

Days to last harvest varied from 85.00 days to 120.67 days with the mean of 101.75 days. The genotype MOD- 1 took minimum number of days 85.00 for first harvest followed by GPR - 2 (85.33) and MDH- 1 took maximum number of days (120.67) Followed by in GPR-1 (112.00).

4.3.1.9 Number of fruit per plant

The highest number of fruits per plant was recorded in genotype MDH -1 (103.40) followed by GPR-1 (43.60) while, the least number of fruits 5.47 per plant was recorded in genotype MOD-2 followed by GPR-5 (5.53). Among all the genotypes, five were found to possess more number of fruits per plant when compared to mean (19.48).

4.3.1.10 Fruit length

The fruit length, range of all genotypes was varied from 2.90 to 4.77 cm. The maximum fruit length was observed in MOD-15 (4.77 cm) followed by in MDH-4 (4.73) and MOD-13, MDH-3 (4.57) While, minimum fruit length was observed in GPR-4 (2.93) followed by in GPR-2 GPR-3 (3.13).The overall mean fruit length of all genotype was 4.05 cm.

Table 4. Mean performance of spine gourd genotypes for its associated traits

Genotypes	Plant height (cm)	Number of primary branches per plant	Internodal length (cm)	No. of nodes at first female flowering	Days to first flowering	Days to 50% flowering	Days to first harvest	Days to last harvest	Number of fruit per plant	Fruit length (cm)
GPR 1	349.84	4.40	5.53	6.93	42.00	53.33	70.00	112.00	43.60	4.50
GPR 2	65.08	4.03	5.53	8.13	54.67	62.67	77.67	85.33	7.73	3.13
GPR 3	74.07	2.37	5.54	7.50	53.67	57.33	73.67	93.67	7.23	3.13
GPR 4	190.48	2.73	5.53	7.50	42.67	54.67	71.33	96.00	6.13	2.93
GPR 5	66.62	3.93	3.47	8.40	38.33	54.33	75.00	93.00	5.53	2.90
MOD 1	153.76	3.50	3.47	6.50	39.00	53.67	72.00	85.00	13.17	3.37
MOD 2	190.12	4.60	3.43	8.93	39.33	54.33	72.33	97.67	5.47	3.33
MOD 3	182.96	2.57	4.23	7.13	41.00	53.33	72.33	106.00	13.33	4.30
MOD 4	187.60	2.97	7.40	5.87	47.00	57.00	76.67	103.33	10.73	4.43
MOD 5	154.45	3.63	5.20	5.80	38.00	55.00	72.00	99.33	11.13	3.34
MOD 7	187.60	4.20	4.67	10.37	36.00	51.33	68.67	108.00	12.20	4.10
MOD 10	180.53	2.67	5.53	8.43	32.67	47.33	60.33	105.00	13.93	5.17
MOD 11	187.72	4.47	5.23	9.27	37.00	52.67	62.67	112.67	25.07	4.47
MOD 12	192.59	3.97	5.13	6.33	42.00	52.67	70.67	104.33	18.73	4.37
MOD 13	184.24	3.93	4.23	8.43	39.33	52.67	71.67	108.33	17.00	4.57
MOD 15	177.64	3.73	5.30	9.20	41.33	50.67	70.33	106.33	9.67	4.77
MDH 1	167.58	3.93	4.47	6.23	40.33	53.67	73.67	120.67	103.40	4.40
MDH 2	185.94	3.80	4.53	4.67	37.33	57.33	66.00	104.33	28.70	4.50
MDH 3	177.88	3.33	5.10	7.63	43.00	48.67	62.33	102.67	24.43	4.57
MDH 4	179.09	3.17	3.67	8.50	45.33	55.33	77.00	91.50	12.50	4.73
Mean	**171.78**	**3.59**	**3.59**	**7.58**	**41.50**	**53.81**	**70.81**	**101.75**	**19.48**	**4.05**
SE ±	1.90	0.30	0.30	0.12	0.93	2.29	1.32	2.40	0.70	0.06
CD@5%	5.42	0.87	0.87	0.34	2.66	6.52	3.75	6.83	2.01	0.17

4.3.1.11 Fruit diameter

The diameter of fruit was ranged from 1.77 cm to 3.17 cm with a mean value of 2.45 cm. The maximum fruit diameter was recorded in MOD-11 (3.17 cm) followed by in MOD-10 (3.07) and MOD-13 (2.77) Whereas, MDH-2, GPR-2 (1.77 cm) genotype were showed the minimum fruit diameter.

4.3.1.12 Fruit pedicel length

The fruit pedicel length range of all genotypes were varied from 1.27 to 1.57 cm. The maximum fruit pedicel length were observed in GPR -1(1.57cm) followed by in GPR -3 and MOD-1 (1.53 cm) and MOD-7 (1.5 cm) While, minimum fruit pedicel length were observed in MOD 12 and MOD-13 (1.27 cm) followed by in MOD-3 and MOD -10 (1.30 cm) .The overall mean fruit pedicel length of all genotype was 1.41 cm.

4.3.1.13 Single fruit weight

Considerable variation was observed with respect to single fruit weight which ranged from 7.20 g to 20.53 g. The highest single fruit weight was recorded in MOD -11 (20.53 g) followed by in MDH -3 (18.73g) and MDH-1 (17.23g) Whereas, minimum single weight of fruit was recorded GPR -2 (7.20 g) followed by in MOD-5 (7.83 g) and overall mean of single fruit weight 12.05g .

4.3.1.14 Average fruit weight

The considerable variation was observed with respect to average fruit weight which was ranged from 32.73 to 97.00 g. The highest average weight of fruit was recorded in MOD-11 **(**97.00g) followed by in MDH-3 **(**85.33). Whereas, minimum average weight of fruit was recorded in GPR 2 (32.73) and followed by in GPR -3 (35.67 g) with average mean 55.66 g.

4.3.2 Mean performance of spine gourd genotypes for quality attributes

Data on mean performance of quality attribute in spine gourd genotypes are presented in Table 5

4.3.2.1 Ascorbic acid

Ascorbic acid content was ranged from 6.44 to 11.53 mg/100 g with a mean of 9.67 mg/100 g of fruit. The highest ascorbic acid content was recorded in. MDH- 3

(11.53/100g) followed by in MOD-7 (11.21 mg/100g). The lowest ascorbic acid content was found in MOD- 4 (6.44 mg/100g).

Table 5. Mean performance of quality parameter in spine gourd genotypes

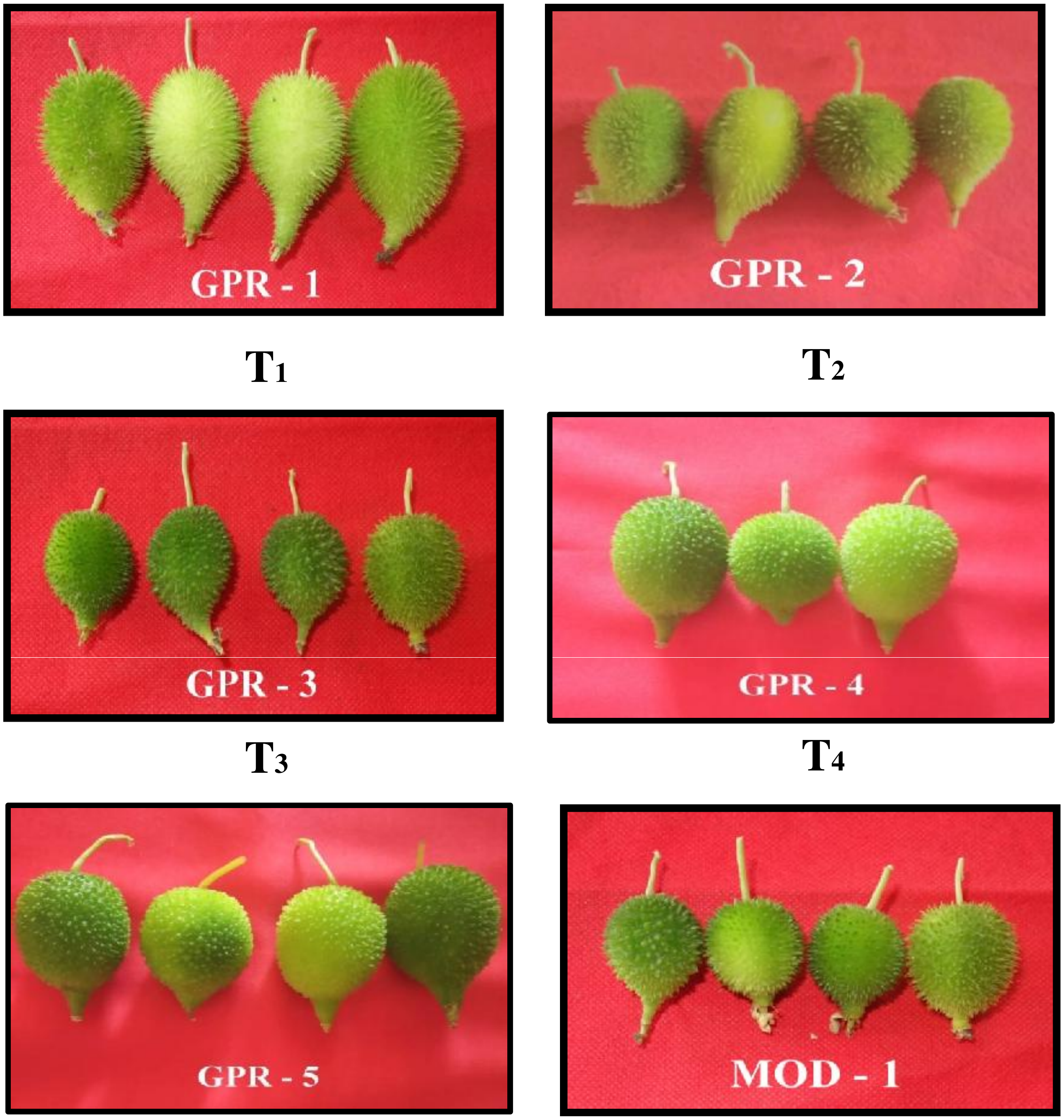
Genotypes	Ascorbic acid (mg/100)	TSS (%)	Titratable Acidity (%)
GPR 1	10.67	2.60	0.70
GPR 2	7.07	2.63	0.56
GPR 3	8.12	2.34	0.64
GPR 4	9.37	2.45	0.82
GPR 5	10.41	2.31	0.91
MOD 1	8.98	3.19	0.43
MOD 2	10.54	3.20	0.66
MOD 3	10.31	3.05	0.37
MOD 4	6.44	2.21	0.84
MOD 5	9.79	3.00	0.38
MOD 7	11.21	2.52	0.44
MOD 10	10.65	2.28	0.72
MOD 11	10.20	3.20	0.62
MOD 12	9.31	2.38	0.45
MOD 13	10.84	2.23	0.90
MOD 15	8.22	2.35	0.73
MDH 1	10.04	3.02	0.55
MDH 2	9.14	2.53	0.65
MDH 3	11.53	2.31	0.63
MDH 4	10.59	3.04	0.36
Mean	**9.67**	**2.64**	**0.61**
SE ±	0.84	0.06	0.01
CD@5%	0.84	0.19	0.03

4.3.2.2 Titratable Acidity

Maximum titratable acidity was recorded in genotype GPR- 5 (0.91 %) followed by in MOD -13 (0.90 %), GPR-4 (0.82 %) whereas, minimum titratable acidity recorded in genotype MDH-4 (0.36%) with overall mean of 0.61 % .

4.3.2.3 Total Soluble Solids

Total soluble solid was ranged from 2.21 to 3.20 % with overall mean 2.64 % .Maximum Total soluble solids was recorded in genotype MOD -2 and in MOD -11 (3.20 %) followed by in MOD 3 (3.05 %), MDH - 4 (3.04 %) and whereas, minimum TSS was recorded in MOD - 4 (2.21 %) followed by in MOD 10 (2.28%) .



T_1 T_2

T_3 T_4

T_5 T_6

Plate – 1a: Variability in the fruits of spine gourd genotypes (T_1-T_6)

T_7

T_8

T_9

T_{10}

T_{11}

T_{12}

Plate – 1b: Variability in the fruits of spine gourd genotypes (T_7-T_{12})

T_{13}

T_{14}

T_{15}

T_{16}

T_{17}

T_{18}

Plate – 1c: Variability in the fruits of spine gourd genotypes (T_{13}-T_{18})

T_{19} T_{20}

Plate – 1d: Variability in the fruits of spine gourd genotypes (T_{19}-T_{20})

4.3.3 Mean performance of spine gourd genotypes for yield attributes

Data on mean performance of fruit yield parameter and its associated traits of spine gourd genotypes are presented in Table 6

4.3.3.1 Fruit yield per plant

The data presented in table 6 revealed that fruit yield per plant was ranged from 44.87g to 1796.67g. The maximum fruit yield per plant was recorded in genotype MDH-1 (1796.67g) followed by in genotype GPR-1 (642.10 g) and MOD-11 (470.33 g). Whereas, minimum fruit yield per plant was observed in genotype GPR-4 (44.87g) followed by in GPR-5 (46.50g). The overall mean of fruit yield per plant was 264.81g.

4.3.3.2 Fruit yield per plot

The data presented in Table 6 that fruit yield per plot was ranged from 0.26 to 11.77 kg. The maximum fruit yield per plot was recorded in genotype MDH-1 (11.77 kg) followed by in GPR-1 (4.61 kg) and MOD-11 (3.51 kg). Whereas, minimum fruit yield per plot was recorded in genotype GPR-3 (0.26 kg) followed by in GPR-4 (0.34 kg) and GPR-5 (0.36 kg) . The overall mean of fruit yield per plot was 1.90 kg.

4.3.3.3 Fruit yield per hectare

The data presented in Table 6 recorded for fruit yield per hectare was ranged from 3.47 to 158.50 q/ha. The maximum fruit yield was recorded in genotype MDH-1 (158.50 q/ha) and followed by in GPR-1 (60.80 q/ha). While, minimum fruit yield per hectare was recorded in genotype GPR -3 (3.47 q/ha) and GPR-4 (4.55 q/ha). The overall mean for fruit yield was 25.34 q/ha.

From the present study, a wide range of variation was estimated for all the traits. Morphological traits are not influenced by the environment , transfer of those characters are fully governed by genes and could be plant breeder. Execution of any breeding programme depends upon the magnitude of genetic variability for different traits and degree of transmission of the trait from one generation to other which would help in selecting the best genotypes from the population.

The above estimated result shows that, there is ample scope of varietal improvement through hybridization and selection in view of good performance of genotypes .

Table 6. Mean performance of spine gourd genotypes for yield parameter

Genotypes	Fruit diameter (cm)	Fruit pedicel length(cm)	Single fruit weight(g)	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield per plot (kg)	Fruit yield per hectare (q)
GPR 1	2.50	1.57	13.47	62.70	642.10	4.61	60.80
GPR 2	1.77	1.53	7.20	32.73	77.13	0.58	7.77
GPR 3	2.13	1.40	8.27	35.67	50.27	0.26	3.47
GPR 4	2.30	1.37	7.93	37.00	44.87	0.34	4.55
GPR 5	2.40	1.37	7.97	37.40	46.50	0.36	4.81
MOD 1	2.20	1.50	8.10	44.90	99.83	0.75	10.21
MOD 2	2.30	1.37	8.73	40.93	59.13	0.38	4.60
MOD 3	2.37	1.30	9.23	44.67	114.43	0.74	9.83
MOD 4	2.40	1.40	8.17	38.33	63.70	0.49	6.51
MOD 5	2.47	1.53	7.83	36.67	82.60	0.62	8.23
MOD 7	2.47	1.50	9.77	45.00	110.37	0.74	9.80
MOD 10	3.07	1.30	16.77	77.67	233.33	1.90	25.23
MOD 11	3.17	1.47	20.53	97.00	470.33	3.51	46.41
MOD 12	2.70	1.27	16.77	77.67	285.13	2.54	33.63
MOD 13	2.77	1.27	16.67	79.33	258.27	1.78	23.63
MOD 15	2.33	1.40	15.80	70.00	141.07	1.50	20.37
MDH 1	2.53	1.37	17.23	79.33	1796.67	11.77	158.50
MDH 2	1.77	1.47	8.23	30.00	201.67	1.58	21.11
MDH 3	3.00	1.37	18.73	85.33	361.30	2.28	30.49
MDH 4	2.43	1.47	13.73	61.00	157.63	1.27	16.93
Mean	**2.45**	**1.41**	**12.05**	**55.66**	**264.81**	**1.90**	**25.34**
SE ±	0.04	0.04	0.31	1.84	3.27	0.12	0.49
CD@5%	0.12	0.13	0.88	5.23	9.29	0.35	1.39

Result on yield and yield contributing traits are conformity with Bhagat *et al.* (2017) exhibited variatioin day to first flowering, stem and leaf fruit characteristics in spine gourd. Rasul and Okubo (2002) in kakrol found no relationship with geographical isolation and genetic diversity of the crop. Chaudhary e*t al.* (2008) reported high range of variability in average number of fruits/plant, fruit per plant and yield per plot in ridge gourd. Bharati *et.al* (2006) observed wide range of varability for fruit length ,fruit width , fruit weight and yield per plant in spine gourd .Ram *et al* .(2004) observed extent of variability fruit length ,fruit width , fruit weight and number of fruits per plant in spine gourd.

4.4 Genetic divergence (D^2 statistic)

The quantitative assessment of genetic divergence was made by adopting Mahalonobis D^2 statistic for yield and its contributing characters. Mahalanobis's D^2 statistic is also an unique tool for discriminance populations considering a set of parameters together rather than interfering from indices based on eco-geographical diversity, phylogenetic relationships and morphological similarities.

4.4.1 Grouping of genotypes into different clusters (D^2 analysis)

Procedure suggested by Tocher (Rao, 1952) has been used to group 20 genotypes into four clusters by treating the estimated D^2 values as the square of the generalized distance. Based on D^2 values, the 20 genotypes were grouped into four highly divergent clusters in Table 7.

Some of genotypes were so divergent in all the characters, hence each single genotype formed a separate cluster. Thus four clusters *viz.,* I II, III, IV were solitary with one genotype in each cluster. Cluster I was biggest accommodated 16 genotypes.

Table 7. Cluster classification of spine gourd genotypes

Cluster	No. of genotypes	Genotypes
I	16	GPR- 1, GPR- 2, GPR -3, GPR -4, GPR- 5, MOD-1, MOD- 2, MOD-3, MOD -4, MOD-5, MOD -7 , MOD- 10, MOD -11, MOD-12, MOD -13, MOD-15.
II	2	MDH -2, MDH- 4
III	1	MDH -1
IV	1	MDH -3

4.4.2 Cluster mean for various characters

The cluster mean for the fourteen characters were studied in spine gourd genotypes are presented in Table 8 and revealed that considerable differences among all the clusters.

The highest plant height was recorded in cluster II (182.51 cm) while, lowest plant height was recorded in cluster III (167.58 cm). The maximum number of primary branches were recorded in cluster III (3.93) whereas, minimum number of branches were recorded in cluster IV (3.33).

The highest node number at first female flower appear was recorded in cluster I (7.79) whereas lowest was recorded in cluster III (6.23). The minimum days to 50% flowering was recorded in cluster IV (48.66 days) whereas, cluster II was recorded maximum days to 50% flowering (56.33 days).

The maximum mean for days to last harvest were observed in cluster III (120.66). Whereas, minimum days to last harvest were found in cluster II (97.91). The maximum number of fruits per plant was recorded in cluster III (103.40) while minimum numbers of fruits per plant was found in cluster I (13.79).

The maximum fruit length was observed in genotypes of cluster II (4.61 cm) followed by in cluster IV (4.56 cm), while, minimum fruit length was observed in the genotypes of cluster I (3.92 cm). Whereas, the maximum fruit diameter was recorded in cluster IV (3.00 cm) while, lowest fruit diameter was recorded in cluster II (2.10 cm). The maximum fruit pedicel length was recorded in cluster II (1.46 cm) while, lowest fruit pedicel length was recorded in cluster III and IV (1.36 cm).

The highest ascorbic acid content was recorded in cluster IV (11.52 mg/100g), while, lowest ascorbic acid content was recorded in cluster I (9.50 mg/100g). The genotypes of cluster III had maximum total soluble solid content (3.02 %) whereas, minimum total soluble sugar was observed in genotypes of cluster IV (2.31 %).

The maximum titratable acidity was recorded in cluster I and cluster IV (0.63%) while, minimum value was recorded in cluster II (.0.50%).

The highest fruit yield per plant was recorded in cluster III (1796.6 g) while, lowest fruit yield per plant was recorded in cluster I (173.69 g). The highest fruit yield per hectare was recorded in cluster III (158.50 q/ha) while, lowest fruit yield per hectare was recorded in cluster I (17.49) q/ha.

Table 8. Mean values of clusters for fourteen characters in spine gourd genotypes

Characters	Cluster			
	I	II	III	IV
Plant height (cm)	170.33	182.51	167.58	177.88
No. of primary branches per plant	3.60	3.48	3.93	3.33
Node no. at first female flower appear	7.796	6.58	6.23	7.63
Days to 50% flowering	53.83	56.33	53.66	48.66
Days to last harvest	101.00	97.91	120.66	102.66
Number of fruit per plant	13.79	20.60	103.40	24.43
Fruit length (cm)	3.92	4.61	4.40	4.56
Fruit diameter (cm)	2.45	2.10	2.53	3.00
Fruit pedicel length (cm)	1.40	1.46	1.36	1.36
Ascorbic acid (mg/100g)	9.50	9.86	10.04	11.52
TSS%	2.62	2.78	3.02	2.31
Titrable Acidity %	0.63	0.50	0.55	0.63
Fruit yield per plant (g)	173.69	179.65	1796.6	361.30
Fruit yield per hectare (q)	17.49	19.02	158.50	30.49

4.4.3 Average intra and inter cluster distances

Data presented in Table 9 are indicated that the mean intra and inter cluster D^2 values among the four clusters.

The intra cluster D^2 value was ranged from 0.0 (Cluster III and IV) to 84.27 and the cluster I had the maximum D^2 value (84.27) followed by the cluster II (30.79)

The inter cluster D^2 values of the four clusters were revealed that highest inter cluster generalized distance (404.46) was between cluster I and cluster III, while the lowest (50.54) was between cluster II and cluster IV.

The nearest and distant clusters from each of the clustesr based on D^2 values were presented in Table10.

Cluster I was nearest to cluster II (62.21) and distant from cluster III (404.46). Cluster I had maximum divergence with cluster III. Hence, it is use as to incorporating diverse traits during the hybridization programme.

Cluster I was found nearest to cluster II (62.21), while which was farthest from cluster III (404.46). Cluster II was found nearest to cluster IV (50.54), while which was farthest from cluster III (398.28) and cluster III was found nearest to cluster IV (354.04), while it was farthest from cluster I (404.46). Cluster IV was found nearest to cluster II (50.54), while it was farthest from cluster III (354.04).

Statistical distance represents the extent of genetic diversity among clusters. The inter cluster distance was minimum between cluster II and IV indicated close relationship and similarity for most of the characters of the genotypes included in these clusters. The maximum inter cluster distance was observed between clusters I and III indicated wider genetic diversity among the genotypes included in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Similar results were obtained in spine gourd Bharathi *et al.* (2010), Bhagat *et al.* (2018).

Cluster III and IV displayed least intra cluster distance denoted the similarity of genotypes. While, maximum intra cluster distance was recorded in cluster I and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters. Therefore, hybridization programme between the genotypes belonging to cluster I and cluster III may be undertaken for getting good segregants.

Emphasis should be laid on characters contributed maximum D^2 values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. Highest contribution towards divergence in this regard by fruit yield per plant followed by, acidity, number of fruits per plant , fruit yield per hectare, node no. at first female flower appear ,fruit length. Thus, these were the major traits contributing to divergence. Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in spine gourd, Similar results were reported in melon by Tomar *et al.* (2008).

Sundaram *et al.* (2008) observed that fruit weight contributed maximum to the divergence followed by yield of fruits per vine in ridge gourd and Tyagi *et al.* (2017)

recorded that vine length contributed maximum towards genetic divergence followed by fruit diameter and average fruit weight in bitter gourd.

Table 9. Average intra (bold) and inter-cluster D^2 values for four clusters in spine gourd genotypes

Clusters	I	II	III	IV
I	**84.27**	62.21	404.46	75.81
II		**30.79**	398.28	50.54
III			**0.000**	354.04
IV				**0.000**

Table 10. The nearest and farthest clusters from each cluster based on D^2 values in spine gourd genotypes

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 value
I	II (62.21)	III (404.46)
II	IV (50.54)	III (398.28)
III	IV (354.04)	I (404.46)
IV	II (50.54)	III (354.04)

4.4.4 Relative contribution of different characters towards divergence

The per cent contribution of each character towards divergence are presented in Table 11. The data presented in Table 11 were showed that the maximum (78.94%) fruit yield per plant were contributed highest towards divergence followed by titrable acidity (7.36 %), Number of fruit per plant (5.52 %) ,fruit yield per hectare (4.21%), Node number at first female flower appearance (2.63%) , plant height (0.52%).

The rest of the characters *viz.*, number of primary branches per plant, days to 50% flowering, days to last harvest, fruit length, fruit pedicel length, ascorbic acid did not contribute to the total divergence.

Table 11. Percent contribution of different traits towards diversity in spine gourd genotypes

Characters	Times ranked 1st	Per cent contribution
Plant height (cm)	1	0.52
No. of primary branches per plant	0	0.00
Node no. at first female flower appear	5	2.63
Days to 50% flowering	0	0.00
Days to last harvest	0	0.00
Number of fruit per plant	11	5.52
Fruit length(cm)	0	0.00
Fruit diameter (cm)	0	0.52
Fruit pedicel length(cm)	1	0.00
Ascorbic acid (mg/100g)	0	0.00
TSS%	1	0.52
Titratable Acidity%	13	7.36
Fruit yield per hectare (q)	8	4.21
Fruit yield per plant (g)	150	78.94
Total	190	100

4.5.5 Variability, Heritability (h^2) and Genetic advance

The results with regard to mean, overall range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GA) for all the twenty characters were furnished in Table 12 and Fig. 3 and 4.

4.5.5.1 Plant height

The data presented in Table 12 were revealed that highly significant phenotypic and genotypic variances (3527.98 and 3517.07) are recorded and coupled with moderate PCV and GCV of 34.58 and 34.52 percent respectively. This trait showed high heritability (99.69 %), moderate genetic advance (121.98) and moderate GA as per cent mean (71.00).

4.5.5.2 Number of primary branches per plant

The data presented in Table 12 showed that the character were recorded least phenotypic and genotypic variances of 0.63 and 0.34 respectively with moderate

PCV (22.08) and GCV (16.30) values, moderate heritability (54.50 %), low genetic advance (0.89) and high GA as per cent mean (24.79).

4.5.5.3 Internodal length

Data presented in Table 12 showed high phenotypic and genotypic variances for, internodal length 0.85 and 0.84 respectively with moderate PCV (18.54) and low GCV (18.46), high heritability (99.21%), least genetic advance (1.88) and GA as per cent mean (37.88).

4.5.5.4 Node number of first female flower appearance

The Lowest phenotypic and genotypic variances of 2.04 and 1.99 respectively were recorded with moderate PCV and GCV of 18.80 and 18.59 values. High heritability (97.79%), low genetic advance (2.87) and high GA as per cent mean (37.88) were recorded for node number at which first female flower appearance .

4.5.5.5 Days to first flowering

Phenotypic and genotypic variance values were recorded 31.01 and 28.84 with low PCV and GCV of 13.42 and 12.84 values, respectively. High heritability (91.50 %), low genetic advance (10.50) and low GA as per cent mean (25.30) were recorded for days to first flowering.

4.5.5.6 Days to 50% flowering

Data presented in Table 12 showed high phenotypic and genotypic variances (21.80 and 5.99 respectively) with low PCV (8.68) and low GCV (4.55), and also low heritability (27.46%), genetic advance (2.64) and low GA as per cent mean (4.91) were recorded for this trait.

4.5.5.7 Days to first harvest

Data presented in Table 12 showed moderate phenotypic and genotypic variances 26.57 and 21.34 respectively with low PCV (7.28) and low GCV (6.52), high heritability (80.30 %), low genetic advance (8.53) and moderate GA as per cent mean (12.04) estimates were recorded for days to first harvest.

4.5.5.8 Days to last harvest

Data presented in Table 12 showed high phenotypic and moderate genotypic variances 94.91 and 77.55 respectively with moderate PCV (9.57) and GCV (8.65), high heritability (81.71 %), low genetic advance (16.40) and moderate GA as per cent mean (16.11) estimates were recorded for trait days to last harvest.

4.5.5.9 Number of fruits per plant

This number of fruits per plant trait showed highest phenotypic and genotypic variances 478.98 and 477.46 respectively with moderate PCV (112.32) and GCV (112.14), high heritability (99.68%), moderate genetic advance (44.94) and high GA as percent mean (230.65) estimates.

4.5.5.10 Fruit length (cm)

Fruit length were recorded low phenotypic and genotypic variances of 0.51 to 0.50 respectively with moderate PCV and GCV 17.59 and 17.40 values.High heritability (97.79 %), low genetic advance (1.44) and moderate GA as per cent mean (35.44) were recorded for fruit length.

4.5.5.11 Fruit diameter (cm)

Fruit diameter were recorded least phenotypic and genotypic variances of 0.14 to 0.13, respectively were recorded with moderate PCV and GCV of 15.11 and 14.79 values. High heritability (95.79 %), low genetic advance (0.73) and moderate GA as per cent mean (29.81).

4. 5.5.12 Fruit pedicel length (cm)

Fruit pedicel length were recorded least phenotypic and genotypic variances of 0.01 and 0.02 respectively, with low PCV and GCV of 7.99 and 5.48 values. Moderate heritability (47.11%), low genetic advance (0.11) and low GA as per cent mean (7.75) were recorded for fruit pedicel length.

4. 5.5.13 Single fruit weight (g)

Single fruit weight were showed moderate phenotypic and genotypic variances 20.55 and 20.26 respectively, with moderate PCV(37.60) and GCV(37.34), high heritability (98.60%), low genetic advance (9.21) and high GA as per cent mean (76.37) estimates.

4.5.5.14 Ascorbic acid (mg/100g)

Low phenotypic (2.01) and genotypic (1.74) variances, moderate PCV (14.65) and GCV (13.64) were recorded for ascorbic acid. High heritability (86.71 %), low genetic advance (2.53) and moderate GA as per cent mean (26.17) estimates were observed for this ascorbic acid.

4.5.5.15 Total soluble solid (%)

With respect to total soluble solid low phenotypic and genotypic variances (0.14 to 0.13), moderate PCV (14.32) and GCV (13.58), high heritability (90.02%), low genetic advance (0.70), and moderate GA as per cent mean (26.55) estimates were recorded .

4.5.5.16 Titratable Acidity (%)

Least phenotypic and genotypic variances (0.03 and 0.03) along with moderate PCV (28.24) and GCV (28.06) were recorded for this titratable acidity .The acidity were showed high heritability (98.75 %), low genetic advances (0.35) and moderate GA as per cent mean (57.44).

4.5.5.17 Average fruit weight (g)

High phenotypic and genotypic variances (451.84 and 441.67) along with moderate PCV (38.19) and high GCV (37.75) were recorded for average fruit weight .The average fruit weight were showed high heritability (97.75 %), moderate genetic advances (42.80) and high GA as per cent mean (76.89).

4.5.5.18 Fruit yield per plant (g)

The maximum phenotypic and genotypic variances (154738.94 and 154706.84) were recorded for fruit yield per plant in spine gourd genotypes with high PCV (148.54) and GCV (148.53) values. Fruit yield per plant were showed high heritability (99.98 %) and high genetic advance (810.17) as well as high GA as per cent mean (305.94) .

4.5.5.19 Fruit yield per plot (kg)

Moderate phenotypic and genotypic variances (6.75 and 6.70) were recorded for fruit yield per plot in spine gourd genotypes with high PCV (136.72) and GCV (136.25) values. Fruit yield per plot were showed high heritability (99.31%) and genetic advance (5.32) but high GA as per cent mean (279.71).

4.5.5.20 Fruit yield per hectare (q)

High phenotypic and genotypic variances (1214.88 to 1214.16) were recorded for fruit yield per hectare in spine gourd genotypes with high PCV (137.52) and GCV (137.48) values. Fruit yield per hectare were showed high heritability (99.94%) and also high genetic advance (71.76) as well as high GA as per cent mean (283.13).

In the present study, twenty genotypes from diverse sources were evaluated. The genotypes exhibited significant differences for all the twenty characters studied and a wide range of variability was observed for fruit yield per plant, fruit yield per plot, fruit yield per hectare, plant height, number of fruits per plant, average fruit weight, single fruit weight, indicated the scope for selection of suitable initial breeding material for further improvement.

The PCV and GCV values were very high particularly for fruit yield per hectare, fruit yield per plot, fruit yield per plant, number of fruit per plant, and ascorbic acid content due to very high variability available in these traits. The PCV and GCV values were moderate for average fruit weight, single fruit weight, plant height, fruit length and suggesting that these characters can be improved through simple selection. Our findings are similar to that earlier work of Naik *et.al* (2012) for number of fruit per plant in teasle gourd, Kumar *et al.* (2011) in bottle gourd, Kumar *et al.* (2013) in sponge gourd, Dora *et al.*(2003) in pointed gourd, Pal *et al*. (2016) in cucumber, Yadav *et al.* (2018) in spine gourd and Rahman *et al* .(2016) in sweet gourd.

Our results also confirmed with Mandal *et al*. 2015) fruit weight, fruit length and number of fruits per plant in bottle gourd . Devi and Mariappan, (2013) for fruit length in snake gourd, Pathak *et al.* (2014) also reported high PCV and GCV for these traits.

Moderate PCV and GCV values for number of branches per plant, average fruit weight, single fruit weight, plant height, fruit length, days to 50 % flowering similar reports were also reported by Basumatary *et al* .(2014) in spine gourd and Maurya *et al* .(2018) in bitter gourd.

Heritability estimates for different the characters were ranged from very high degree to low i.e. from 99.98 to 27.46 per cent. Highest heritability was recorded for fruit yield per plant (99.98), fruit yield per hectare (99.94%) followed by plant height

(99.69 %) ,number of fruit per plant (99.68%), number of fruit per plot (99.31%) ,fruit length (97.79 %) and node number at which first female flower appearance (97.79 %).

This suggested the greater effectiveness of selection due to less influence of environment and improvement to be expected for these characters in future breeding programme. These findings are in conformity with Kumar *et al.* (2011) for fruit yield per plant in bitter gourd, Ananthan *et.al* (2017) in ridge gourd, Usha Rani *et.al* (2017) , Pathak *et al* .(2014) in bitter gourd and Jena *et al* . (2017) in pointed gourd.

Johnson *et al.* (1955) suggested that high heritability coupled with high genetic advance as percentage of mean were more useful than heritability alone in predicting the resultant effect during selection of best individual genotype. Genetic advance is the measure of genetic gain under selection and expression in percentage of mean.

In present investigation genetic advance as per cent of mean was high for fruit yield per plant, fruit yield per plot, number of primary branches per plant, number of fruit per plant, fruit yield per hectare, plant height, node number at which first female flower appearance, fruit length, fruit diameter, ascorbic acid, single fruit weight, acidity, average fruit weight.

A similar results of high heritability coupled with high genetic advance was observed for days to first male and female flowering, TSS, weight of fruit (Muralidhara *et al.*, 2014), fruit yield per plant followed by fruit length (Singh *et al.,* 2015), number of fruits per plant also reported by Mandal et. al (2015), Sanwal *et al.* (2007), Dey *et al.* (2009) in bitter gourd , Rambabu *et.al* (2017) in bottle gourd, ,Resmi and Sreelathakumary (2011) in ash gourd, Rani *et al.*(2012) and Chakraborthy *et al.* (2013) in bitter gourd, Devi and Mariappan (2013) in snake gourd, Gautam (2013) in ridge gourd, Kumar *et al.* (2013) in sponge gourd. Damor *et. al* (2016) in bottle gourd.

Table 12. Estimation of variability, heritability and genetic advance as per cent of mean for twenty characters in spine gourd genotypes

Characters	Range		Mean	Variance		PCV (%)	GCV (%)	h^2 (%)	Genetic Advance	GA as per cent of mean
	Mini	Maxi		σ^2 (p) (Phenotypic)	σ^2 (g) (Genotypic)					
PH (cm)	65.08	349.84	171.78	3527.98	3517.07	34.58	34.52	99.69	121.98	71.00
NPB	2.37	4.60	3.59	0.63	0.34	22.08	16.30	54.50	0.89	24.79
IL(cm)	3.43	7.40	4.96	0.85	0.84	18.54	18.46	99.21	1.88	37.88
NNFFF	4.67	10.37	7.59	2.04	1.99	18.80	18.59	97.79	2.87	37.88
DF	32.67	54.67	41.50	31.01	28.84	13.42	12.84	91.50	10.50	25.30
DFF	47.33	62.67	53.82	21.80	5.99	8.68	4.55	27.46	2.64	4.91
DFH	60.33	77.67	70.82	26.57	21.34	7.28	6.52	80.30	8.53	12.04
DLH	85.00	120.67	101.76	94.91	77.55	9.57	8.65	81.71	16.40	16.11
NFP	5.47	103.40	19.49	478.98	477.46	112.32	112.14	99.68	44.94	230.65
FL(cm)	2.90	4.77	4.05	0.51	0.50	17.59	17.40	97.79	1.44	35.44
FD(cm)	1.77	3.17	2.45	0.14	0.13	15.11	14.79	95.79	0.73	29.81
PDL(cm)	1.27	1.57	1.41	0.01	0.01	7.99	5.48	47.11	0.11	7.75
SFW(g)	7.20	20.53	12.06	20.55	20.26	37.60	37.34	98.60	9.21	76.37
ASCB	6.44	11.53	9.67	2.01	1.74	14.65	13.64	86.71	2.53	26.17
TSS%	2.21	3.20	2.64	0.14	0.13	14.32	13.58	90.02	0.70	26.55
ACD%	0.36	0.91	0.63	0.03	0.03	28.24	28.06	98.75	0.35	57.44
AFW(g)	32.73	97.00	55.67	451.84	441.67	38.19	37.75	97.75	42.80	76.89
FYPT (g)	44.87	1796.67	264.82	154738.94	154706.84	148.54	148.53	99.98	10.17	305.94
FYPL(kg)	0.26	11.77	1.90	6.75	6.70	136.72	136.25	99.31	5.32	279.71
FYH (q)	3.47	158.50	25.34	1214.88	1214.16	137.52	137.48	99.94	71.76	283.13

PH (plant height), NPB (Number of primary branches), NNFFF (Number of nodes at first female flower appearance), DFF (Days to 50% flowering) ,DFH (days to first harvest), DLH (days to last harvest), SFW (single fruit weight), NFPP (Number of fruits per plant), FL (Fruit length), FD (Fruit diameter), PDL (pedicel length), ASCB (ascorbic acid), TSS (Total soluble solid), ACD (Titratable acidity), AFW (average fruit weight) , FYPH (Fruit yield per hectare) and FYPP (Fruit yield per plant)

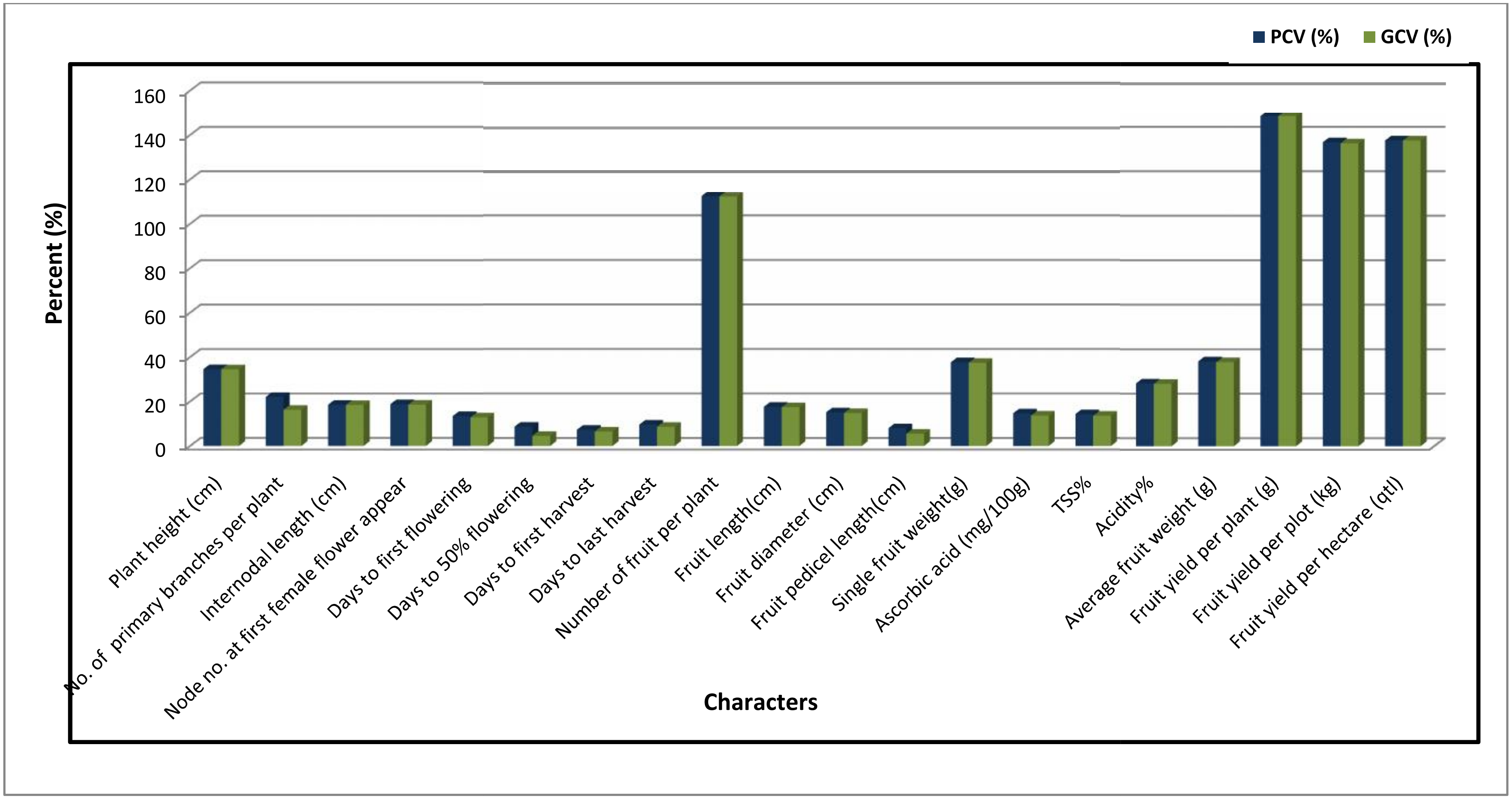


Fig. 3 . PCV and GCV of twenty quantitative traits in spine gourd genotypes

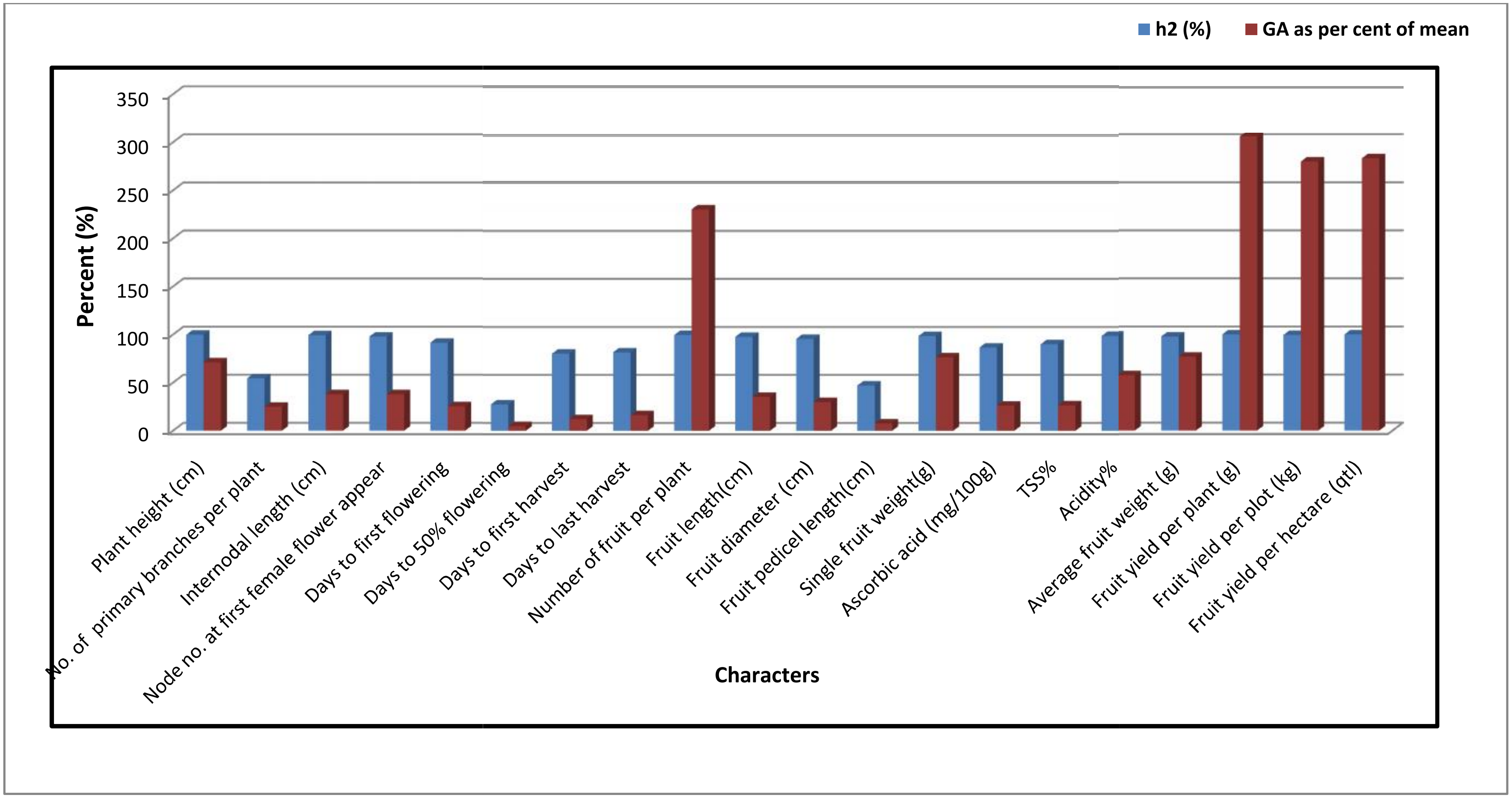


Fig. 4 Heritability (H^2) and genetic advance as per cent mean for twenty quantitative traits in spine gourd

Table 13. Phenotypical correlation coefficient for different fruit yield contributing characters in spine gourd

C/G	PH	NPB	NFFF	DFF	DLH	NFP	FL	FD	PDL	VTC	TSS %	ACIDITY	FYPH	FYPP
PH	**1.0000**	0.2078	-0.1044	-0.2882*	0.5338**	0.2968*	0.5403**	0.3193*	0.0871	0.3415**	0.0827	0.0012	0.2890*	0.2637*
NPB		**1.0000**	0.1947	-0.0447	0.1653	0.2065	-0.0158	0.0322	0.2312	0.1969	0.2039	0.0103	0.2332	0.2214
NFFF			**1.0000**	-0.2379	-0.0113	-0.3195*	0.0328	0.3193*	-0.0543	0.3438**	-0.0177	0.1095	-0.2019	-0.2035
DFF				**1.0000**	-0.4000**	-0.0757	-0.3710**	-0.5432**	0.3171*	-0.4842**	0.1537	-0.0896	-0.1350	-0.1188
DLH					**1.0000**	0.6206**	0.5962**	0.4759**	-0.1418	0.2954*	-0.0532	0.1125	0.6425**	0.6260**
NFP						**1.0000**	0.3314**	0.1571	0.0149	0.1884	0.2120	-0.0885	0.9783**	0.9836**
FL							**1.0000**	0.5015**	-0.1718	0.2512	-0.1420	-0.0382	0.3661**	0.3290*
FD								**1.0000**	-0.2919*	0.5470**	-0.0608	0.0998	0.2752*	0.2595*
PDL									**1.0000**	-0.1285	0.3065*	-0.2544*	-0.0402	-0.0376
VTC										**1.0000**	0.1587	-0.1258	0.2027	0.2138
TSS%											**1.0000**	-0.6054**	0.2061	0.2164
ACD												**1.0000**	-0.0615	-0.0610
FYPH													**1.0000**	0.9966**
FYPP														**1.0000**

*** Significant** at 5 per cent level**, ** Significant** at 1 per cent level.

PH (plant height) , NPB (Number of primary branches), NFFF (Number of nodes at first female flower appearance), DFF (Days to 50% flowering), DLH (days to last harvest), NFPP (Number of fruits per plant), FL (Fruit length), FD (Fruit diameter), PDL (pedicel length), ASCB (ascorbic acid), TSS (Total soluble solid), ACD (titratable acidity), FYPH (Fruit yield per hectare) and FYPP (Fruit yield per plant).

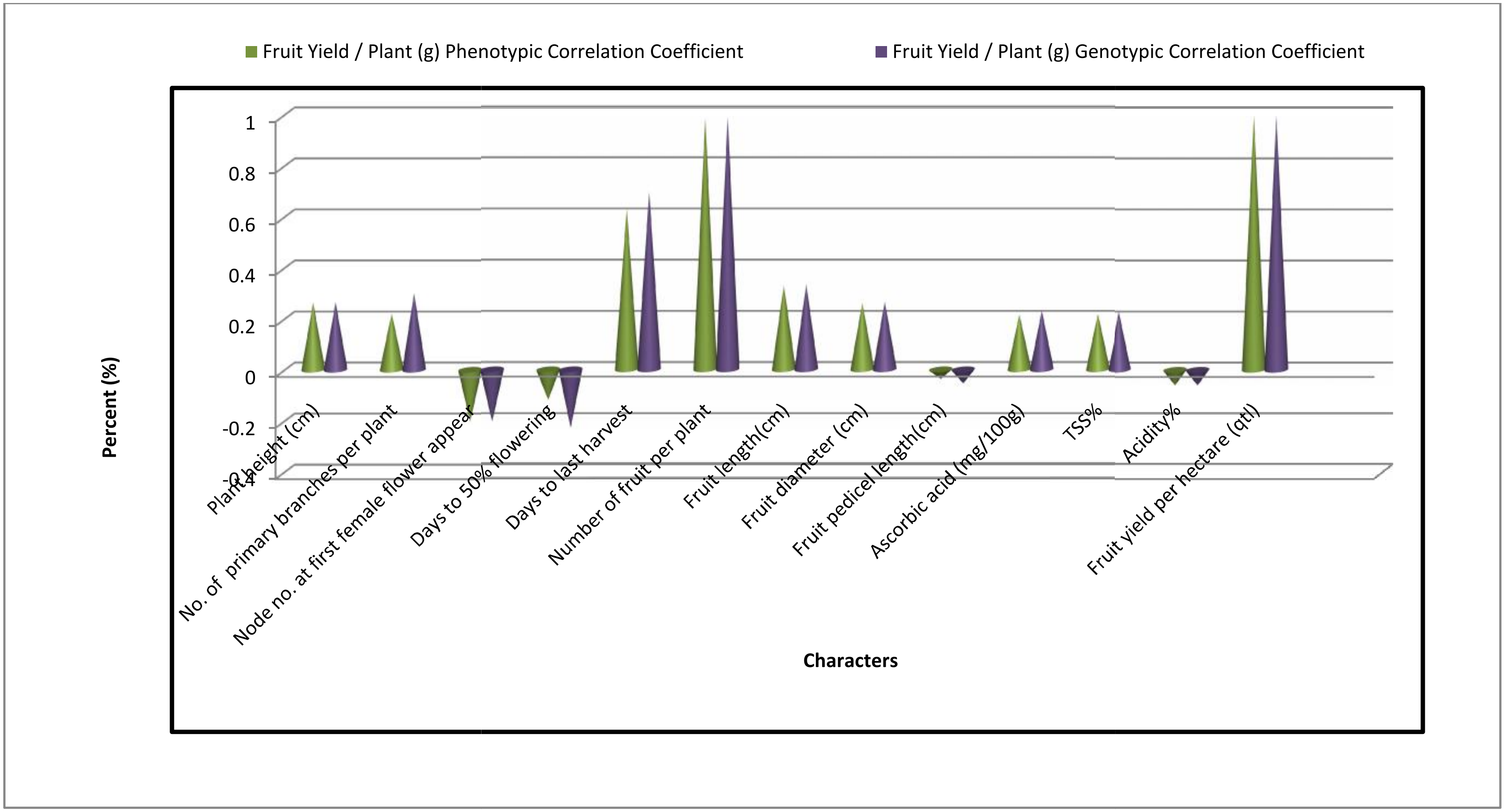


Fig. 5 Phenotypic and genotypic correlation coefficient for fourteen characters in spine gourd

Table 14. Genotypical correlation coefficient for different fruit yield contributing characters in spine gourd

C/G	PH	NPB	NNFFF	DFF	DLH	NFP	FL	FD	PDL	VTC	TSS%	ACIDITY	FYPH	FYPP
PH	**1.0000**	0.2855*	-0.1047	-0.5624**	0.5920**	0.2980*	0.5488**	0.3273*	0.1299	0.3767**	0.0874	-0.0001	0.2898*	0.2645*
NPB		**1.0000**	0.2532	0.0956	0.3378**	0.2866*	0.0128	0.0632	0.4281**	0.2728*	0.3248*	0.0303	0.3202*	0.2995*
NNFFF			**1.0000**	-0.4642**	-0.0158	-0.3241*	0.0273	0.3270*	-0.0556	0.3518**	-0.0182	0.1138	-0.2035	-0.2059
DFF				**1.0000**	-0.6306**	-0.1501	-0.7891**	-1.1225**	0.6576**	-0.9415**	0.1950	-0.1328	-0.2491	-0.2292
DLH					**1.0000**	0.6830**	0.6659**	0.5350**	-0.3049*	0.3865**	-0.0490	0.1207	0.7072**	0.6922**
NFPP						**1.0000**	0.3330**	0.1634	0.0141	0.1998	0.2240	-0.0896	0.9803**	0.9854**
FL							**1.0000**	0.5231**	-0.2754*	0.2670*	-0.1520	-0.0358	0.3705**	0.3324**
FD								**1.0000**	-0.4566**	0.5797**	-0.0584	0.1087	0.2812*	0.2653*
PDL									**1.0000**	-0.2124	0.3971**	-0.3671**	-0.0589	-0.0552
ASCB										**1.0000**	0.2104	0.1323	0.2183	0.2289
TSS %											**1.0000**	-0.6433**	0.2157	0.2276
ACD												**1.0000**	-0.0621	-0.0611
FYPH													**1.0000**	0.9969**
FYPP														**1.0000**

*** Significant** at 5 per cent level**, ** Significant** at 1 per cent level.

PH (plant height), NPB (Number of primary branches), NNFFF (Number of nodes at first female flower appearance), DFF (Days to 50% flowering), DLH (days to last harvest), NFPP (Number of fruits per plant), FL (Fruit length), FD (Fruit diameter), PDL (pedicel length), ASCB(ascorbic acid), TSS (Total soluble solid), ACD (acidity), FYPH (Fruit yield per hectare) and FYPP (Fruit yield per plant)

4.6 Correlation studies

The phenotypic and genotypic correlation co-efficient were determined to obtain information on the relationship among fourteen quantitative characters in Spine gourd are presented in Tables 13 and 14 respectively.

4.6.1 Plant height (cm)

Plant height were exhibited positive significant correlation with number of branches per plant (0.2078 P, 0.2855 G) , days to last harvest (0.5338 P, 0.5920 G) , number of fruit per plant (0.2968 P, 0.2980 G) , fruit length (0.5403 P, 0.5488 G), fruit diameter (0.3193 P ,0.3273 G), fruit pedicel length (0.0871 P, 0.1299 G), ascorbic acid (0.3415 P, 0.3767 G), acidity (0.0012 P, -0.0001 G) , TSS (0.0827 P, 0.0874 G), fruit yield per hectare (0.2890 P, 0.2898 G) and fruit yield per plant (0.2637 P, 0.2645 G) at both genotypic and phenotypic level .

Negative significant correlation was noticed with first female flower appearance (-0.1044 P ,-0.1047 G) ,days to 50% flowering (-0.2882 P, -0.5624 G) at both genotypic and phenotypic level.

4.6.2 Number of primary branches per plant

Number of primary branches per plant were recorded positive significant correlation with node number at first female flower appearance (0.1947 P, 0.2532 G) ,number of fruit per plant (0.2065 P, 0.2866 G),days to last harvest (0.1653 P, 0.3378 G) , fruit yield /ha (0.2332 P, 0.3202 G), fruit yield per plant (0.2214 P, 0.2995G), ascorbic acid (0.1969 P, 0.2728 G), TSS (0.2039 P, 0.3248 G), acidity (0.0103 P, 0.303 G) at both genotypic and phenotypic level. Days to 50% flowering (0.0956 G) has recorded positive and significant association with plant height at genotypic level.

Negative and significant correlation was observed in fruit length (-0.0158 G) at phenotypic level. Days to 50% flowering (-0.0447 P) were exhibited significant and negative association with number of primary branches per plant at phenotypic level.

4.6.3 Node number at first female flower appearance

Phenotypic and genotypic correlation were recorded significant positive correlation with node number at first female flower appearance to fruit length (0.0328 P, 0.0273 G) , fruit diameter (0.3193 P, 0.3270 G) ,ascorbic acid (0.3438 P, 0.3518 G),acidity (0.1095 P, 0.1138 G).

Days to50% flowering (-0.2379 P,-0.4642 G) ,days to last harvest (-0.0113 P -0.0158 G) , number of fruit per plant (-0.3195 P,-0.3241 G), Fruit pedicel length (-0.0543 P -0.0556 G) , TSS (- 0.0177 P , -0.0182 G), fruit yield per hectare (-0.2019 P, -0.2035 G) and fruit yield per plant (-0.2035 P, -0.2059 G) were exhibited negative correlation for both phenotypic and genotypic correlation in these trait.

4.6.4 Days to 50 per cent flowering

Days to 50 per cent flowering showed significant positive correlation with fruit pedicel length (0.3171 P, 0.6576 G), TSS (0.1537 P, 0.1950 G) at phenotypic and genotypic correlation, fruit yield per hectare (-0.1350 P) showed negative correlation at phenotypic level and (0.7072 G) significant positive correlation at genotypic level.

Both phenotypic and genotypic correlation were exhibited significant negative correlation with days to last harvest (-0.4000 P, -0.6306 G), number of fruit per plant (-0.0757 P ,-0.1501 G) fruit length (-0.3710 P, -0.7891 G) ,fruit diameter (-0.5432 P,-1.1225 G) ,ascorbic acid (-0.4842 P -0.9415 G) acidity (-0.0896 P , -0.1328 G) ,fruit yield per plant (-0.1188 P, -0.2292 G) recorded for the trait.

4.6.5 Days to last harvest

Both phenotypic and genotypic correlation were exhibited significant positive correlation with fruit length (0.5962 P, 0.6659 G), fruit diameter (0.4759 P, 0.5350 G) ascorbic acid (0.2954 P, 0.3865 G), fruit yield per hectare (0.6425 P, 0.7072 G) and fruit yield per plant (0.6260 P, 0.6922G) was recorded for the trait. TSS (-0.0532 P) showed significant positive correlation at phenotypic level.

Fruit pedicel length (-0.1718 P, -0.3049 G), were recorded negative and significant association with days to last harvest at phenotypic and genotypic level.

4.6.6 Number of fruit per plant

Number of fruit per plant showed positive significant correlation with fruit length (0.3314 P, 0.3330 G), fruit diameter (0.1571 P, 0.1634 G) ,fruit pedicel length (0.0149 P 0.0141 G), ascorbic acid (0.1884 P ,0.1998 G),fruit yield per hectare (0.9783 P , 0.9803 G) and fruit yield per plant (0.9836 P, 0.9854 G) at phenotypic and genotypic level.

Negative and significant correlation was noticed with fruit pedicel length (-0.1718 P) at phenotypic level (0.0141 G) showed positive correlation at genotypic level .Acidity (-0.0885 P, -0.0896 G) showed negative correlation at phenotypic and genotypic level.

4.6.7 Fruit length (cm)

Length of fruit were recorded positive, significant correlation with fruit diameter (0.5231 P , 0.5015 G), ascorbic acid (0.2512 P , 0.2670 G) , fruit yield per hectare (0.4604 P, 0.4752 G) and fruit yield per plant (0.3171 P, 0.3259 G).

Fruit pedicel length (-0.1718 P, -0.2754 G), acidity (-0.0382 P, -0.0358 G) and TSS (-0.1420, -0.1520 G) has recorded negative and significant association was noticed with length of fruit at both genotypic and phenotypic level**.**

4.6.8 Fruit diameter (cm)

Diameter of fruit were recorded positive, significant correlation with fruit yield per hectare (0.2752 P, 0.2812 G), ascorbic acid (0.5470 P, 0.5797 G), Acidity (0.0998 P ,0.1087 G) and fruit yield per plant (0.2595 P ,0.2653 G) and negative significant correlation was noticed with fruit pedicel length (-0.4566 P,-0.2919 G) and TSS (-0.0608 P, -0.0584 G) at both genotypic and phenotypic level**.**

4.6.9 Fruit pedicel length (cm)

Fruit pedicel length were recorded positive, significant correlation with TSS (0.3065 P ,0.3971 G) whereas ascorbic acid (-0.1285 P,-0.2124 G) ,acidity (-0.2544 P, -0.3671 G),fruit yield per hectare (-0.0402 P, -0.0589 G), fruit yield per plant (-0.0376 P ,-0.0552) noticed negative significant correlation at both genotypic and phenotypic level**.**

4.6.10 Ascorbic acid (mg/100g of fruit)

Ascorbic acid content were showed positive significant correlation with TSS (0.1587 P ,0.2104 G) and fruit yield per hectare (0.2027 P, 0.2183 G), fruit yield per plant (0.2138 P, 0.2289 G). Negative significant correlation was found with acidity (-0.1258 P) at phenotypic level while found positive (0.1323 G) genotypic level.

4.6.11 TSS %

At phenotypic and genotypic level total soluble solid content were showed positive significant correlation with fruit yield per hectare (0.2061 P, 0.2157 G), fruit yield per plant (0.2164 P, 0.2276 G) Negative, significant correlation was found with acidity (--0.6054, -0.6433 G) .

4.6.12 Titratable acidity %

Titratable acidity showed negative significant correlation with fruit yield per hectare (-0.0615 P, -0.0621 G) and fruit yield per plant (-0.0610 P, -0.0611 G) at phenotypic and genotypic level.

4.6.13 Fruit yield per hectare (q)

Fruit yield per hectare showed positive significant correlation with fruit yield per plant (0.9966 P, 0.9969 G) at phenotypic and genotypic level.

4.6.14 Fruit yield per plant (kg)

Fruit yield per plant was recorded positive significant correlation with characters plant height (0.2637 P , 0.2645 G) , number of primary branches per plant (0.2214 P, 0.2995 G), days to last harvest (0.6260 P, 0.6922 G), fruit length (0.3290 P, 0.3324 G), fruit diameter (0.2595 P , 0.2653 G) and fruit yield per hectare (0.9966 P, 0.9969G), ascorbic acid (0.2138 P, 0.2289 G) and TSS (0.2164 P ,0.2276 G) at phenotypic and genotypic level.

Fruit pedicel length (-0.0376 P, -0.0552 G), node number of first female flower appearance (-0.2035 P-0.2059 G), Days to 50% flowering (-0.1188 P, -0.2292 G) and acidity (-0.0610 P, -0.0611 G) has recorded negative and significant association with fruit yield per plant at phenotypic and genotypic level.

In general, it is evident from the recorded data (Table 13 and 14), genotypic correlation was higher than phenotypic correlation indicating a less influence of environmental factors and relative stability of the genotypes and revealed that Fruit yield per plant exhibited high significant positive association with plant height, number of branches per plant, days to last harvest ,number of fruit plant ,fruit length, fruit diameter, ascorbic acid ,TSS, fruit yield per hectare at both phenotypic and genotypic level .

Similar investigation for significant positive correlation between fruit yield per plant and fruit length at phenotypic and genotypic level in spine gourd reported by Aaliya *et al.* (2014), by Choudhary *et al.* (2014) in ridge gourd, Dora *et al*. (2003) in bottle gourd. Kumar *et al.* (2013a) observed total yield per vine was found to be positively and significantly correlated with average weight of fruit, number of fruits per vine and number of seeds per fruit in sponge gourd. Similar work was also done by Akhter *et al.* (2013) in pumpkin, Rahman *et al* . (2011) in Teasle gourd, Rabbani *et al.* (2012) in ridge gourd, Janaranjani *et al.* (2015) in Bottle gourd.

The study showed that selection for those characters positively related to yield would be effective to get more yield per plant. Similarly, those characters which are positively related to days to last havest are effective in selection to get long fruiting span varieties .

4.7 Path coefficient analysis

Association of characters determined by correlation indicates the association pattern of component traits with yield. It simply represents the general association of a particular trait with yield rather than providing cause and effect relation. It may not provide an exact picture of the relative significance of direct and indirect influence of each of the yield attributing components towards yield. In order to find a clear picture of inter-relationships among the fruit yield and yield contributing characters, direct and indirect effects were worked out using path analysis.

The technique of path coefficient of analysis was developed by Wright (1934) and demonstrated by Dewy and Lu (1959). As it measures both the direct and indirect effects of one variable upon other, it has immense value for the breeder to identify important component traits of yield and utilize in a proper way. Path coefficient analysis is important for those traits which showed significant correlations with fruit yield per plant as it partitions the correlation between traits into direct and indirect effect via other traits used in the analysis. Path analysis has been described for those traits only which showed significant correlation with fruit yield per plant as it partitions the correlation between traits into direct and indirect effect via other traits used in the analysis. Path analysis has been described for those traits only which showed significant correlation with fruit yield per plant

Path analysis was carried out at phenotypic and genotypic level considering fruit yield per plant as dependent character and its attributes as independent characters with two path actions *viz.,* direct effect on yield and indirect effect through components which are not revealed by correlation studies and data presented in Table 15 and 16 and Fig. 6 and Fig. 7.

4.7.1 Plant height (cm)

Plant height showed maximum negative direct effect (-0.0564) on fruit yield per plant. It had shown maximum positive indirect effect on fruit yield per plant through days to 50% flowering (0.0317) followed by node number of first flower appearance (0.0059) While, it had shown negative indirect effect on days to last harvest (-0.0334) followed by fruit length (-0.0309), ascorbic acid (-0.0212), fruit diameter (-0.0184), number of fruit per plant (-0.0168) number of primary branches (-0.0161) at genotypic level.

At phenotypic level, plant height was recorded maximum negative direct effect (-0.0096) on fruit yield per plant. It had shown maximum positive indirect effect through days to 50% flowering (0.0028) followed by node number of first female flower appearance (0.0010) While, characters fruit length (-0.0052) ,days to last harvest (-0.0051) followed by ascorbic acid (-0.0033), fruit diameter (-0.0031) and fruit yield per ha. (-0.0028) had shown maximum negative indirect effect on fruit yield per plant.

4.7.2 Number of primary branches per plant

Number of primary branches had a maximum negative direct effect (-0.0809) on fruit yield per plant. It exhibited negative indirect effect through fruit pedicel length (-0.0346), days to last harvest (-0.0273), fruit yield per hectare (-0.0259) , number of fruit per plant (-0.0232) , plant height (-0.0231) , TSS (- 0.0263) , ascorbic acid (-0.0221) and days to 50% flowering (-0.0077) at genotypic level and no one character showed indirect positive effect at genotypic level.

The number of primary branches showed negative direct effect (-0.0107) on fruit yield per plant. It exhibited negative indirect effect on fruit yield per plant *viz.,* fruit yield per ha (-0.0025) ,fruit pedicel length (-0.0025), followed by number of fruit per plant (-0.0022), total soluble solid (-0.0022) , plant height (-0.0022) , days to last harvest (-0.0018), Whereas, two characters had shown positive indirect effect on fruit

Table 15. Genotypic (G) path coefficient analysis indicating direct and indirect effects of components characters on yield per plant in spine gourd genotypes.

characters	Plant Height	No. of primary Branch	Node no. first female flower	Days to 50% Flowering	Days to last Harvest	No. of fruits /plant	Fruit Length	Fruit Diameter	Fruit Pedicel Length	Ascorbic Acid	Total soluble solid	Titratable acidity	Fruit yield/ha	Fruit yield /plant
PH	**-0.0564**	-0.0161	0.0059	0.0317	-0.0334	-0.0168	-0.0309	-0.0184	-0.0073	-0.0212	-0.0049	0.0000	-0.0163	0.2645
NPB	-0.0231	**-0.0809**	-0.0205	-0.0077	-0.0273	-0.0232	-0.0010	-0.0051	-0.0346	-0.0221	-0.0263	-0.0024	-0.0259	0.2995
Fff	-0.0002	0.0005	**0.0018**	-0.0008	0.0000	-0.0006	0.0000	0.0006	-0.0001	0.0006	0.0000	0.0002	-0.0004	-0.2059
DFF	0.0050	-0.0008	0.0041	**-0.0089**	0.0056	0.0013	0.0070	0.0099	-0.0058	0.0083	0.0017	0.0012	0.0022	-0.2292
DLH	0.0503	0.0287	-0.0013	-0.0536	**0.0850**	0.0580	0.0566	0.0455	-0.0259	0.0328	-0.0042	0.0103	0.0601	0.6922
NFP	0.0167	0.0161	-0.0182	-0.0084	0.0384	**0.0562**	0.0187	0.0092	0.0008	0.0112	0.0126	-0.0050	0.0551	0.9854
FL	-0.0221	-0.0005	-0.0011	0.0318	-0.0268	-0.0134	**-0.0403**	-0.0211	0.0111	-0.0107	0.0061	0.0014	-0.0149	0.3324
FD	-0.0061	-0.0012	-0.0061	0.0210	-0.0100	-0.0031	-0.0098	**-0.0187**	0.0085	-0.0108	0.0011	-0.0020	-0.0053	0.2653
PDL	0.0086	0.0283	-0.0037	0.0434	-0.0201	0.0009	-0.0182	-0.0301	**0.0660**	-0.0140	0.0262	-0.0242	-0.0039	-0.0552
VTC	0.0188	0.0136	0.0176	-0.0471	0.0193	0.0100	0.0134	0.0290	-0.0106	**0.0500**	0.0105	-0.0066	0.0109	0.2289
TSS	0.0034	0.0127	-0.0007	0.0076	-0.0019	0.0088	-0.0059	-0.0023	0.0155	0.0082	**0.0391**	-0.0251	0.0084	0.2276
ACD	0.0000	0.0015	0.0056	-0.0065	0.0059	-0.0044	-0.0018	0.0053	-0.0180	-0.0065	-0.0316	**0.0491**	-0.0030	-0.0611
FY/HA	0.2695	0.2977	-0.1893	-0.2316	0.6576	0.9115	0.3445	0.2615	-0.0547	0.2029	0.2006	-0.0577	**0.9298**	0.9969

Residual effect = 0.0316

PH (plant height) , NPB (Number of primary branches), NNFFF (Number of nodes at first female flower appearance), DFF (Days to 50% flowering), DLH (days to last harvest), NFPP (Number of fruits per plant), FL (Fruit length), FD (Fruit diameter), PDL (pedicel length), ASCB (ascorbic acid), TSS (Total soluble solid),ACD (titratable acidity) and FYPH (Fruit yield per hectare).

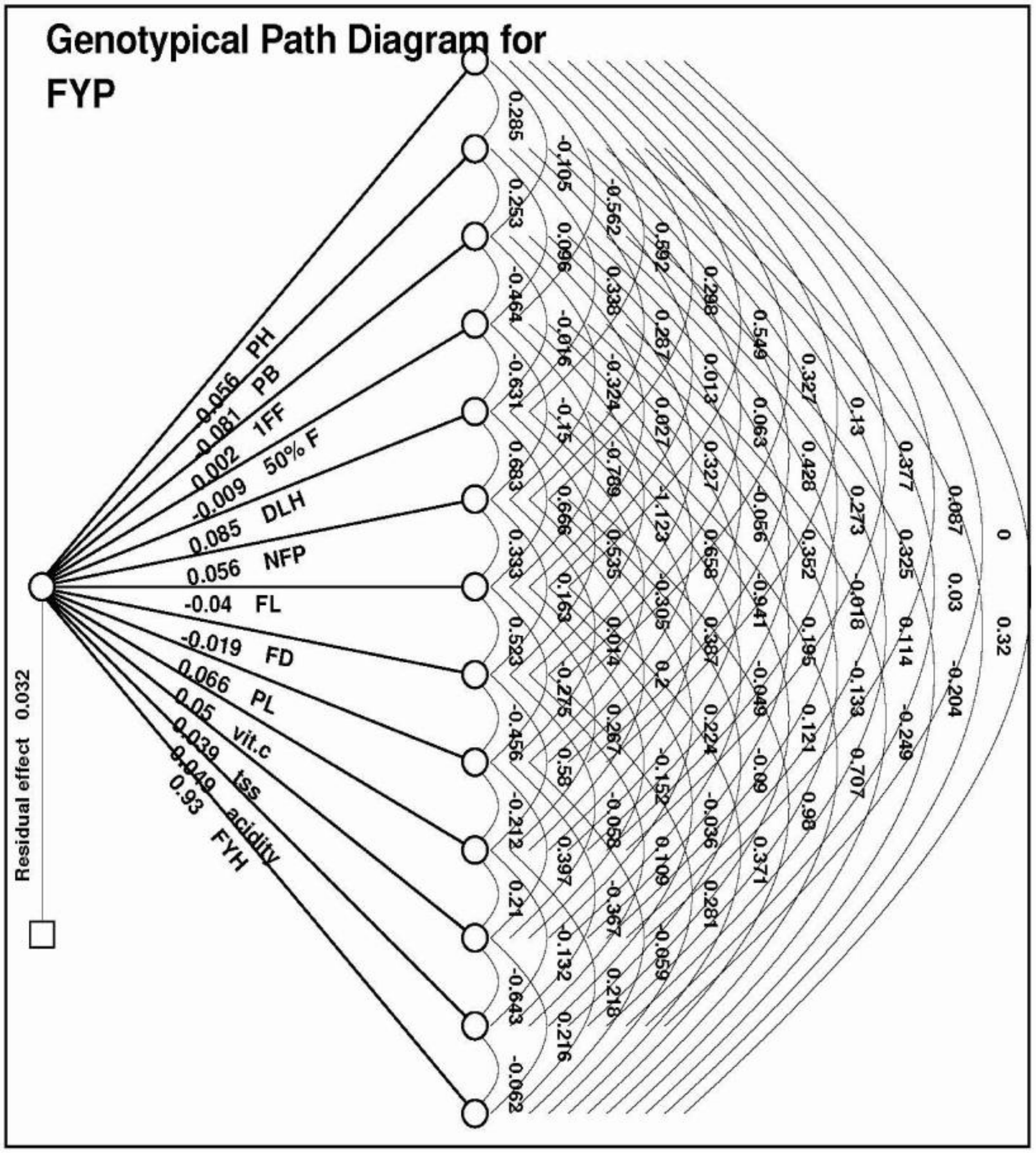


Fig.6. Genotypic path diagram representing direct and indirect effects on fruit yield per plant

Table 16. Phenotypic (G) path coefficient analysis indicating direct and indirect effects of components characters on yield per plant in spine gourd genotypes.

Characters	Plant Height	No. of primary Branch	Node no. first female flower	Days to 50% Flowering	Days to last Harvest	No. of fruits /plant	Fruit Length	Fruit Diameter	Fruit Pedicel Length	Ascorbic Acid	Total soluble solid	Titrable acidity	Fruit yield/ha	Fruit yield /plant
PH	**-0.0096**	-0.0020	0.0010	0.0028	-0.0051	-0.0029	-0.0052	-0.0031	-0.0008	-0.0033	-0.0008	0.0000	-0.0028	0.2637
NPB	-0.0022	**-0.0107**	-0.0021	0.0005	-0.0018	-0.0022	0.0002	-0.0003	-0.0025	-0.0021	-0.0022	-0.0001	-0.0025	0.2214
NNFFF	-0.0052	0.0097	**0.0497**	-0.0118	-0.0006	-0.0159	0.0016	0.0159	-0.0027	0.0171	-0.0009	0.0054	-0.0100	-0.2035
DFF	-0.0013	-0.0002	-0.0011	**0.0046**	-0.0018	-0.0003	-0.0017	-0.0025	0.0015	-0.0022	0.0007	-0.0004	-0.0006	-0.1188
DLH	-0.0093	-0.0029	0.0002	0.0070	**-0.0175**	-0.0108	-0.0104	-0.0083	0.0025	-0.0052	0.0009	-0.0020	-0.0112	0.6260
NFPP	0.1351	0.0940	-0.1454	-0.0345	0.2825	**0.4552**	0.1509	0.0715	0.0068	0.0858	0.0965	-0.0403	0.4453	0.9836
FL	-0.0225	0.0007	-0.0014	0.0155	-0.0248	-0.0138	**-0.0417**	-0.0209	0.0072	-0.0105	0.0059	0.0016	-0.0153	0.3290
FD	0.0163	0.0016	0.0163	-0.0277	0.0243	0.0080	0.0256	**0.0511**	-0.0149	0.0279	-0.0031	0.0051	0.0141	0.2595
PDL	-0.0013	-0.0034	0.0008	-0.0046	0.0021	-0.0002	0.0025	0.0043	**-0.0146**	0.0019	-0.0045	0.0037	0.0006	-0.0376
ASCB	-0.0048	-0.0028	-0.0048	0.0068	-0.0042	-0.0027	-0.0035	-0.0077	0.0018	**-0.0141**	-0.0022	0.0018	-0.0029	0.2138
TSS	0.0008	0.0020	-0.0002	0.0015	-0.0005	0.0021	-0.0014	-0.0006	0.0031	0.0016	**0.0100**	-0.0060	0.0021	0.2164
ACD	0.0000	0.0001	0.0006	-0.0005	0.0007	-0.0005	-0.0002	0.0006	-0.0015	-0.0007	-0.0036	**0.0059**	-0.0004	-0.0610
FYPH	0.1677	0.1353	-0.1171	-0.0784	0.3728	0.5676	0.2124	0.1597	-0.0233	0.1176	0.1196	-0.0357	**0.5803**	0.9966

Residual effect = 0.0408

PH (plant height) , NPB (Number of primary branches) , NNFFF (Number of nodes at first female flower appearance), DFF (Days to 50% flowering), DLH(days to last harvest), NFPP (Number of fruits per plant), FL (Fruit length), FD (Fruit diameter), PDL(pedicel length), ASCB (ascorbic acid), TSS (Total soluble solid), ACD (Titratable acidity) , FYPH (Fruit yield per hectare) and FYPP (Fruit yield per plant).

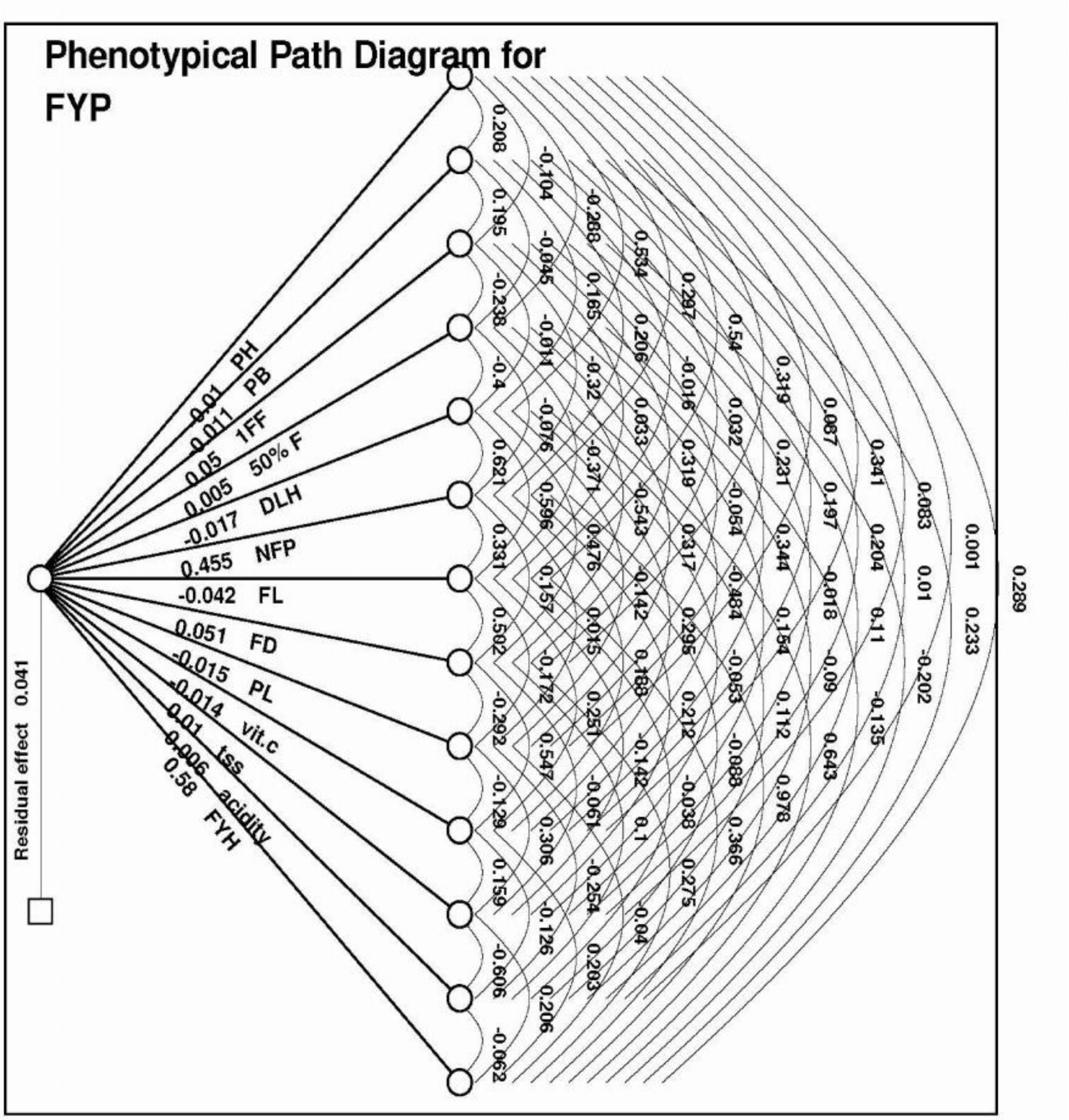


Fig.7. Phenotypic path diagram representing direct and indirect effects on fruit yield per plant

yield per plant through days to 50% flowering (0.0005), fruit length (0.0002) at phenotypic level.

4.7.3 Node number of first female flower appearance

First female flower appearance node number had a positive direct effect (0.0018) on fruit yield per plant. It showed a positive indirect effect through characters *viz.,* fruit length (0.0006), ascorbic acid (0.0006) followed by number of primary branches per plant (0.0005) While, it showed maximum negative indirect effect through days to 50% flowering (0.0008), Fruit yield per hectare (-0.0004) followed by number of fruit per plant (-0.0006) at genotypic level.

The character First female flower appearance node number showed positive direct effect (0.0497) on fruit yield per plant. It exhibited maximum positive indirect effect on fruit yield per plant *viz.* ascorbic acid (0.0171) ,fruit diameter (0.0159), number of primary branches per plant (0.0097), acidity (0.0054) Whereas, it had shown maximum negative indirect effect on fruit yield per plant through number fruit per plant (-0.0159) ,days to 50% flowering (-0.0118) ,fruit yield per hectare (-0.0100), plant height (-0.0052) at phenotypic level.

4.7.4 Days to 50 per cent flowering

Days to 50 per cent flowering was exerted by maximum negative direct effect (-0.0089) on fruit yield per plant and it had maximum positive indirect effect on fruit diameter (0.0099) ascorbic acid (0.0083), fruit pedicel length (0.0070), plant height (0.0050), number of fruit per plant (0.0013) While, traits exerted negative indirect effect on fruit yield per plant *viz.* fruit pedicel length (- 0.0058), total soluble solid (-0.0017) at genotypic level.

At phenotypic level, days to 50 per cent flowering had shown maximum positive direct effect (0.0046) on fruit yield per plant. While, it were recorded maximum negative indirect effect *viz* fruit diameter (-0.0025), ascorbic acid (-0.0022), days to last harvest (-0.0018) , fruit length (-0.0017) and fruit yield per hectare (-0.0006) While, fruit pedicel length (0.0015),TSS (0.0007) had shown positive indirect effect on fruit yield per plant.

4.7.5 Days to last harvest

At genotypic level, days to last harvest were recorded maximum positive direct effect (0.0850) on fruit yield per plant. Its positive indirect effect on fruit yield was exerted through fruit yield per hectare (0.0601) followed by and number of fruit per plant (0.0580), fruit length (0.0566), plant height (0.0503), fruit diameter (0.0455), ascorbic acid (0.0328), acidity (0.0103) Whereas, days to 50% flowering (-0.0536) showed maximum negative indirect effect on fruit yield per plant followed by fruit pedicel length (-0.0259), TSS (-0.0042) node number of first female flower appearance (-0.0013) .

At phenotypic level, days to last harvest exerted maximum negative direct effect (- 0.0175) on fruit yield per plant. While, it had shown negative indirect effect through fruit yield per hectare (-0.0112) followed by number of fruit per plant (-0.0108), fruit length (-0.0104), plant height (-0.0093) and fruit diameter (-0.0083). It had maximum positive indirect effect on fruit yield per plant viz., days to 50% flowering (0.0070) and fruit pedicel length (0.0025).

4.7.6 Number of fruit per plant

Number of fruits per plant had a positive direct (0.0562) on fruit yield per plant. It showed a maximum positive indirect effect through characters *viz.,* fruit yield per hectare (0.0551) followed by days to last harvest (0.0384), fruit length (0.0187), number of primary branches per plant (0.0161), plant height (0.0167) While, it showed maximum negative indirect effect through node number of first female flower appearance (-0.0182) followed by days to 50% flowering (-0.0084), acidity (-0.0050) at genotypic level.

The number of fruit per plant showed positive direct effect (0.4552) on fruit yield per plant. It exhibited maximum positive indirect effect on fruit yield per plant *viz.,* fruit yield per hectare (0.4453) , days to last harvest (0.2825) , fruit length (0.1509) ,TSS (0.0965) and plant height (0.1351), ascorbic acid (0.0858) ,fruit diameter (0.0715) While, it showed maximum negative indirect effect through node number of first female flower appearance (-0.1454), acidity (-0.0403), days to 50% flowering (-0.0345) at phenotypic level.

4.7.7 Fruit length (cm)

At genotypic level, length of fruit had shown negative direct effect (-0.0403) on fruit yield per plant. The characters exerted maximum positive indirect effect on fruit yield per plant through days to 50% flowering (0.0318), fruit pedicel length (0.0111), TSS (0.0061), acidity (0.0014) While, it had shown negative indirect effect through days to last harvest (-0.0268), plant height (-0.0221), fruit diameter (-0.0211), fruit yield per hectare (-0.0149), number of fruit per plant (-0.0134) and ascorbic acid (-0.0107).

Length of fruit were exhibited negative direct effect (-0.0417) on fruit yield per plant. It had maximum positive indirect effect on fruit yield per plant viz, days to 50% flowering (0.0155), days to last harvest (0.0155) ,fruit pedicel length (0.0072) Whereas, it had shown maximum negative indirect effect through days to 50% flowering (-0.0248) , plant height (-0.0225) and fruit yield per hectare (-0.0153) and fruit diameter (-0.0209) at phenotypic level.

4.7.8 Fruit diameter (cm)

Diameter of fruit had shown negative direct effect (-0.0187) on fruit yield per plant. It had maximum positive indirect effect on fruit yield per plant through days to 50% flowering (0.0210), fruit pedicel length (0.0085) TSS (0.0011) while ,It had maximum negative indirect effect on fruit yield per plant through followed by ascorbic acid (-0.0108), days to last harvest (-0.0100) ,fruit length (-0.0098), plant height (-0.0061) number of fruit per plant (-0.0031) and acidity (-0.0020) and Number of primary branches (-0.0012) at genotypic level.

The diameter of fruit was recorded positive direct effect (0.0511) on fruit yield per plant. The traits ascorbic acid (0.0279) exhibited maximum positive indirect effect on fruit yield per plant followed by fruit length (0.0256), days to last harvest (0.0243), node number of first female flower appearance (0.0163) , plant height (0.0163) fruit yield per hectare (0.0141) , number of fruit per plant (0.0080) While, diameter of fruit had shown maximum negative indirect effect on fruit yield per plant through days to 50% flowering (-0.0277), fruit pedicel length(-0.0149) and total soluble solid (-0.0031) at phenotypic level.

4.7.10 Fruit pedicel length (cm)

The pedicel length of fruit was recorded positive maximum direct effect (0.0660) on fruit yield per plant. It had exerted highest positive indirect effect on fruit yield per plant through the traits days to 50% flowering (0.0434) , Number of primary branches (0.0283) , TSS (0.0262), plant height (0.0086) While, diameter of fruit (-0.0301) had shown maximum negative indirect effect on fruit yield per plant followed by acidity (-0.0242), days to last harvest (-0.0201) fruit length (-0.0182), ascorbic acid (-0.0140) and fruit yield per hectare (-0.0039) at genotypic level.

Fruit pedicel length were exhibited negative direct effect (-0.0146) on fruit yield per plant. It had maximum positive indirect effect on fruit yield per plant via., fruit diameter (0.0043) acidity (0.0037) , fruit length (0.0025), days to last harvest (0.0021) , ascorbic acid (0.0019) Whereas, it had shown maximum negative indirect effect through days to 50% flowering (-0.0046) ,TSS (-0.0045) and number of primary branches (-0.0034) at phenotypic level.

4.7.11Ascorbic acid (mg/100 g)

Ascorbic acid content was recorded positive direct effect (0.0500) on fruit yield per plant. It had exerted highest positive indirect effect on fruit yield per plant through fruit diameter (0.0290) days to last harvest (0.0193), plant height (0.0188) , fruit yield per hectare (0.0109) ,number of branches per plant (0.0136) , fruit length (0.0134), number of branches per plant (0.0136), number of fruit per plant (0.0100), TSS (0.0105) Whereas, it had maximum negative indirect effect on fruit yield per plant days to 50% flowering (-0.0471), fruit pedicel length (-0.0106) and acidity (-0.0066) genotypic level.

At phenotypic level, ascorbic acid content was recorded positive direct effect (-0.0141) on fruit yield per plant. However, it had maximum positive indirect effect on fruit yield through days to 50% flowering (0.0068) , fruit pedicel length (0.0018), acidity (0.0018) While, fruit diameter (-0.0077), node number of first female flower appearance (-0.0048) , plant height (-0.0048), days to last harvest (-0.0042), fruit yield per hectare (-0.0029) and number of fruit per plant (-0.0027) were recorded maximum negative indirect effect on fruit yield per plant .

4.7.12 Total soluble solid (%)

At genotypic level, the total soluble solid content showed positive direct effect (0.0391) on fruit yield per plant. It had maximum positive indirect effect on fruit yield through followed by fruit pedicel length (0.0155), ascorbic acid (0.0105) ,number of primary branches per plant (0.0127) ,number of fruit per plant (0.0088), fruit yield per hectare (0.0084) ,plant height (0.0034),While, It had shown maximum negative indirect effect on fruit yield per plant through acidity (-0.0251), fruit length (-0.0059) and days to last harvest (-0.0019).

At phenotypic level, total soluble solid content had shown positive direct effect (0.0100) on fruit yield per plant. It showed maximum positive indirect effect on fruit yield per plant through fruit pedicel length (0.0031), number of fruit per plant (0.0021), fruit yield per hectare (0.0021) While, acidity (-0.0060) were exerted maximum negative indirect effect on fruit yield per plant followed by fruit length (-0.0014).

4.7.13 Titratable acidity (%)

Titratable acidity was exerted positive direct effect (0.0491) on fruit yield per plant. It had maximum positive indirect effect on fruit yield through days to last harvest (0.0059), fruit diameter (0.0053) Whereas, the maximum negative indirect effect was exerted through followed by and TSS (-0.0316) and fruit pedicel length (-0.0180) at genotypic level.

At phenotypic level, Titratable acidity was recorded positive direct effect (0.0059) on fruit yield per plant. The traits days to last harvest (0.0007) showed positive indirect effect While, total soluble solid (-0.0036) and fruit pedicel length (-0.0015) had exerted highest negative indirect effect on fruit yield per plant.

4.7.14 Fruit yield per hectare (q)

Fruit yield per hectare had shown positive direct effect (0.9298) on fruit yield per plant. It was exerted maximum negative indirect effect through characters *viz.,* days to 50% flowering (-0.2316) , node number of First female flower appearance (-0.1893), acidity (-0.0577) ,fruit pedicel length (-0.0547) ,number of primary branches per plant (0.2977) , plant height (0.2695) Whereas, it had shown maximum positive indirect effect through days to last harvest (0.6576), fruit length (0.3445) followed by number of fruit per plant (0.9115) and ascorbic acid (0.2029) at genotypic level .

At phenotypic level, fruit yield per hectare was exhibited positive direct effect (0.5803) on fruit yield per plant. The traits exhibited maximum positive indirect effect on fruit yield per plant through ,number of fruit per plant (0.5676) ,days to last harvest (0.3728), fruit length (0.2124) ,fruit diameter (0.1597), plant height (0.1677) ,number of primary branches (0.1353), ascorbic acid (0.1176) While, node number of first female flower appearance (-0.117) ,days to 50% flowering (-0.0784) were recorded highest negative indirect effect on fruit yield per plant.

The result showed that in genotypic path coefficient ,the traits node number of First female flower appearance, days to last harvest, number of fruit per plant, fruit pedicel length, ascorbic acid, total soluble solid, acidity, fruit yield per hectare were exhibited positive direct effects on fruit yield where as negative direct effect showed by plant height, number of primary branches per plant, days to 50 per cent flowering, fruit and fruit diameter at genotypic level.

Whereas, in phenotypic path coefficient traits node number of first female flower appearance, number of fruit per plant, days to 50 per cent flowering, fruit diameter, total soluble solid, acidity, fruit yield per hectare were exhibited positive direct effects on fruit yield while, negative direct effect shown by plant height , number of primary branches per plant , days to last harvest , fruit length, fruit pedicel length and ascorbic acid at phenotypic level.

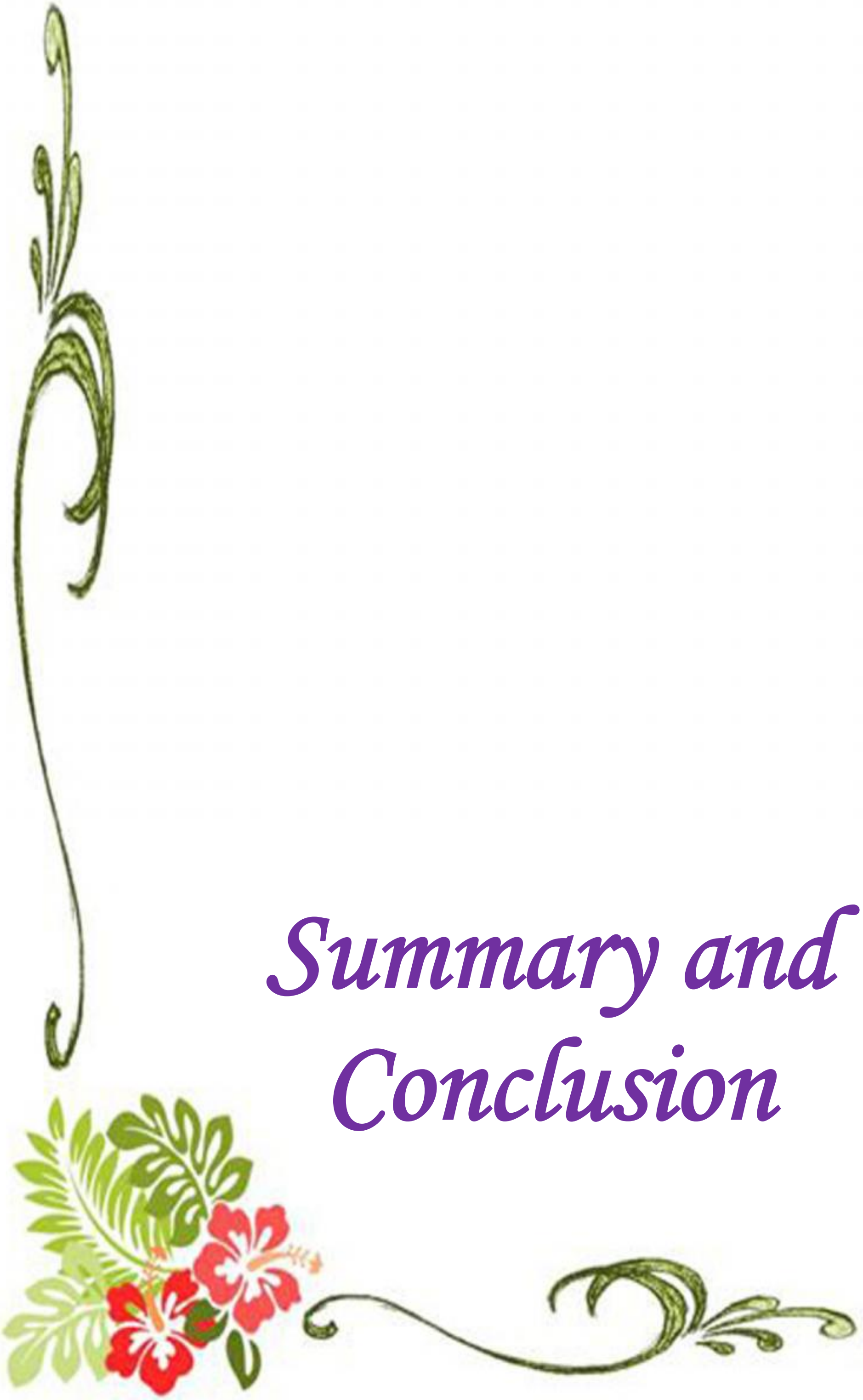
This suggested that, direct selection based on these traits will be rewarding for crop yield improvement. These findings, in general conformity with earlier, Chakraborty *et al.* (2013) found that the maximum direct effect on fruit yield per vine was through traits like number of fruits per vine followed by fruit weight at phenotypic level in bitter gourd and also Sundaram *et al* .(2010) in bitter gourd.

Khule *et al* .(2011) reported in sponge gourd number of fruit per plant, days to appear first female flower, fruit length, fruit diameter, number of seeds per fruit and 100-seed weight had direct positive effects on marketable fruit yield per plant.

Kumar *et al.* (2013) revealed that ,diameter of fruit, number of primary branches, number of fruits per vine, average weight of fruit and total soluble solids showed positive direct effects on total yield per vine.

Similar results were also reported by Pandey *et al.* (2009) in snap melon, Kumar *et al.* (2006) in bottle gourd, Chetariya *et al* .(2018) in bottle gourd , Muralidhara *et al.* (2014) in pumpkin.

Out of fourteen characters studied, path analysis revealed that traits like, days to last harvest ,node number of first female flower appearance , number of fruit per plant, fruit pedicel length, ascorbic acid ,TSS, acidity , fruit yield per hectare was directly contributed to yield.



Summary and Conclusion

CHAPTER -V

SUMMARY AND CONCLUSIONS

The present research work on **"Genetic divergence studies in Spine gourd (*Momordica dioica* Roxb.)** was undertaken to study the nature and magnitude of genetic diversity available in the germplasm, correlation and path analysis studies on component attributes with yield and to screen the genotypes against major problems. The salient findings are summarized below.

In present investigation, twenty spine gourd germplasm lines were grown in a Randomized Block Design with three replications during *kharif* 2018-19 at Horticulture Research Scheme, (Vegetable's) VNMKV, Parbhani. The observations were recorded on twenty characters viz, plant height (cm), number of primary branches per plant, days to first flowering, days to 50% flowering, node number of first female flower appearance, number of fruit per plant, days to first harvest , days to last harvest, fruit length (cm), fruit diameter (cm), fruit pedicel length (cm), fruit color, fruit shape, ascorbic acid (mg/100g), total soluble solid (%), titratable acidity (%), average weight of fruit (g), fruit yield per plant (g), fruit yield per plot (kg), fruit yield per hectare (q). The data was analyzed by following standard statistical techniques.

The considerable variability in genotypes studied for improvement of various traits based on the mean performance it was observed that maximum plant height was recorded in genotype GPR-1 followed by in MOD-12 , Number of primary branches per plant was recorded maximum in genotype MOD-2 and GPR-2. Maximum inter nodal length was observed in genotype MOD-3 followed by in GPR- 4, MOD-10. The genotype MHD-2 showed lower node MDH-2 and higher node position in MOD-7 for appearance of first female flower.

The minimum number of days for first flowering was found in genotype MOD -10 followed by in MOD-7 whereas, minimum days taken to 50 per cent flowering was found in MOD-10 followed by in genotype MDH-3, MOD-7.

The considerable variation was observed with respect to minimum days to first harvest recorded in MOD-10 whereas, maximum number of days to first harvest was recorded in GPR-2.

The highest number of fruits per plant was recorded in genotype MDH -1 followed by in GPR-1 .The maximum fruit length was observed in genotype MOD-15, MDH-4. Maximum fruit diameter was recorded in MOD-11 followed by in MOD-10. Whereas, maximum fruit pedicel length was observed in genotype GPR -1 followed by in GPR -3 .The highest single fruit weight was recorded in MOD -11 followed by in MDH -3 and MDH-1. The highest ascorbic acid content was found in MDH-3. Maximum acidity was recorded in genotype GPR-5 whereas, maximum Total Soluble Solids (TSS) was recorded in MOD 2 and MOD -11. The maximum fruit yield per plant was observed in genotype MDH-1 followed by in GPR-1 and MOD-11.

Genetic diversity was assessed by using Mahalanobis's D^2 statistics for twenty attributes. Grouping of genotypes into clusters using Tocher's method (Rao, 1952) resulted in formation of four clusters. Among four clusters, cluster I had highest number of genotypes GPR 1, GPR 2, GPR 3, GPR 4, GPR 5, MOD1, MOD 2, MOD3, MOD 4, MOD5, MOD 7, MOD 10, MOD 11, MOD12, MOD 13, MOD15 and cluster II had two genotypes MDH 2, MDH 4 and cluster III had only one genotype MDH 1 and cluster IV also had only one genotype MDH 3.

The maximum intra-cluster distance was found in cluster I (84.279), while minimum for cluster II (30.79).

The maximum inter-cluster distance (404.46) was recorded between cluster I and cluster III and minimum inter-cluster distance was recorded (50.54) between cluster II and cluster IV.

Among all characters the maximum (78.94%) fruit yield per plant contributed highest towards divergence followed by characters like titratable acidity (7.36 %), number of fruit per plant (5.52 %), fruit yield per plant (4.21%), node number at first female flower appear (2.63%) and plant height (0.52%) contributed considerably to the total divergence.

The analysis of variance revealed significant difference for twenty attributes studied and reported that ,there was considerable amount of variability exist among the genotypes. Wide range of variability was observed in plant height, number of fruits per plant, average fruit weight, fruit yield per plant, fruit yield per plot and fruit yield per hectare indicated the scope for selection of suitable initial breeding material for further improvement.

Highest phenotypic and genotypic coefficient of variation were recorded for the attributes viz., fruit yield per plant (148.54 P, 148.53G) , fruit yield per hectare (137.52 P,137.48 G), number of fruit per plant (112.32 P , 112.14 G) and average fruit weight (38.19 P, 37.75 G). The moderate values of phenotypic coefficient of variation were observed for plant height (34.58 P , 34.52 G) , number of primary branches (22.08 P, 16.30 G) ,single fruit weight (37.60 P , 37.34 G) ,average fruit weight (38.19 P, 37.75 G).The low values of phenotypic and genotypic coefficient of variation were observed for days to 50% flowering , days to first harvest, days to last fruit harvest, fruit length, fruit diameter, TSS, acidity ,fruit pedicel length. For all the traits PCV was found higher than the GCV which indicate that, the predominance role of environment on the expression of characters.

Heritability estimates for different the attributes were ranged from very high degree to low i.e. from 99.98 to 27.46 per cent. Highest heritability was recorded for fruit yield per plant (99.98), fruit yield per hectare (99.94 %) followed by plant height (99.69 %), number of fruit per plant (99.68%) , number of fruit per plant (99.31%), fruit length (97.79 %), node number at which first female flower appearance (97.79 %) . The high value of heritability for these character expressed that they were influenced by environmental factor. Most of these attribute exhibited high heritability estimates, which has extended the hope for reliability of selection in the present material.

The high value of genetic advance as per cent mean for fruit yield per plant, fruit yield per plot, number of branches per plant, number of fruit per plant, fruit yield per hectare, plant height, node number at which first female flower appearance, fruit length, fruit diameter, ascorbic acid, single fruit weight, acidity and average fruit weight. This reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

From the correlation studies it revealed that, fruit yield per plant exhibited high significant positive association with plant height, number of branches per plant, days to last harvest, number of fruit plant, fruit length, fruit diameter, ascorbic acid ,total soluble solid, fruit yield per hectare at both phenotypic and genotypic level .

In general, genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficient indicated that, the environment have influence on yield and yield contributing attributes of spine gourd. These characters should form selection criterion in breeding programmes.

Path coefficient analysis showed that, the attributes plant height ,days to last harvest, node number of first female flower appearance , number of fruit per plant, fruit pedicel length, ascorbic acid ,TSS, acidity , fruit yield per hectare were exhibited positive direct effects on fruit yield at genotypic level. Whereas, negative effect showed by number of primary branches per plant, days to 50 % flowering, fruit length, fruit diameter.

In present investigation path analysis observed that plant height, days to last harvest, node number of first female flower appearance, number of fruit per plant, fruit pedicel length, ascorbic acid, TSS, acidity, fruit yield per hectare were the important yield component which might be suggested that, selection of genotypes based on these characters as selection criteria would be helpful in improving yield potential of genotypes.

Conclusions

From the present investigation it may be concluded that, a rich diversity exists among the genotypes collected from different regions of Maharashtra in spine gourd for fruit yield and yield related traits.

1. On the basis of mean performance of the genotypes among the different traits studied, genotypes MDH-1, GPR-1, GPR-5, MOD-11, MOD-15, MDH-4, MDH-3, MOD -10, MOD-13 were identified as promising lines.
2. Considering the magnitude of genetic distance, direct and indirect effect of traits on yield, intra and inter-cluster distances, magnitude of cluster means for different characters and contribution of characters towards the total divergence, the genotypes GPR-1, MDH-1, MDH-2 were identified as genetically divergent for plant height and hence, these genotypes can be utilized in crop improvement programme as donor parents for improving plant height. The genotype MDH-2, MDH-3, MDH-4 were observed more divergent for improving number of primary branches per plant. The genotype MDH-3 which found to be a promising line for minimum number of days to 50 % flowering .
3. The genotype MDH-1, GPR-1, MOD -11 can be used for improving number of fruit per cluster whereas, days to last harvest highest in genotypes MDH -1, MDH-3 and lowest in MDH-2, fruit length was maximum in the genotypes of MDH-2, MDH-4, maximum diameter of fruit and fruit pedicel length was observed in the genotype MDH-3 and MDH-2. Highest average fruit weight was recorded in MOD -10 while highest ascorbic acid content was found in MDH-3. Highest fruit yield per plant were highest in MDH-1, GPR-1 whereas, highest fruit yield per plot and fruit yield per hectare was observed in MDH-1.
4. From the correlation studies, it revealed that, fruit yield per plant exhibited high significant positive association with plant height, number of primary branches per plant, days to last harvest, number of fruit plant, fruit length, fruit diameter, ascorbic acid, TSS and fruit yield per hectare at both phenotypic and genotypic level.
5. Path coefficient analysis showed that the attributes like node number of first female flower appearance, number of fruit per plant, ascorbic acid, total soluble solid, acidity, fruit yield per hectare were exhibited positive direct effects on fruit yield at

genotypic as well as phenotypic level except fruit pedicel length, ascorbic acid, days to last harvest at genotypic level while days to 50% flowering, fruit diameter at phenotypic level. This suggested that, direct selection based on these traits will be rewarding for crop yield improvement.

6. Considering all the qualitative and quantitative traits among the twenty genotypes as MDH-1, GPR-1, GPR-5 , MOD 10, MOD-11 MOD-13, MOD-15, MDH- 3, MDH-4 were selected and suggested to be selfed for the development of inbred line for use in future breeding programme.

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Appendix

APPENDIX-I

WEEKLY WEATHER DATA 2018-19

WK No.	**Period**	**Rainfall (mm)**	**Temperature ^{O}C**		**Humidity (%)**		**EVP (mm)**	**BSS (Hrs.)**	**W.V. (kmph^{-1})**
			Max.	**Min.**	**Max.**	**Min.**			
23	04-10 June 18	112.8	33.1	21.7	89	59	4.8	4.2	5.9
24	11-17 June 18	53.2	36.1	23.8	78	41	9.0	8.1	8.1
25	18-24 June 18	112.5	34.0	22.8	84	57	5.6	6.6	5.2
26	25-01 July 18	26.3	31.8	22.3	84	57	4.5	4.4	4.4
27	02-08 July 18	48.3	31.8	22.4	87	64	4.0	4.4	5.2
28	09-15 July 18	39.9	28.9	21.9	92	80	2.4	0.3	5.0
29	16-22 July 18	103.4	29.6	21.8	88	76	2.8	2.2	5.4
30	23-29 July 18	2.2	29.9	21.9	83	65	3.1	1.5	4.9
31	30-05 Aug 18	0.0	32.8	21.7	79	50	5.3	6.7	5.3
32	06-12 Aug 18	7.2	30.5	22.0	84	68	4.9	2.1	6.3
33	13-19 Aug 18	148.4	28.3	21.5	90	75	3.2	0.8	5.5
34	20-26 Aug 18	110.2	28.7	20.5	91	73	3.1	4.8	5.8
35	27-02 Sept 18	8.8	29.7	20.8	84	61	3.6	4.9	4.8
36	03-09 Sept 18	2.4	30.9	20.2	83	54	5.1	7.6	5.4
37	10-16 Sept 18	0.0	33.0	20.7	83	49	5.9	9.1	2.9
38	17-23 Sept 18	1.8	32.4	21.2	83	56	4.6	3.5	4.5
39	24-30 Sept 18	4.0	34.6	20.8	82	41	5.7	8.2	3.2
40	01-07 Oct 18	0.0	34.9	20.0	78	40	6.2	9.0	3.4
41	08-14 Oct 18	0.0	35.5	16.3	72	20	6.6	8.7	4.3
42	15-21 Oct 18	0.0	34.5	16.5	75	27	6.2	8.8	3.2
43	22-28 Oct 18	0.0	34.7	16.2	72	26	5.7	8.7	2.8
44	29-04 Nov 18	0.0	32.9	14.8	73	30	5.9	9.7	4.8
45	05-11 Nov 18	0.0	33.9	16.3	71	33	5.5	8.4	2.8
46	12-18 Nov 18	0.0	33.3	11.4	75	23	4.9	9.5	2.9
47	19-25 Nov 18	0.0	32.2	16.3	77	35	4.5	7.5	3.6
	Total Rainfall	615.4							

VITAE

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