CHARACTERIZATION AND DIVERSITY ANALYSIS OF RIDGE GOURD (*Luffa acutangula*) GERMPLASMS

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CHARACTERIZATION AND DIVERSITY ANALYSIS OF RIDGE GOURD (*Luffa acutangula*) GERMPLASMS

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This is to certify that thesis entitled, **“Characterization and diversity analysis of ridge gourd germplasms”** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the results of a piece of bona fide research work carried out by **Zannatul Anika**, Registration No. **19-10247** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: December, 2021 **(Prof. Dr. Md. Shahidur Rashid Bhuiyan)**

Place: Dhaka, Bangladesh Supervisor

Dedicated
To
My Honorable Teachers
&
Beloved Parents
Whose Blessings Always
With Me

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SAU, Dhaka **The Author**

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ABSTRACT

An experiment was carried out at Sher-e-Bangla Agricultural University in kharif season with thirty ridge gourd germplasms to study the diversity among the germplasms. The germplasms were examined for seventeen yield and yield contributing characters. Significant variation was observed among all the germplasms for all the characters studied. High heritability along with high genetic advance in percentage of mean were observed for fruit yield per plant, fruit weight and no. of fruits per plant. High heritability along with moderate genetic advance in percentage of mean were observed for seed breadth and hundred seed weight. High heritability along with low genetic advance in percentage of mean were observed for days to male flower appearance. Highly significant positive correlation of yield per plant were observed with internode length (r_g=0.44, r_p=0.43), fruit length (r_g=0.33, r_p=0.32), fruit weight (r_g=0.55, r_p=0.53), no. of fruits per plant (r_g=0.83, r_p=0.81) at both genotypic and phenotypic level. Path analysis indicated that, yield per plant had positive and direct effect through days to emergence, days to male flower appearance, internode length, leaf length, petiole length, fruit breadth, seed length and hundred seed weight. The germplasms were grouped into five clusters. Cluster IV was the largest and containing fourteen germplasms followed by cluster III and V with five germplasms and cluster I and II with only three germplasms. Cluster I showed maximum performance for fruit yield per plant (2.28 kg) and fruit weight (2.06 g). Cluster II showed maximum performance for days to emergence (0.42). Cluster III recorded highest mean performance for peduncle length (1.44 cm), fruit breadth (1.41 cm), days to emergence (1.28) and petiole length (1.10 cm). Cluster IV showed maximum performance for leaf breadth (0.38 cm) followed by seed length (0.32cm) and hundred seed weight (0.32 g). Cluster V showed maximum performance for leaf length (1.33 cm) and no. of fruits per plant (1.05). Considering the degree of variability, heritability, genetic advance in percent of mean, correlation with fruit yield, path analysis, magnitude of distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and performance, the germplasms G4, G5, and G24 for yield per plant from cluster I; G1 and G19 for fruit length from cluster III might be considered better parents for efficient hybridization program.

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Some commonly used abbreviations

Full Word	**Abbreviation**
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
and others (at elli)	*et al.*
At the rate	@
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	cm
Degree Celsius (Centigrade)	^{0}C
Coefficient of variation	CV
Days after sowing	DAS
Degree of freedom	df
Environmental variance	σ_e^2
Et cetera	etc
Food and Agricultural Organization	FAO
Financial Year	FY
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genotypic correlation	r_g
Genotypic variance	σ_g^2
Gram	g
Heritability in broad sense	h^2b
Kilogram	kg
Meter	m
Milliliter	ml
Mean sum of square	MS
Market Year	MY

Full Word	**Abbreviation**
Metric ton	MT
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of coefficient of variation	CV%
Phenotypic variance	σ_p^2
Phenotypic coefficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	*sp.*
Square meter	m^2
Standard error	SE
Triple Super Phosphate	TSP
Variety	Var.
United States Department of Agriculture	USDA
Zinc Oxide	ZnO

CHAPTER I

INTRODUCTION

Ridge gourd (*Luffa acutangula*) is a noteworthy vegetable, an important member of the family Cucurbitaceae which is accessible throughout the summer season of Bangladesh and having the chromosome number 2n = 26. Ridge gourd is an annual, climbing herb, unisexual and monoecious crop. The name "Luffa" or "Loofah" is of Arabic origin and refers to the spongy characteristics mature fruit. It is also known as ribbed gourd. Its origin is not definitely known, although wild forms of this crop are found in India, the Sunda Island and Java (Yawalkar, 1985). Now it is cultivated in Bangladesh, China and many regions of India such as Assam, West Bengal, Uttar Pradesh etc. It is a fast-growing vine that often requires some support to facilitate its spread. At the same time, there is an inadequacy of vegetables. It is dark green in color and has a tapering end to it. It is a climbing annual grown primarily for its immature fruits which are eaten raw, pickled or cooked commonly used in soups and curries (Tindall, 1987). The pulp of this vegetable is white in color and consumed after peeling off the skin.

The luffaculin, a protein isolated from ridge gourd seed, exhibited abortifacient, antitumor, ribosome inactivating and immunomodulatory activities (Ng *et al*., 1992). The seeds are a good source of iron, magnesium and phosphorous and contain high amounts of essential amino acids such as lysine (Kamel and Blackman, 1982). The pure seed oil is tasteless and contains 68% of glycerides of oleic and linoleic acids, thus providing a good substitute for other vegetable oils such as from olive, safflower, and rape seed (Kamel and Blackman, 1982; Martin, 1979; Girgis and Said, 1968). It is rich in vitamin C and iron (Fe) content (Yawalkar, 1985). It has considerable curative value. It also has a reasonable medicinal importance (Bora *et al*., 2015) such as Vit-C for keeping away colds, Vit-B for good mood and vitality, zinc for strengthening our immune system, iron for anemia, manganese and magnesium for enzyme production and immunity and calcium and phosphorus for strong bones. Currently, this crop has been tested for its antioxidant (free radical scavenging-FRS) activity confirming the great interest of the nutraceutical sciences (Ansari *et al*., 2005). As fresh ridge gourd contains folates, in the expectant mothers, this folate-rich food may help in reducing the incidences of neural tube defects in the newborns. Its high fiber content assists with healthy digestion and proper functioning of the excretory system. The charantin and peptide which are present in this vegetable have insulin regulatory properties and thus helps in lowering blood sugar levels as well as urine sugar levels. So far, 106 local landraces of *L. acutangula* have been reported in Bangladesh (Rabbani, 2007). However, the area and production of ridge gourd is 9766.39 ha and 47335 metric tons, respectively (BBS, 2016) in Bangladesh. The average yield of the crop in Bangladesh is about 1.83 MT per acre in 2007-2008 (BBS, 2008) indicating low yield performances of the cultivars. Several factors are accountable for such a low yield. Among many reasons, the lack of high yielding variety is one of the most important reasons for low yield of this crop in Bangladesh. For most of the improved cultivars, variety uniformity is one of the main requirements. On the other hand, variability is a desirable goal in germplasm collection, since the material observed in such collection can be used for breeding and developing new varieties in near future. In crop improvement programme, genetic diversity is one of the most important tools to quantify genetic variability in both cross and self-pollinated crops (Gaur *et al.,* 1978).

Yield is complex character and various morphological and physiological characters contribute to yield. It is essential to have knowledge on variability of different characters for the yield improvement. The available variability in a population can be partitioned into heritable and non-heritable parts with the aid of genetic parameters such as genetic coefficient of variation, heritability and genetic advance. The variability of a biological population is an outcome of genetic constitution of individuals making up that population in relation to prevailing environment. It arises either due to geographical separation or due to genetic barriers to cross ability. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme. Varietal uniformity is one of the foremost necessities for the improved cultivars. Variability, on the other hand, is tremendously preferred in germplasm collection and conservation purposes as genetic variation may exist or created, is the first step to any crop improvement programme (Singh, 2000). The knowledge of genetic diversity is necessary to identify the diverse genotypes for breeding purpose. Characterization like disease resistance, earliness, quality or even performance of a particular character should also be considered in case of genetic divergence (Belaj *et al.,* 2002 and Chowdhury *et al.,* 1975). Because genetic diversity provides information about the relationship among elite breeding population and helps in selecting desirable parents for establishing new breeding population. But this genetic diversity within a population depends on the number and frequency of all loci and the genetic constitution of the population (Crossa *et al.,* 1993). Now the quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents (Jain *et al.,* 1975). It is also essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield and wider adaptation, desirable quality, pest and diseases resistance (Joshi and Dhawan, 1966). Knowledge of genetic diversity among existing cultivars of any crop is essential for long-term success in breeding program and to maximize the exploitation of the germplasm resources (Belaj *et al*., 2002).

Under such circumstances, this study was conducted to assess the variability among the 30 genotypes of ridge gourd collected from BARI, Joydebpur, Gazipur for yield and yield contributing characters, their interrelationship and genetic diversity through biometrical procedures. Hence, the present study has been designed to study the genetic diversity, to identify useful traits and predict their potentiality for utilization and conservation. Information on genetic divergence among the plant material is vital to a plant breeder for efficient choice of parents for hybridization (Methela *et al.,* 2019). There is tremendous genetic diversity within the family, and the range of adaptation for Luffa species includes tropical and subtropical regions, arid deserts, and temperate regions. There are eight species originated in Indian Sub-continent of which only two *L. acutangula* and *L. cylindrica* (Sponge gourd) are important vegetable crops while others are wild type. More diverse the parents greater are the chances of obtaining high heterotic F_1 and broad spectrum of heritability in segregating generations (Murty and Arunachalam, 1966). Precise information on the extent of genetic diversity among population is crucial in any crop improvement program, as selection of plants based on genetic diversity has become successful in several crops (Manoj *et al.*,2018; Ananda and Rawat, 1984) The parent's identified on the basis of divergence analysis would be more promising. Cluster analysis and principal component analysis (PCA) are the important genetic diversity measuring tools employed for exhibiting relative genetic differences among the genotype collection of various crop species. Thus, this information may promote to design efficient breeding programme for the development of new varieties of ridge gourd in

Bangladesh. Under such circumstances, the present study was conducted with the following objectives:

I. To characterize collected ridge gourd germplasms morphologically
II. To assess variability, heritability and genetic advance and predict gene action
III. To assess interrelationship among yield and yield contributing characters
IV. To study genetic diversity among the germplasms in respect of different yield contributing characters
V. To identify useful traits with potential germplasm for utilization in future breeding program

CHAPTER II

REVIEW OF LITERATURE

Ridge gourd is one of the important warm season vegetables grown all over the country of Bangladesh. Its tender fruits are popular and well known for culinary vegetable with good nutritive value. Very few research reports are available on the improvement of this crop that has been done in various part of the world including Bangladesh. The work so far been done in Bangladesh is not adequate and conclusive. Research effort on genetic variability, character association and path co-efficient analysis seems to be also inadequate and not conclusive. However, some of the important and informative works conducted at home and abroad in this aspect are reviewed below:

2.1 Variability and heritability of ridge gourd germplasms

Genetic variability studies in ridge gourd (*L. acutangula*) were undertaken by Gowda (2011) during the year 2010-2011 at Department of Vegetable Science, Karnataka, India. Totally 30 ridge gourd genotypes were evaluated and significant differences were observed among genotypes for all the characters studied.

Eleven pointed gourd (*T. dioica*) selections were assessed by Dora *et al.*, 2003 to estimate genetic variability and correlation for yield and its attributes. High genetic coefficient of variation (GCV) estimate was observed for the characters such as node at which first female flower appeared, length of vine, number of nodes per plant and number of fruits per plant. The heritability estimate was high for all the characters. The character having high GCV also exhibited high genetic advance.

Apu *et al*. **(**2013**)** conducted an experiment and reported that, the highest weight of individual fruit (137.55 g) was obtained in LA-211 and the lowest weight (73.55 g) in LA-208. The highest fruit yield (22.41 t/ha) was found in LA-211 and the lowest yield (8.04 t/ha) in LA-210. For 10 traits phenotypic variation was higher than the genotypic variance with moderate to high heritability and moderate genetic advance and in percentage of mean. Positive significant association was observed for fruit yield per ha in respect of individual fruit weight (0.526), number of fruits per plant (0.711), fruit yield per plant (0.968) and fruit yield per hectare (1.00).

Genetic variability studies were undertaken by Gowda (2011) with 30 ridge gourd genotypes and reported that significant differences were observed among genotypes for all the characters studied. PCV was higher than GCV for all the characters studied. High PCV and GCV were observed for the characters, viz. vine length and number of leaves at 90 DAS, node to first female flower, sex ratio, fruit yield per plant, fruit yield per plot, fruit yield per hectare, average fruit weight, fruit length, number of seeds per fruit and seed yield per fruit indicates maximum variability and offers good scope for improvement by simple selection. High heritability coupled with high genetic advance over per cent of mean was observed for the character vine length and number of leaves at 90 DAS, node to first female flower, sex ratio, fruit yield per plant, fruit yield per plot, fruit yield per hectare, average fruit weight, fruit length, number of seeds per fruit and seed yield per fruit indicates these characters were governed by additive gene action and offers good scope for improvement by simple selection through these characters.

Fifteen diverse genotypes of ridge gourd were evaluated by Devmore *et al.* (2010) in Dapoli, Maharashtra, India, for their variability, heritability and genetic advance for 15 traits: days to first male flower, nodal position for first male flower, days to first female flower, nodal position for first female flower, vine length, primary branches per vine, node number per vine, days to fruit development, days to first fruit harvest, fruit number per vine, fruit length, fruit breadth, fruit weight, 100-seed weight and fruit yield per vine.

Guffar (2008) was conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. Among the characters the highest GCV recorded for yield per plant (63.90) followed by top fruit perimeter (46.60) and average fruit weight (39.52).

Genetic variability, heritability (h^2), genetic advance studies were carried out by Choudhary *et al.* (2008) in 22 accession of ridge gourd (*L. acutangula*) during rainy season. Highly significant differences between genotypes were recorded for all the characters. Maximum range of mean values was observed 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 which in female flower appears and fruits per plant. High estimates of heritability in broad sense were obtained for fruit weight and fruit length suggesting hereby both these traits are governed by additive gene action.

A field experiment was conducted by Kumar *et al.,* (2007) during summer in Varanasi, Uttar Pradesh, India, with twenty diverse genotypes (VRBG-1, VRBG2, VRBG-8, VRBG-14, VRBG-18, VRBG-33, VRBG-36, VRBG-37, VRBG-40, VRBG-44, VRBG-48, VRBG-101, VRBG-110, NDBG-56, Pusa-Naveen, Pusa Summer Prolific Long (PSPL), PBOG-61, IC-42345, DVBG-2 and NDBG-58) of ridge gourd. Observations were recorded on 14 characters, i.e. days to 50% germination, days to first male and female flower anthesis, number of branches per vine, vine length, node number of the first male and female flower, days to first fruit harvest, length of edible fruits, number of fruits per vine, individual edible fruit weight, number of seeds per fruit, hundred seed weight and fruit yield per 42 vine. Among all the genotypes, 'VRBG-110', 'NDBG-56', 'VRBG-44', 'PBOG61', 'Pusa Naveen' and 'VRBG-40' gave promising results.

Ram *et al.,* (2006) were evaluated twenty-four accessions of *L. hermaphrodita* in randomized complete block design for 12 economic characters to study genetic variability of traits and contribution towards yield and its association with each other. The analysis of variance revealed considerable genetic variability among the accessions for aggregate effect of all the characters. Of the 24 genotypes. SP-59 recorded highest edible fruit yield/hectare (107.9 q) while DR/Y-1 expressed earliness with respect to days to first hermaphrodite flower anthesis (40.6) and maximum mean value for number of fruits per plant (185.3). High heritability for number of seeds per fruit, seed weight and edible fruit yield per hactare suggests that characters phenotypic value could provide fair and reliable measure of good genotype. High heritability and high genetic advance for number of seeds per fruit and edible fruit yield per hectare indicated the presence of high amount of fixable variation among genotypes for these traits, which provides ample scope for varietal improvement through hybridization and selection in *L. hermaphrodita*.

Five promising F_1 hybrids of ridge gourd involving 7 parents (LA-46, LA-99, LA12, LA-76, LA-32, LA-37 and LA-17), along with 2 commercial hybrids (Surekha and NS-3), were evaluated by Gautham et al. (2004), at Hyderabad, Andhra Pradesh, India. Data were recorded for days to 50% female flowering, node number at which first female flower appeared, number of fruits per vine, fruit weight, length and girth, and yield per vine. Pooled data of 2 years revealed that LA-46 × LA-99 was the earliest to flower. Desirable fruit length and girth were observed in LA-12 × LA-37, LA-12 × LA-17 and LA-12 × LA-76. The highest fruit yield was recorded in LA-12 ×

LA-37 (1.76 kg/vine), which was at par with LA-12 × LA-76 (1.63 kg/vine). These hybrids recorded 32.5 and 19.5% higher fruit yield over the superior control hybrid NS-3. High estimates of heritability were recorded for fruit length and girth, number of fruits per vine and yield per vine, indicating the possibility of improving these characters through selection.

Zaman *et al.* (2004) reported the performance of three sponge gourd lines at the farm of' Olericulture Division. HRC and in different RARS, BARI during the summer season of 2004. The line Sg 6-3-2-2-10-10 and Sg 6-3-1-2-1-6 produced the highest number of fruits per plant (34) and lower was recorded in Local (26). Maximum individual fruit weight was obtained from Local (189 g). The line Sg 6-3-2-2-10-10 gave the highest yield (20.0 t/ha) closely followed by Sg 6-3-1-2-1-6 (19.4 t/ha).

Hedau and Sirohi (2004) conducted an experiment with 10 ridge gourd cultivars and reported that the narrow-sense heritability was less than 0.5 for number of fruits per plant and fruit yield per plant, indicating the predominance of dominance gene action. Partial dominance and high narrow-sense heritability were recorded for fruit length and weight.

Shinde *et al.* (2003) evaluated fruit characteristics of 18 strains and 2 cultivars of *L. acutangula* during summer in India. The lowest number of days to fruit set was recorded in DPL-RG-12 (36.99), l) DPL-RG-4 (40.33) Punjab Sadabahar (40.66) and DPL-RG-2 (41.00). The average fruit number per vine (15.55) was recorded in DPL-RG-12, whereas Punjab Sadabahar recorded the highest average fruit length (28.73 cm) and fruit weight (115.33 g). The superior lines in terms of fruit yield and quality were DPI-RG-12, DPL-RG-2 and Punjab Sadabahar.

A field experiment was conducted by Shinde *et al.* (2003) during 1995 at the Department of Horticulture, Marathwada Agricultural University, Parbhani (Maharashtra, India) studied the growth and yield attributes of 20 ridge gourd (*L. acutangula*) genotypes. Tabulated data showed that genotype Punjab Sadabahar recorded significantly highest vine length of 4.80 m. The internodal length (14.57 cm) recorded by ‘DPL-RG-17’ was the highest and significantly more that the remaining 19 treatments. Punjab Sadabahar produced the highest number of leaves per vine (36.55) while DPL-RG-12 recorded the highest number of branches per vine. Punjab Sadabahar produced the highest number of male flowers (59.07) while DPL-RG-12 had the highest number of female flowers (17.33). The lowest sex ratio (male:female) of 2.04 was recorded for DPL-RG-12. The variety Punjab Sadabahar recorded the highest yield with 1.76 kg/vine and 117.33 q/ha.

An experiment was conducted by Singh *et al.* (2002) on 80 ridge gourd genotypes to determine the genetic variability and heritability. High phenotypic coefficient of variation (pcv) and genetic coefficient of variation (gcv) were observed for node number for appearance of first male flower, male flowers per plant, sex ratio on whole plant, main axis and branches, fruits per plant, fruit weight, seeds per fruit and yield per plant. The gcv and pcv values were almost equal for most of the characters studied. The broad sense heritability estimates were high for all the characters. High heritability with high genetic advance was observed for number of nodes for appearance of first male and female flower, length of main axis, number of primary branches, male and female flowers per plant, sex ratio on the whole plant, main axis and branches, fruits per plant, fruit set, fruit length, fruit weight, seeds per fruit, 100-seed weight and yield per plant. Genetic variation, heritability and genetic advance for yield and yield components were studied by Chowdhury and Sharma (2002) in 12 *L. acutangula* cultivars (AAUJ-1, AAUJ-2, AAUJ-3, Mangaldoi, Tezpeu, Tihu, Mirza Short, Rangamati Long, Borpeta Long, Tiniali Long, Pusa Nazder, and HRS C-2) grown in Gwuahati, Assam, India. The genetic coefficient of variation (GCV) was higher than the phenotypic coefficient of variation (PCV) for all characters. High values of heritability, PCV, GCV, and genetic advance were recorded for vine length, yield per hectare, and fruit weight, indicating that these traits were characterized by additive gene effect. A field experiment was conducted by Jawadagi *et al.* (2002) in Gangavati, Dharwad, Karnataka, India, to evaluate ten *L. acutangula* cultivars for resistance to natural salinity gradient of 4, 6, 8, and 10 ds/m. Yield reduction increased with the increase in soil salinity. Among the cultivars, Kotiyal local had the highest yield under a soil salinity gradient of up to 8 ds/m.

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was observed for all the characters at phenotypic as well as genotypic level with a very wide range of values.

2.2 Characters associations

The character association studies by Gowda (2011) revealed that the fruit yield per plant highly significant and positively associated with vine length, number of branches at 90 days after sowing, number of leaves at 45 and 90 DAS, days to last harvest, sex ratio, per cent fruit set, number of fruits per plant, fruit yield per plot, fruit yield per hectare, fruit length, fruit diameter, rind thickness, flesh thickness, number of seeds per fruit, seed yield per fruit, 100 seed weight. Since, these association of characters are in the desirable direction, selection for these traits will improve the yield per plant. The correlation between the yield and yield components of ridge gourd (*L. acutangula*) was studied by Prasanna *et al.*, (2002) in Bangalore, Karnataka, India, during the rabi. Fruit yield per hectare was positively associated with vine length at 90 days after sowing (DAS), number of leaves at 90 DAS, number of female flowers, total dry weight of plant, number of fruits, and fruit girth and weight. Correlation coefficient analysis of yield components was conducted by Shah and Kale (2002) on 55 genotypes (10 parents and 45 hybrids) of ridge gourd (*L. acutangula*). The fruit weight per vine was positively and significantly correlated with the fruit number per vine, average fruit weight, number of female flowers per vine and vine length, indicating the close association and dependency of yield on these characters. The fruit length was negatively correlated with fruit diameter and fruit number per vine, while it was positively correlated with the average fruit weight. Significant correlations were found in the following characters: fruit number per vine with number of female flowers per vine; branch number with vine length, internode length and number of male flowers per vine; internodal length with average fruit weight. It is concluded that fruit number per vine, number of female flowers per vine, vine length and average fruit weight could be considered while selecting for high yielding ridge gourd genotypes. Correlation for yield and yield components were studied by Chowdhury and Sharma (2002) with 12 *L. acutangula* cultivars (AAUJ-1, AAUJ-2, AAUJ-3, Mangaldoi, Tezpeu, Tihu, Mirza Short, Rangamati Long, Borpeta Long, Tiniali Long, Pusa Nazder, and HRS C-2) in Gwuahati, Assam, India. The correlation coefficients revealed that yield per hectare can be improved through selection for greater fruit number per plant, fruit length and girth, and individual fruit weight. Correlation and path coefficient analysis were conducted by Rao *et al.,* (2000) in the segregating population of ridge gourd. The magnitude of genotypic correlation coefficient was higher than the phenotypic coefficients indicating strong inherent association among the various characters studied. Yield per vine exhibited significant positive correlation with volume of fruit, fruits per vine, fruits per branch and length of the vine at both phenotypic and genotypic levels while girth and weight of fruit at genotypic level only. Days to first male and female flower and days to 50% flowering exhibited significant negative correlation with yield.

Correlation and path-coefficient analyses were conducted by Rao *et al.*, (1999) in 36 genotypes of ridge gourd. The majority of genotypic correlation coefficients were higher than phenotypic correlation coefficients, indicating a strong inherent association among various characters studied. Yield per vine was significantly and positively correlated with number of fruits per vine, fruits per branch, girth, weight and volume of the fruit, but was negatively correlated with days to first female flower.

Singh and Ram (2003) conducted an experiment on 28 musk melon genotypes to determine the correlation among fruit characters. The simple correlation among fruit traits showed that polar diameter, latitudinal diameter, flesh thickness and seed cavity size were positively correlated with fruit weight.

Shah and Kale (2002) conducted an experiment on correlation coefficient analysis of yield components of 55 genotypes of ridge gourd. The fruit weight per vine was positively and significantly correlated with number of fruits per vine, average fruit weight, number of female flower per vine and vine length, indicating the close association and dependency of yield on these characters. The fruit length was negatively correlated with fruit diameter and fruit number per vine, while it was positively correlated with average fruit weight.

Singh *et al.* (2002) were carried out an experiment on 98 hybrids of cucumber derived from crosses involving 14 male and 7 female parents and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation coefficient was higher than phenotypic co-efficient which indicated strong association among these traits. Path coefficient analysis also indicated that fruit weight had the highest direct effect on fruit yield.

Badade *et al.* (2001) conducted an experiment to study the correlation of 20 bottle gourd (*Lagenaria vuIgaris*) genotypes. Yield was found significantly and positively correlated with number of branch per vine, number of fruits per vine and significantly and negatively correlated with clays to first male and female flower appearance and weight of deformed fruits per vine at both phenotypic and genotypic levels. Fruit length showed positive but non-significant correlation with fruit yield.

Miah *et al.* (2000) noted that fruit yield in bitter gourd showed significant positive association with average fruit weight, fruit breadth and number of nodes per vine in genotypic and phenotypic correlation with days to male flowering. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield.

Sarker *et al.* (1999) studied correlation and path coefficient of 16 divergence types of pointed gourd indicated that fruit weight, fruit diameter and number of primary branches per plant were positively and significantly correlated with yield per plant at genotypic and phenotypic levels. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield.

Li *et al.* (1997) noted that number of fruits per plant, average fruit per plant, average fruit weight, fruiting rate and leaf area of cucumber genotypes were positively correlated to yield. Days to flowering and vine Length were negatively correlated. From path analysis, they also concluded that fruits per plant and average fruit weight affected the yield directly.

Ananthan and Pappoah (1997) reported that fruit number per vine and seed number per fruit were positively correlated with total yield while days to first female flowering, days to first male flowering, sex ratio, fruit girth, pulp thickness and total soluble solids content were negatively correlated with total yield in cucumber.

Rajput *et al*. (1991) also found significant positive correlation between number of fruit and yield and number of branches with yield. Harvest period also influenced the yield and its degree of association with increasing vine length. Characters association were studied by Abusaleha and Dutta (1990) in cucumber. They found positive and significant correlation between yield and nodal position of first female flower (r= 0.225) in cucumber.

2.3 Partitioning contribution of various character on yield

Rao *et al.* (2000) conducted an experiment on the segregating population of ridge gourd for and performed path coefficient analysis. Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth of fruit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd.

Path co-efficient analysis revealed that number of fruits per plant and average fruit weight had high direct effect on fruit yield per plant. The genotypes Arka Sumeet, Arka Sujat and Jaipur Long were superior genotypes for fruit size, quality and yield parameters. Selection of superior genotypes involves crossing and making selection in segregating generations. Character association and path analysis were carried out by Choudhary *et al.*, (2008) in 22 accession of ridge gourd (*Luffa acutangula*) during rainy season. Positive and significant association of yield per plant was observed with fruit length and fruit weight at both genotypic and phenotypic level indicating that selection based on these characters either in combination or alone will help to identify the genotypes having high yield potential. The average fruit weight, fruits per plant and days taken to initiation of female flower had maximum direct effect on yield followed by number of primary branches per plant. Therefore, fruit weight, fruits per plant, days taken to initiation of in female flower and number of primary branches per plant should be considered as selection criteria for yield improvement in ridge gourd breeding.

Path coefficient analysis showed that vine length at 90 DAS, number of female flowers per vine, number of branches per vine, number of fruits per vine, fruit girth, and fruit weight had direct positive effects on fruit yield, whereas the number of leaves at 90 DAS, total dry weight of the plant, and fruit length had negative direct effects on fruit yield. The fruit yield of ridge gourd can be enhanced through the improvement of vine length at 90 DAS, number of female 51 flowers, number of branches, number of fruits per vine, fruit girth, and fruit weight.

Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth of fruit, fruits per vine, fruits per branch and length of the vine in ridge gourd.

Path coefficient analysis confirmed that number of fruits per vine, weight of the fruit and days to first female flower were the major yield components having high direct effect on yield per vine. The above cited review revealed that the importance of a systematic research on ridge gourd genotypes in genetic diversity, correlation among yield contributing characters, path co-efficients patents and gene actions of governing characters for improvement of the crop.

2.4 Diversity among ridge gourd germplasms

Quamruzzaman *et al.* (2008) were conducted an experiment on the genetic divergence among thirty genotypes of ridge gourd *(L. acutangula*) at the farm of Olericulture Division, HRC and in different RARS, BARI during the summer season of 2005. The genotype RGN05, RGN06, RGN07, RGN08, RGN13, RGN17, RGN18, RGN27, RGN29 recorded for highest cluster mean values for days to first male flower open (56.0 days), single fruit weight (141.0g) and RGN03, RGN12 lowest mean values for days to first female flower open (27 days), single fruit weight (85.0 g). The highest fruit length (23 cm), fruit number per plant (26) and yield per plant (9.7 kg) obtained from RGN16 and RGN20. The role of days to 1st male flower open, days to first female flower open, fruit diameter, single fruit weight and fruit number in PCA indicates their importance in genetic divergence.

According to the experiment by Guffar (2008), Genotypes included in cluster I were suitable for yield per plant (6.55), cluster III for having the highest mean value for internode length (17.62). Cluster V for Leaf length (30.43), leaf breadth (24.65), petiole length (13.28), days to first male flower (103.28), days to first female flower (107.80) and other characters.

According to the experiment by Jawadagi *et al.* (2002), The cultivars were grouped based on genetic diversity under various salinity levels. The high-yielding cultivars Kotiyal local, Malapur-2, and Japanese Long were grouped under the first category. The 47 second category was marked by lower maximum yield but lower yield reduction (Ittnalli local-1, Poona local, and Pusa Nasdar). Ittnalli local-2, Jumnal local, Raichur local-2, and Deodurga local, grouped under the third category, were characterized by lower yield potential and high yield reduction.

CHAPTER III

MATERIALS AND METHODS

The present research work was designated as “Characterization and diversity analysis of ridge gourd germplasms’’ carried out in the experimental field of Sher-e-Bangla Agricultural University, Dhaka during Kharif season July to October 2021. The materials and methods that were used for conducting the experiment have been presented in this chapter. It includes a short description of the location of experimental site, climate and soil condition of the experimental plot, materials used for the experiment, design of the experiment, data collection procedure and procedure of data analysis. The explicit information regarding the materials and methods of this experiment is discussed below:

3.1 Experimental site

The study was conducted at the experimental plot of Sher-e-Bangla Agricultural University, Dhaka under the Agro-ecological Zone of Madhupur Tract. The experimental site location was located at 23^0 77’ N latitude and 90^0 37’ E longitudes with an elevation of 13.03 meters (9ft) from the sea level (www.distancesfrom.com). The experimental field belongs to the Agro ecological zone AEZ 28 (The Madhupur Tract) (Appendix I).

3.2 Soil and climate

The experimental land was clay loam in texture; medium-high with medium fertility level. The pH of the soil was around 6.2 and it contains 0.82% organic carbon content (Appendix II). The experimental site was located in the subtropical climatic zone with wet summer and dry winter. Generally, high rainfalls, high temperature and short day length are observed during the Kharif season. The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

Bangladesh Agricultural Research Institute (BARI) provided the healthy and vigorous seeds of twenty-seven (27) genotypes and three genotypes of *L. acutangula* which were collected from Bogura district used as experimental materials. The materials used in the experiment are showed in Table 1.

Table 1. List of the genotypes used in the study and their sources

Sl. No.	**Genotype No.**	**BARI Accession No.**	**Source**
1.	G1	BD-3048	PGRC, BARI
2.	G2	BD-3049	PGRC, BARI
3.	G3	BD-3050	PGRC, BARI
4.	G4	BD-3053	PGRC, BARI
5.	G5	BD-8891	PGRC, BARI
6.	G6	BD-8892	PGRC, BARI
7.	G7	BD-8893	PGRC, BARI
8.	G8	BD-8894	PGRC, BARI
9.	G9	BD-8895	PGRC, BARI
10.	G10	BD-8896	PGRC, BARI
11.	G11	BD-8897	PGRC, BARI
12.	G12	BD-8898	PGRC, BARI
13.	G13	BD-8905	PGRC, BARI
14.	G14	BD-8907	PGRC, BARI
15.	G15	BD-8912	PGRC, BARI
16.	G16	BD-8918	PGRC, BARI
17.	G17	BD-8919	PGRC, BARI
18.	G18	BD-8920	PGRC, BARI
19.	G19	BD-8923	PGRC, BARI
20.	G20	BD-8925	PGRC, BARI
21.	G21	BD-8926	PGRC, BARI
22.	G22	BD-8928	PGRC, BARI
23.	G23	BD-8930	PGRC, BARI
24.	G24	BD-10275	PGRC, BARI
25.	G25	BD-10280	PGRC, BARI
26.	G26	BD-10281	PGRC, BARI
27.	G27	BD-10283	PGRC, BARI
28.	G28	HAJARI	Bogura
29.	G29	RAJA	Bogura
30.	G30	PRATIK	Bogura

Here, PGRC= Plant Genetic Resource Centre; BARI= Bangladesh Agricultural Research Institute

3.4 Experimental design and layout

The research was laid out in a Randomized Complete Block Design (RCBD) with three replications. The total area of the experimental plot was 540 m^2 with length 27.0 m and width 20.0 m. The experimental field was divided into three blocks, representing three replications. Two to three seedlings per pit were transplanted maintaining 2.5 m × 1.5 m spacing from row to row and plant to plant, respectively. Thirty germplasm of ridge gourds were distributed in each of the block through randomization process. The distance maintained between two blocks was in 1m.

3.5 Polybag preparation and raising seedling

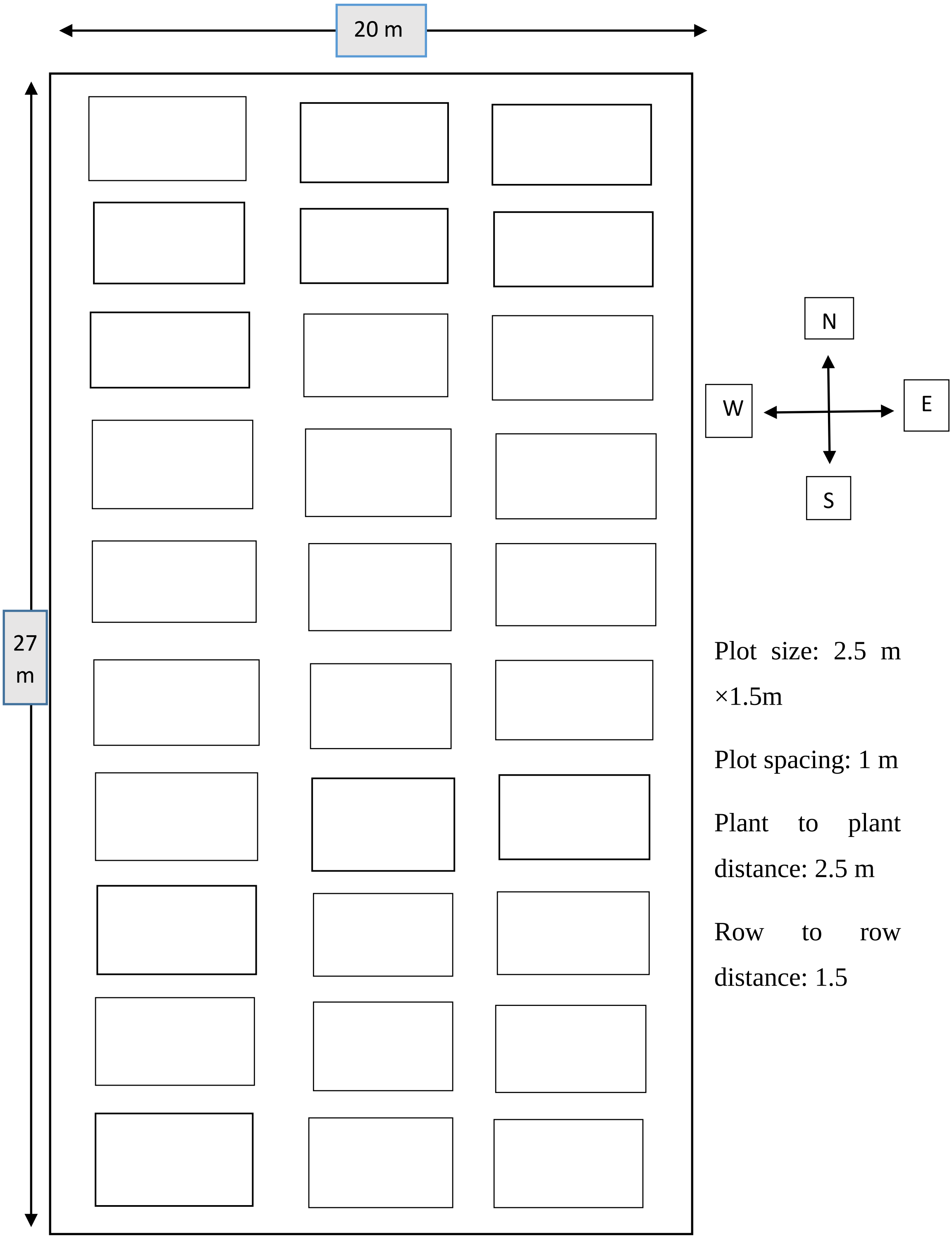
Due to uncertain rainfall during the period of the study, the seeds were dibbled in polybag for higher germination percentage and to get healthy seedlings and when the seedlings become 25 days old, those were transplanted in the main field in the pit. Seeds were sown in polybag on 1st July 2021. Before sowing, seeds were soaked in water for 24 hours and seeds were treated with Bioderma (*Trichoderma viride*) for 5 minutes.

3.6 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the third week of June, 2021. Weeds and other stables were removed carefully from the experimental plot and leveled properly.

3.7 Pit preparation

After final land preparation, pits of 50 cm × 50 cm ×45 cm were prepared in each plot with a spacing of a spacing of 2.5 m×1.0 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5g Furadan was also mixed with the soils of each pit before making it ready for dibbling.



Plot size: 2.5 m ×1.5m

Plot spacing: 1 m

Plant to plant distance: 2.5 m

Row to row distance: 1.5

Figure 1. Layout of experimental plot

Plate 1. The pictorial view of seedlings emergence

Plate 2. Observation of seedlings

Plate 3. Pit formation in the main field

3.8 Application of manure and fertilizers

Urea, Triple Super Phosphate (TSP) and Muriate of Potash (MP) were used as a source of nitrogen, phosphorous, and potassium, respectively. Manures and fertilizers that were applied to the experimental plot according to Fertilizer Recommendation Guide (2005) and presented in Table 2. According this 750 g cowdung, 23 g urea, 10 g TSP, 18 g MP, 5 g gypsum and 0.5 g boron was applied in each pit. The total amount of cowdung, TSP and MP were applied as basal dose at the time of final land preparation. Urea was applied at 30, 60 and 90 days after sowing (DAS) of seeds.

Table 2. Dose and method of application of fertilizers in ridge gourd field

Fertilizers	Dose/ha	Application (%)			
		Basal	30 DAS	60 DAS	90 DAS
Cowdung	5 tons	100	---	---	---
Nitrogen (as urea)	100 kg	----	33.33	33.33	33.33
P_2O_5 (as TSP)	45 kg	100	---	---	---
K_2O (as MP)	80 kg	100	---	---	---
S (as gypsum)	25 kg	100	---	---	---
B (as borax)	2.0 kg	100	---	---	---

3.9 Transplanting of seedlings

Germination of seeds was completed within 15 days and the seedlings of different accessions were planted in the pit on 26th July, 2021. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand. The field view of this experiment shown in below.

Plate 4. Seedlings transplanting in the main field

Plate 5. Pictorial view of research field at early stage

Plate 6. Pictorial view of research field at fruiting stage

3.10 Intercultural operation

After raising seedlings, various intercultural operations such as gap filling by healthy seedlings, weeding, earthing up, irrigation pest and disease control etc. were accomplished for better growth and development of the ridge gourd seedlings.

3.10.1 Weeding

Weeding was done at 30, 60 and 90 days after sowing to keep the plots free from weeds.

3.10.2 Irrigation

Light watering was given by a watering cane at every morning and afternoon and was continued for a week for rapid and well establishment of the germinated seedlings.

3.10.3 Pest and disease control

Insect infestation was a serious problem during the period of establishment of seeding in the field. In my experiment, I didn’t apply any insecticide and pesticide. I was followed the bagging method to control insect and pest. That’s why I was bagged every fruit instead of insecticide application. Discolored and yellowish diseased leaves were also collected from the plant and removed from the field.

3.11 Harvesting

Fruits were harvested based on the attaining of eating quality. Harvesting was started from at the time of last September, 2021 and was continued up to November, 2021.

3.12 Data collection

Data were collected in respect of the following parameters to assess plant growth; yield attributes and yields. The details of data recording are given below on individual plant basis.

3.12.1 Days to first flowering

Days to first flowering was counted when plants of a plot produced first flower. Difference between the dates of sowing to the date of first flowering of a plot was counted as days to first flowering.

BD-3048 G1

BD-3049 G2

BD-3050 G3

BD-3053 G4

BD-8891 G5

BD-8892 G6


BD-8893 G7


BD-8894 G8


BD-8895 G9

Plate 7. Female flower appearance of 30 ridge gourd germplasms


BD-8896 G10


BD-8897 G11


BD-8898 G12


BD-8905 G13


BD-8907 G14


BD-8912 G15

BD-8918 G16

BD-8919 G17

BD-8920 G18

Plate 7 (Cont.). Female flower appearance of 30 ridge gourd germplasms

BD-8923 G19

BD-8925 G20

BD-8926 G21

BD-8928 G22

BD-8930 G23

BD-10275 G24

BD-10280 G25

BD-10281 G26

BD-10283 G27

Plate 7 (Cont.). Female flower appearance of 30 ridge gourd germplasms

HAJARI G28

RAJA G29

PRATIK G30

Plate 7 (Cont.). Female flower appearance of 30 ridge gourd germplasms

3.12.2 Days to first harvest

Days to first harvest was counted when plants of a plot produced first marketable fruit. Difference between the dates of sowing to the date of first harvest of a plot and counted as days to first harvest.

3.12.3 Fruit length

The length of fruit was measured with a meter scale from the neck of the fruit to the bottom of 10 selected marketable fruits from each plant and their average was taken and expressed in cm.

3.12.4 Fruit diameter

Diameter of fruit was measured at the middle portion of 10 selected marketable fruit from each plot with a digital calipers-515 (DC-515) and average was taken and expressed in cm.

3.12.5 Individual fruit weight

The weight of individual fruit was measured with a digital weighing machine from 10 selected marketable fruits from each selected plots and their average was taken and expressed in gram.

3.12.6 Number of fruits per plant

The number of fruits per plant was counted from the sample plants for the whole growing period and the average number of fruits produced per plant was recorded and expressed in fruits per plant.

3.12.7 Fruit yield per plant

Fruit yield of ridge gourd was recorded as the total number of fruits per plant by weighing a digital machine for the whole growing period and was expressed in gram.

BD-3048 G1

BD-3049 G2

BD-3050 G3

BD-3053 G4

BD-8891 G5

BD-8892 G6

Plate 8. Fruit appearance of 30 ridge gourd germplasms

BD-8893 G7

BD-8894 G8

BD-8895 G9

BD-8896 G10

BD-8897 G11

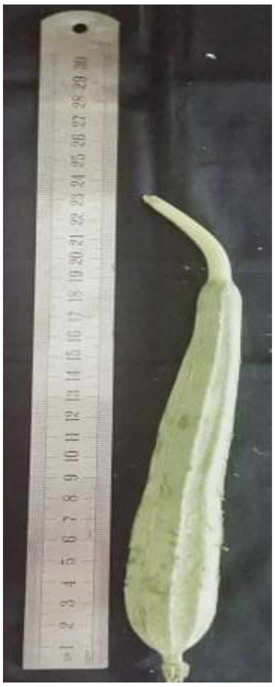
BD-8898 G12

Plate 8 (Cont.): Fruit appearance of 30 ridge gourd germplasms

BD-8905 G13

BD-8907 G14

BD-8912 G15

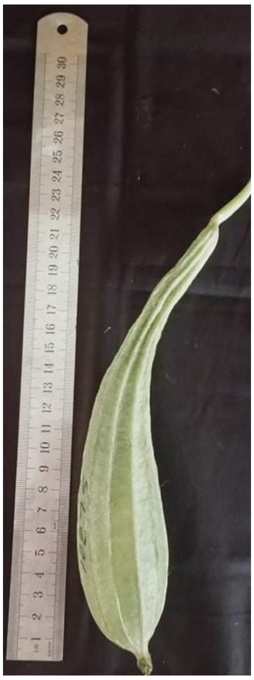


BD-8918 G16

BD-8919 G17

BD-8920 G18

Plate 8 (Cont.): Fruit appearance of 30 ridge gourd germplasms



BD-8923 G19

BD-8925 G20

BD-8926 G21

BD-8928 G22

BD-8930 G23

BD-10275 G24

Plate 8 (Cont.): Fruit appearance of 30 ridge gourd germplasms

BD-10280 G25

BD-10281 G26

BD-10283 G27

HAJARI G28

RAJA G29

PRATIK G30

Plate 8 (Cont.): Fruit appearance of 30 ridge gourd germplasms

BD-3048

BD-3049

BD-3050

BD-3053

BD-8891

BD-8892

Plate 9. Seed appearance of 30 ridge gourd germplasms

BD-8893

BD-8894

BD-8895

BD-8896

BD-8897

BD-8898

Plate 9 (Cont.): Seed appearance of 30 ridge gourd germplasms

BD-8905

BD-8907

BD-8912

BD-8918

BD-8919

BD-8920

Plate 9 (Cont.): Seed appearance of 30 ridge gourd germplasms

BD-8923

BD-8925

BD-8926

BD-8928

BD-8930

BD-10275

Plate 9 (Cont.): Seed appearance of 30 ridge gourd germplasms

BD-10280

BD-10281

BD-10283

HAJARI

RAJA

PRATIK

Plate 9 (Cont.): Seed appearance of 30 ridge gourd germplasms

3.12.8 Weight of hundred seeds

One hundred seeds were counted randomly from the total cleaned harvested seeds of each individual plot and then weighed and recorded in grams.

3.12.9 Fruit yield per plot

Fruit yield of ridge gourd was recorded as the yield of whole plot by weighing a digital balance for the whole growing period and was expressed in kg.

3.12.10 Fruit yield per hectare

Fruit yield per hectare of ridge gourd was estimated by converting the weight of plot yield into hectare and was expressed in ton.

3.13 Statistical analysis

The data obtained for different characters were statistically analyzed by using R (Version 4.1.2) software. The mean values of all the recorded characters were evaluated and analysis of variance was performed by the 'F' (variance ratio) test. The significance of the difference among the means of treatment combinations was estimated by Duncan's Multiple Range Test (DMRT) at 5% level of probability (Gomez and Gomez, 1984).

3.14 Analysis of variance

The variance analysis for different characters was carried out utilizing mean data. The level of significance was tested at 5% and 1% using the F test. The model of ANOVA used is presented below:

Sources of variation (S.V)	**Degree of freedom (d.f.)**	**Mean sum of squares (MS)**	**Expected MS (EMS)**
Replication	(r-1)	Mr	$p\,\sigma_r^2 + \sigma_e^2$
Population	(p-1)	Mp	$r\,\sigma_p^2 + \sigma_e^2$
Error	(p-1) (r-1)	Me	σ_e^2
Total	(rp-1)		

Where, p = number of treatments (population)**;** r = number of replications;

σ_r^2 = variance due to replications; σ_p^2 = variance due to treatments (population); and

σ_e^2= variance due to error

To test the significance of the difference between any two-adjusted genotypic mean, the standard error of the mean was computed using the formula**:**

$$S.E = \sqrt{\frac{2Me}{r}}\left(1 + \frac{rqu}{q+1}\right)$$

Where, S. E = Standard error of mean; Me = Mean sum of square for error (Intra block); r = Number of replications; q = Number of population in each sub-block; and u = Weightage factor computed

3.14.1 Estimation of least significant differences (LSD)

Least Significant Differences were estimated according to the formula of Gomez and Gomez (1984).

$$LSD_\alpha = t_\alpha \sqrt{\frac{s^2}{r}}$$

Here, α = Level of significance; t= tabulated t value with concerned df at same level of significance; s^2= Error Mean Sum of Square; and r = Number of replications.

3.14.2 Study of variability parameters

Estimation of the variability among the ridge gourd germplasms for traits related to yield per plant in *L. acutangula* L. were explained below:

3.14.3 Estimation of genotypic variance and phenotypic variance

To estimate phenotypic and genotypic components of variance, Johnson *et al.* (1955) suggested a formula which is mentioned below:

a. Genotypic variance, $\sigma_g^2 = \frac{MSG - MSE}{r}$

Where, MSG = Mean sum of square for genotypes; MSE = Mean sum of square for error; and r = Number of replication

b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where, σ_p^2= Phenotypic variance; σ_g^2= Genotypic variance; and σ_e^2 = Environmental variance = Mean square of error (MSE)

3.14.4 Estimation of genotypic and phenotypic coefficient of variation

To compute the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters, the following formula was given by Burton, (1952):

$$GCV = \frac{\sigma_g \times 100}{\underline{x}}$$

$$PCV = \frac{\sigma_p \times 100}{\underline{x}}$$

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; σ_g= Genotypic standard deviation; σ_p= Phenotypic standard deviation; and $\underline{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) as

Low (0-10%); Moderate (10-20%); and High (>20%)

3.15 Estimation of heritability in broad sense

Singh and Chaudhary (1985) suggested a formula to estimate broad sense heritability which is given below:

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, h_b^2= Heritability in broad sense; σ_g^2= Genotypic variance; σ_p^2= Phenotypic variance

Robinson *et al.* (1966) suggested the following categories for heritability estimates in cultivated plants.

Categories: Low: 0-30%; Moderate: 30-60; and High: >60%

3.15.1 Estimation of genetic advance

Allard (1960) suggested the following formula, which was used to estimate the expected genetic advance for different characters under selection:

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

Where, GA = Genetic advance; σ_g^2 = Genotypic variance; σ_p^2 = Phenotypic variance; σ_p= Phenotypic standard deviation; and K= Standard selection differential which is 2.06 at 5% selection intensity.

Categories: Low (<10%); Moderate (10-20%); and High (>20%)

3.15.2 Estimation of genetic advance in percentage of mean

Following formula was given by Comstock and Robinson (1952) to compute genetic advance in the percentage of mean:

$$\text{GA in percent of mean} = \frac{GA}{Grand\ mean} \times 100$$

Johnson *et al.* (1955) suggested that genetic advance in percent of mean was categorized into following groups:

Categories: Less than 10% - Low; 10-20% - Moderate; and More than 20% - High

3.15.3 Correlation coefficient analysis

To determine the level of relationship of characters with yield and among the yield parts, the correlation coefficients were computed. Both genotypic and phenotypic correlation coefficients between two characters were determined by utilizing the variance and covariance components, as suggested by Al-Jibouri *et al.* (1958).

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma_{gx}^2 \cdot \sqrt{\sigma_{gy}^2}}} \qquad r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma_{px}^2 \cdot \sqrt{\sigma_{py}^2}}}$$

Where, $r_g(xy), r_p(xy)$ the genotypic and phenotypic correlation coefficients of x and y, respectively.

Cov_{gxy}, Cov_{pxy} are the genotypic and phenotypic covariance of x and y, respectively.

σ_{gx}^2= Genotypic variance of the trait x and σ_{gy}^2 = Genotypic variance of the trait y.

σ_{px}^2= Phenotypic variance of the trait x and σ_{py}^2= Phenotypic variance of the trait y.

The calculated value of ‘r’ was compared with table ‘r’ value with n-2 degrees of freedom at 5% and 1% level of significance, where, n refers to the number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of ridge gourd populations.

3.15.4 Path coefficient analysis

According to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), Path coefficient analysis was done utilizing simple correlation values. In path analysis, the correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3} + \ldots\ldots\ldots\ldots\ldots\ldots + P_{yx11}.r_{x1x11}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3} + \ldots\ldots\ldots\ldots\ldots\ldots + P_{yx11}.r_{x2x11}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3} + \ldots\ldots\ldots\ldots\ldots\ldots + P_{yx11}.r_{x3x11}$$

To estimate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where r's denoted simple correlation coefficient and P's indicate path coefficient (unknown).

P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, the residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$$\mathrm{P}_{\mathrm{RY}}^2 = 1 - \sum \mathrm{P}_{\mathrm{iy}} \cdot \mathrm{r}_{\mathrm{iy}}$$

Where, $\mathrm{P}_{\mathrm{RY}}^2 = (\mathrm{R}^2)$; Hence, residual effect, $R = (P_{RY}^2)^{\frac{1}{2}}$; P_{iy}= Direct effect of the character on yield; and r_{iy}=Correlation of the character with yield

Categories: Negligible (0.00 to 0.09); Low (0.10 to 0.19); Moderate (0.20 to 0.29);

High (0.30 to 1.0); and Very High (>1.00)

3.16 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component Analysis (PCA) and Cluster Analysis (CA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows,

3.16.1 Principal Component Analysis (PCA)

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.16.2 Cluster Analysis (CA)

Cluster Analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to identify the breeding values in respect of genotypic effects and comparative performances of different ridge gourd genotypes. For this, the mean performance of 30 ridge gourd in respect of different quantitative characters such as days to emergence, days to first male flowering, days to first female flowering, internode length, number of primary branches per plant, leaf length, leaf breadth, petiole length, peduncle length, fruit length, fruit breadth, fruit weight, length of seed, breadth of seed, hundred seed weight, number of fruits per plant and yield per plant were analyzed by Duncan's Multiple Range Test (DMRT). Heritability of a trait is important in determining its response to selection. Character association derived by correlation coefficient gives the basis for selecting desirable plant, aiding in evaluation of relative influence of various component characters on yield. Path coefficient analysis discerns correlation into direct and indirect effects. Diversity is the function of parent selection and also heterosis. The availability of transgressive segregates in a breeding program depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the prerequisite of an effective breeding program. Data pertaining to seventeen yield and its contributing characters were recorded and statistically analyzed and the results of the present investigation are presented under the following headings:

4.1 Morphological characterization of ridge gourd;

4.2 Characterization of ridge gourd on the basis of mean performance of yield and yield contributing characters;
4.3 Variability, heritability and genetic advance;

4.4 Correlation coefficient studies;

4.5 Path coefficient analysis; and

4.6 Assessment of genetic diversity

4.1 Characterization of ridge gourd

4.1.1 Cotyledon colour

Cotyledon color is a significant trait for choosing a genotype in a future breeding programme. As cotyledon the first and base for the development of a plant from seed, three different color cotyledons were found in the accessions. Among the 30 genotypes, seven genotypes (G1, G3, G7, G11, G13, G15, and G18) were observed intermediate cotyledon colour, six genotypes were (G5, G14, G16, G22, G23, and G26) showed light green and rest of the seventeen genotypes were expressed dark green cotyledon colour (Table 3). Karuppaiah *et al.* (2005) also reported findings related to cotyledon colour in ridge gourd.

4.1.2 Leaf shape

Leaf shape is one of the important traits for ridge gourd. Various types of leaves were found in ridge gourd genotypes. Among the genotypes, G8, G11, G16, G21, and G25 produced ovate leaves and rest of the twenty five genotypes produced orbicular leaves (Table 3). Guffar (2008) findings in sponge gourd were also similar to these findings.

4.1.3 Male and female ratio

Male and female ratio is another important trait in ridge gourd, because male it has great impact on yield. High male and female ratio plays significant role on higher yield as G4, G5, G6, G16, G19 and G24 genotypes produced high male female flower ratio. Only G3 and G7 produced low ratio and the rest of the genotype were produced medium ratio of the male as well as female flower (Table 3).

These findings were also similar to Karuppaiah *et al.* (2005) findings in ridge gourd, where highest number of male flower was 79.3 and number of female flower was 23.2. Singh *et al.* (2002) reported high sex ratio in ridge gourd.

4.1.4 Blossom-end fruit shape

Blossom-end fruit shape is an important character for ridge gourd, because it plays a vital impact on consumer preference. Genotype G3, G8, G9, G12, G17, G18, G19, G20, G22, G23, G25, G27, G28 and G29 produced pointed blossom-end fruit shape and the rest of the genotypes produced rounded blossom-end shape fruits (TabIe 3). Guffar (2008) findings in sponge gourd were support these findings.

Table 3. Morphological characteristics of different ridge gourd germplasms

Genotype	**Cotyledon color**	**Leaf shape**	**Male female ratio**	**Blossom-end fruit shape**	**Stem-end fruit shape**
G1	Intermediate	Orbicular	Medium	Pointed	Rounded
G2	Dark green	Orbicular	Medium	Rounded	Rounded
G3	Intermediate	Orbicular	Low	Rounded	Rounded
G4	Dark green	Orbicular	High	Pointed	Pointed
G5	Light green	Orbicular	High	Rounded	Rounded
G6	Dark green	Orbicular	High	Rounded	Pointed
G7	Intermediate	Orbicular	Low	Rounded	Rounded
G8	Dark green	Ovate	Medium	Pointed	Rounded
G9	Dark green	Orbicular	Medium	Rounded	Rounded
G10	Dark green	Orbicular	Medium	Pointed	Pointed
G11	Intermediate	Ovate	Medium	Pointed	Pointed
G12	Dark green	Orbicular	Medium	Rounded	Rounded
G13	Intermediate	Orbicular	Medium	Rounded	Rounded
G14	Light green	Orbicular	Medium	Pointed	Pointed
G15	Intermediate	Orbicular	Medium	Rounded	Pointed
G16	Light green	Ovate	High	Rounded	Rounded
G17	Dark green	Orbicular	Medium	Rounded	Pointed
G18	Intermediate	Orbicular	Medium	Rounded	Pointed
G19	Dark green	Orbicular	High	Rounded	Pointed
G20	Dark green	Orbicular	Medium	Pointed	Pointed
G21	Dark green	Ovate	Medium	Pointed	Pointed
G22	Light green	Orbicular	Medium	Pointed	Rounded
G23	Light green	Orbicular	Medium	Pointed	Pointed
G24	Dark green	Orbicular	High	Rounded	Rounded
G25	Dark green	Ovate	Medium	Pointed	Rounded
G26	Light green	Orbicular	Medium	Rounded	Rounded
G27	Dark green	Orbicular	Medium	Pointed	Pointed
G28	Dark green	Orbicular	Medium	Rounded	Pointed
G29	Dark green	Orbicular	Medium	Rounded	Rounded
G30	Dark green	Orbicular	Medium	Rounded	Rounded

(a) Blossom-end pointed fruit shape

(b) Blossom-end rounded fruit shape

(c) Stem-end pointed fruit shape

(d) Stem-end rounded fruit shape

Plate 10. Blossom and stem end fruit shape

Table 3 (Cont.): Morphological characteristics of different ridge gourd germplasms

Genotype	Fruit shape	Fruit ribs	Fruit color	Fruit skin hardiness	Seed surface
G1	Elongated slim	Superficial	Light green	Soft	Shallow pitted
G2	Elliptical tapered	Deep	Light green	Soft	Smooth
G3	Elongated slim	Deep	Light green	Soft	Shallow pitted
G4	Elongated slim	Deep	Dark green	Soft	Shallow pitted
G5	Elongated tapered	Deep	Dark green	Soft	Shallow pitted
G6	Elongated tapered	Superficial	Light green	Soft	Smooth
G7	Short elliptical tapered	Deep	Green	Intermediate	Smooth
G8	Elongated slim	Deep	Green	Soft	Smooth
G9	Elongated slim	Deep	Light green	Soft	Smooth
G10	Elongated tapered	Deep	Green	Soft	Smooth
G11	Elongated slim	Deep	Light green	Soft	Shallow pitted
G12	Elongated slim	Deep	Dark green	Intermediate	Smooth
G13	Short elliptical tapered	Deep	Light green	Intermediate	Smooth
G14	Elongated slim	Deep	Green	Soft	Smooth
G15	Elongated tapered	Deep	Green	Soft	Shallow pitted
G16	Elongated tapered	Deep	Dark green	Soft	Smooth
G17	Elongated tapered	Deep	Dark green	Soft	Shallow pitted
G18	Elongated slim	Deep	Green	Soft	Shallow pitted
G19	Elongated slim	Deep	Dark green	Soft	Shallow pitted
G20	Elongated slim	Deep	Green	Soft	Shallow pitted
G21	Elongated elliptical tapered	Deep	Green	Soft	Shallow pitted
G22	Elongated tapered	Deep	Dark green	Soft	Smooth
G23	Short elliptical tapered	Deep	Green	Intermediate	Smooth
G24	Elongated slim	Deep	Dark green	Intermediate	Shallow pitted
G25	Elongated tapered	Deep	Light green	Soft	Shallow pitted
G26	Elongated tapered	Deep	Green	Soft	Shallow pitted

Table 3 (Cont.): Morphological characteristics of different ridge gourd germplasms

G27	Elongated tapered	Deep	Green	Intermediate	Smooth
G28	Elongated tapered	Deep	Green	Soft	Shallow pitted
G29	Elongated slim	Deep	Dark green	Soft	Smooth
G30	Elongated elliptical tapered	Deep	Green	Soft	Smooth

4.1.5 Stem-end fruit shape

Stem-end fruit shape is another significant trait for ridge gourd, because it also plays a critical impact on client favoritism. Genotypes G3, G4, G8, G11, G12, G14, G15, G16, G19, G20, G24, G27, G28 and G29 produced pointed stem-end shape fruits and the rest of the genotypes produced rounded blossom-end shape fruits (Table 3). This result was reported to Guffar (2008) findings in sponge gourd.

4.1.6 Fruit shape

Fruit shape is an essential consumer preference criteria of ridge gourd market. Different types of ridge gourd were found according to their shape. Genotypes G7, G13, G23 and G27 produced short elliptical tapered shape fruits and genotypes G21 and G30 produced elongated elliptical tapered. Genotypes G2, G5, G10, G15, G16, G17, G22, G25, G26, G27 and G28 produced elongated tapered shape fruits and the rest of the genotypes produced elongated slim shape fruits (Table 3). Chen *et al.* (2002); Sharma *et al.* (2000) reported wide range of variation in respect to fruit shape in cucumber and sponge gourd, respectively.

4.1.7 Fruit ribs

Fruit rib is another trait in respect of ridge gourd. Superficial type fruit ribs were observed in genotypes G2 and G6, the rest genotypes showed deep type fruit ribs (Table 3). Sing *et al.* (2002) also found significant variation in ridge gourd on fruit ribs 80 genotypes.

4.1.8 Fruit colour

Fruit color generally light green, green and dark green found; in the market fruit color effect on consumer choices. Among 30 genotypes, genotypes G4, G12, G16, G17, G19, G22, G24 and G29 were produced dark green fruits and genotypes G7, G8, G10, G14, G15, G18, G20, G21, G23, G26, G27, G28 and G30 were produced green fruits and rest genotypes were produced light green fruits. These variations offer a better scope for breeding of consumer preference (Table 3). Guffar (2008), Singh *et al*. and Chen *et al.* (2002) also found significant variation in respect to fruit color in ridge gourd, cucumber and sponge gourd genotypes.

4.1.9 Fruit skin hardiness

Fruit skin hardiness is other kind of important feature for consumer liking to ridge gourd in market. Because consumer prefer soft skin fruits to other types fruits. Among the genotypes G7, G12, G13 G23, G24 and G27 had intermediate type fruit skin hardiness and other genotypes were soft feelings (Table 3). This trait might be an option for breeder for the developing new combination. Ashok and Rajan (2002) findings in snake gourd was also related to fruit skin hardiness.

4.1.10 Seed surface

Seed surface variation in ridge gourd is another trait. The genotypes G1, G3, G4, G5, G11, G15, G17, G18, G19, G20, G21, G25, G26 and G29 had shallow pitted seed surface and the rest of genotypes were smooth (Table 3). Seed appearance of different ridge gourd accessions were shown in Plate 9. Ashok and Rajan (2002) in snake gourd, Chen *et al.* (2002) in cucumber reported related observations.

4.2 Characterization of ridge gourd on the basis of mean performance of yield and yield contiributing characters

4.2.1 Days to emergence

Different germplasm varied significantly for days to emergence of ridge gourd (Table 4). The maximum days to emergence (11.00) was observed in G1 (BD-3048) which was statistically different with other germplasm except Local variety RAJA and PRATIK which have the minimum days to emergence (5.00). The average days to emergence was recorded 7.11 (Table 5).

4.2.2 Days to first male flower appearing

It was observed that different germplasm varied significantly for days to first flowering of ridge gourd (Table 4) and ranged from 29.66 to 43.00 days (Table 5). The maximum days (43.00) for first male flower bud appearance was observed in G11 (BD-8897) and minimum days (29.66) was recorded in G4 (BD-3053). The average days to first male flowering was found as 35.69 days. Hossain (1996) also found significant difference in male, female and hermaphrodite flower buds appearance and ranging from 29-38 days after seeding. Joseph (1978) also found significant difference in respect of days to first male flower opening in snake gourd.

4.2.3 Days to first female flower appearing

Similarly, days to first female flower buds appearing varied significantly among the genotypes (Table 4) and ranged from 35.00 days to 57.67 days (Table 5). The minimum days (35.00) for first female flower bud appearance was observed in G8 (BD-8920) and a maximum day (57.67 days) to first female bud appearance was recorded in G11 (BD-8897). A minimum day to female flowering is desirable for vegetable producer. Islam (1993) in bottle gourd, Rahman *et al.,* (1990. 1991) also found significant variation for days to first flowering in ridge gourd.

4.2.4 Internode length (cm)

In case of internode length meaningful differences was observed among 30 accession of the ridge gourd (Table 4). Among the accession the largest length was occupied by G15 and the shortest length was occupied by G29 which were followed by 18.33 cm and 7.00 cm respectively. The mean of internode length was 12.36 cm (Table 5).

4.2.5 Number of primary branches

Number of primary branches per plant showed a significant mean differences due to genotypes, which indicated considerable range of variation among the genotypes for this character (Table 4). The mean value of primary branches number was 5.73 that ranged from 3.63 to 11.33 (Table 5). Banik (2003) also found significant difference in number of primary branches (5.23-11.88) in 26 genotypes of snake gourd.

4.2.6 Leaf length (cm)

In case of internode length meaningful differences was observed among 30 accession of the ridge gourd (Table 4). Among the accession the largest length was occupied by G2 and the shortest length was occupied by G22 which were followed by 18.33 cm and 7.00 cm respectively. The mean of internode length was 20.29 cm (Table 5).

Table 4. Analysis of variances for yield and yield related seventeen characters of ridge gourd germplasms

Source of variances	**DF**	**DE**	**DMF**	**DFF**	**IL**	**NPB**	**LL**	**LB**	**PL**	**PeL**
Replications	2	0.01	139.14	139.30	21.09	46.53	30.13	13.71	10.51	9.42
Genotypes	29	5.18**	19.56**	80.67**	32.25**	8.70**	16.20**	25.65**	16.51**	27.15**
Errors	58	0.01	6.24	2.31	0.36	0.90	0.34	0.23	0.50	0.05

Source of variances	**DF**	**FL**	**FB**	**FW**	**NFP**	**SL**	**SB**	**HSW**	**FYP**
Replications	2	10.29	0.53	245.51	182.63	0.0004	0.001	0.93	0.90
Genotypes	29	107.31**	0.83**	6468.72**	280.79**	0.09**	0.02**	5.13**	3.01**
Errors	58	0.44	0.02	1.20	1.31	0.003	0.002	0.45	0.05

** indicates significant at 0.01 probability level

Here, DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

4.2.7 Leaf breadth (cm)

In terms of leaf breadth significant differences was existed among 30 accession of the ridge gourd (Table 4). The highest value of leaf breadth (32.00 cm) was observed in G2 while the lowest leaf breadth was recorded in G28 (17.23 cm). The mean value of leaf breadth was 22.02 cm (Table 5).

4.2.8 Petiole length (cm)

The meaningful differences were observed among 30 accession of the ridge gourd in case of petiole length (Table 4). Among the accession the largest length was occupied by G11 and the shortest length was occupied by G28 which were 16.00 and 7.33 (cm) respectively. The mean of internode length was 11.86 cm.

4.2.9 Peduncle length (cm)

In respect of peduncle length significant differences were observed among 30 accession of the ridge gourd (Table 4). Among the accessions studied, highest length (15.70 cm) was observed in G14 while the lowest length was recorded in G2 (3.87 cm). The mean value of peduncle length was 8.37 cm (Table 5).

4.2.10 Fruit length (cm)

In case of fruit length significant differences were existed among 30 accession of the ridge gourd (Table 4). The highest value of fruit length (42.50 cm) was observed in G1 while the lowest fruit length was recorded in G7 (12.87 cm). The mean value of fruit length was 30.05 cm (Table 5). Fruit appearance of different ridge gourd accessions were shown in Plate 9. Shinde *et al*. (2003) reported wide range of fruit length variation in ridge gourd. Significant variation for the fruit length was noticed in ribbed gourd and bottle gourd by Rahman *et al*., 1991.

4.2.11 Fruit breadth (cm)

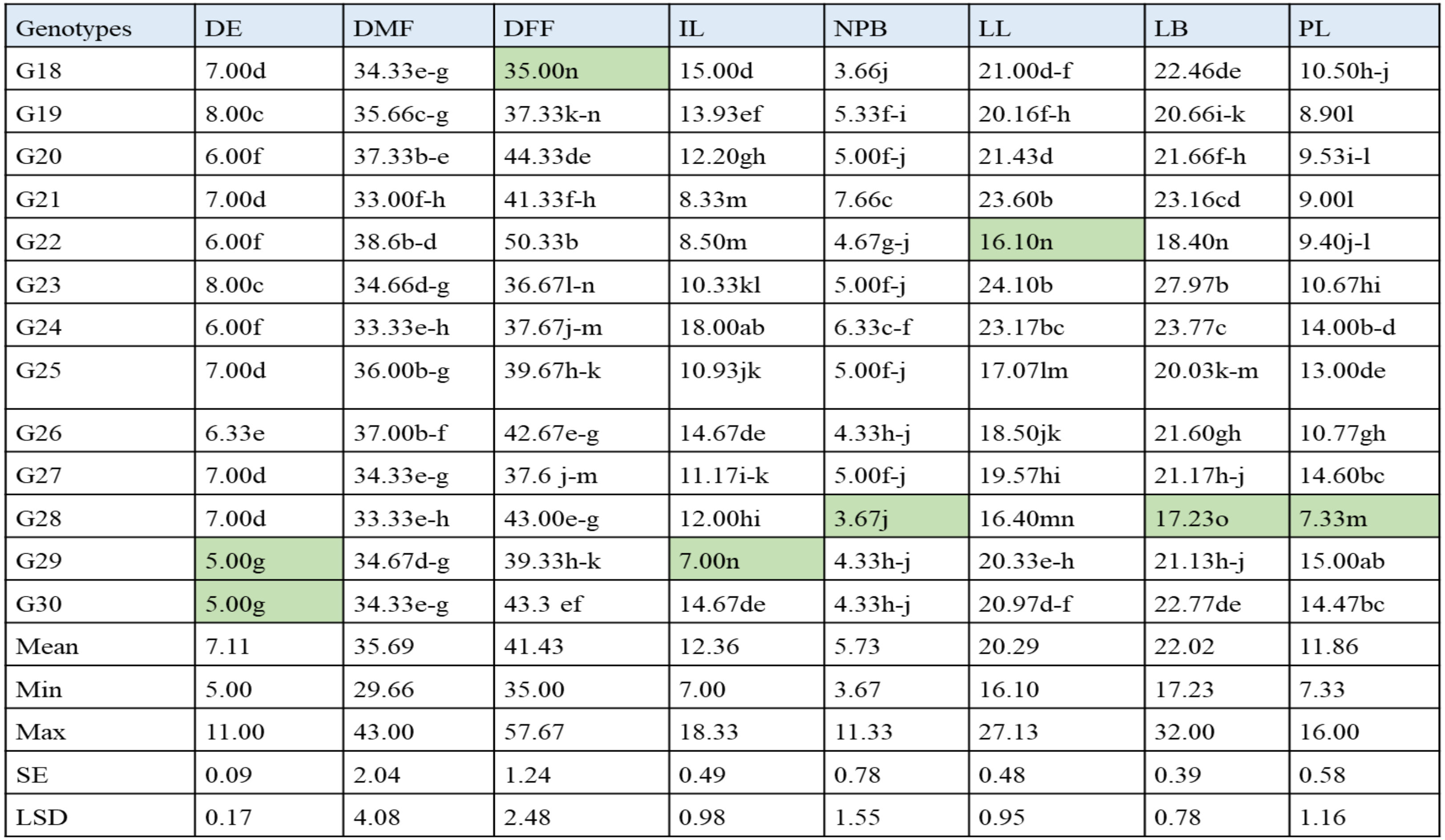
Circumference or breadth of edible fruit varied significantly among 30 ridge gourd accessions (Table 4) and range observed from 2.43 cm to 4.47 cm**.** Among the accession the largest value was occupied by G23 and the shortest value was occupied by G18 which were 4.47 and 2.43 respectively (cm). The mean value of fruit circumference was 3.41 cm. Varghese (1991), Guffar (2008) in snake gourd, Mondal *et al*., (1989) in watermelon, Rahman *et al.* (1991) in bottle gourd and Quamruzzaman *et al.*, (2008) in ridge gourd reported almost similar results to the above findings.

Table 5. Mean performance of 17 characters of 30 genotypes of ridge gourd

Genotypes	DE	DMF	DFF	IL	NPB	LL	LB	PL
G1	11.00a	34.33e-g	37.33k-n	13.36f	9.33b	19.76gh	19.33m	9.26kl
G2	6.00f	37.33b-e	42.66e-g	13.00fg	4.66g-j	27.13a	32.00a	10.43h-j
G3	7.00d	35.00c-g	36.66l-n	11.33h-j	7.00c-e	18.00kl	20.46j-l	13.76cd
G4	7.00d	29.66h	38.33i-l	17.33bc	5.66e-h	19.43h-j	23.10c-e	14.00b-d
G5	6.00f	39.00a-c	38.66i-l	14.93d	6.33c-f	19.96gh	23.73c	10.60hi
G6	9.00b	34.66d-g	50.33b	7.83mn	6.33c-f	20.16f-h	20.50i-l	11.03gh
G7	9.00b	32.33gh	37.66j-m	7.86mn	5.33f-i	18.33k	19.73lm	10.33h-k
G8	7.00d	35.00c-g	35.66mn	16.50c	4.00ij	20.56d-g	20.16kl	11.06gh
G9	7.00d	37.00b-f	38.66i-l	10.76jk	4.00ij	17.90kl	19.73lm	11.83fg
G10	8.00c	35.33c-g	46.33cd	7.53mn	7.33cd	21.00d-f	22.40d-f	10.40h-k
G11	9.00b	43.00a	57.67a	13.90ef	7.00c-e	19.86gh	22.33e-g	16.00a
G12	7.00d	36.66b-f	40.66g-i	9.53l	6.33c-f	19.46hi	20.70i-k	14.50bc
G13	6.00f	35.00c-g	36.66l-n	13.60f	5.66e-h	22.4c	22.33e-g	14.70bc
G14	9.00b	36.00b-g	40.00h-j	10.53jk	7.00c-e	18.66i-k	21.26hi	12.53ef
G15	6.00f	40.00ab	47.33c	18.33a	11.33a	21.20de	27.43b	11.83fg
G16	7.00d	35.00c-g	46.00cd	17.00c	4.33h-j	21.16de	22.73de	16.00a
G17	7.00d	38.66b-d	44.00de	10.83jk	6.00d-g	21.16de	20.66i-k	10.43h-j

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

Table 5 (Cont.) Mean performance of 17 characters of 30 genotypes of ridge gourd



Genotypes	DE	DMF	DFF	IL	NPB	LL	LB	PL
G18	7.00d	34.33e-g	35.00n	15.00d	3.66j	21.00d-f	22.46de	10.50h-j
G19	8.00c	35.66c-g	37.33k-n	13.93ef	5.33f-i	20.16f-h	20.66i-k	8.90l
G20	6.00f	37.33b-e	44.33de	12.20gh	5.00f-j	21.43d	21.66f-h	9.53i-l
G21	7.00d	33.00f-h	41.33f-h	8.33m	7.66c	23.60b	23.16cd	9.00l
G22	6.00f	38.6b-d	50.33b	8.50m	4.67g-j	16.10n	18.40n	9.40j-l
G23	8.00c	34.66d-g	36.67l-n	10.33kl	5.00f-j	24.10b	27.97b	10.67hi
G24	6.00f	33.33e-h	37.67j-m	18.00ab	6.33c-f	23.17bc	23.77c	14.00b-d
G25	7.00d	36.00b-g	39.67h-k	10.93jk	5.00f-j	17.07lm	20.03k-m	13.00de
G26	6.33e	37.00b-f	42.67e-g	14.67de	4.33h-j	18.50jk	21.60gh	10.77gh
G27	7.00d	34.33e-g	37.6 j-m	11.17i-k	5.00f-j	19.57hi	21.17h-j	14.60bc
G28	7.00d	33.33e-h	43.00e-g	12.00hi	3.67j	16.40mn	17.23o	7.33m
G29	5.00g	34.67d-g	39.33h-k	7.00n	4.33h-j	20.33e-h	21.13h-j	15.00ab
G30	5.00g	34.33e-g	43.3 ef	14.67de	4.33h-j	20.97d-f	22.77de	14.47bc
Mean	7.11	35.69	41.43	12.36	5.73	20.29	22.02	11.86
Min	5.00	29.66	35.00	7.00	3.67	16.10	17.23	7.33
Max	11.00	43.00	57.67	18.33	11.33	27.13	32.00	16.00
SE	0.09	2.04	1.24	0.49	0.78	0.48	0.39	0.58
LSD	0.17	4.08	2.48	0.98	1.55	0.95	0.78	1.16

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

Table 5 (Cont.) Mean performance of 17 characters of 30 genotypes of ridge gourd

Genotypes	PeL	FL	FB	FW	NFP	SL	SB	HSW	FYP
G1	10.33f	42.50a	3.70c-e	258.42a	22.00h-j	1.34c-e	0.70f	16.67cd	2.48e
G2	3.86q	24.53j	3.70c-e	110.00lm	26.00g	1.23gh	0.87ab	15.00 ef	1.82g-j
G3	8.23j	20.93l	3.53e-g	83.00rs	8.33q	1.13i	0.50g	14.33f	0.59m
G4	7.50k	30.43f	2.63m-o	182.67d	43.00b	1.33c-e	0.73ef	16.3cd	4.57a
G5	6.47l	24.77 j	3.63d-f	153.33g	54.33a	1.40bc	0.80b-e	15.00ef	4.65a
G6	5.60no	37.97c	3.97b	159.74f	20.67i-l	1.20hi	0.83a-d	16.33cd	2.24ef
G7	4.83p	12.86m	2.90kl	52.36w	11.00p	1.23gh	0.77d-f	14.00fg	0.74m
G8	6.30lm	31.90e	3.96b	184.60c	22.33hi	1.30d-g	0.79c-e	15.00ef	1.78 h-j
G9	12.17d	28.20h	2.90kl	70.83u	17.66n	1.30d-g	0.86ab	15.66de	1.64i-k
G10	7.43k	30.43f	3.90bc	117.42k	23.33h	1.80a	0.80b-e	15.00ef	1.99f-i
G11	9.53h	28.60h	3.00k	95.42p	20.33j-l	1.33c-e	0.76d-f	14.33f	1.62i-k
G12	7.60k	34.13d	3.80b-d	108.91m	20.00k-m	1.40bc	0.83a-d	14.33f	1.52j-l
G13	8.60j	26. 90i	3.50e-h	105.67n	18.33mn	1.22gh	0.90a	14.00fg	1.29kl
G14	15.70a	38.07c	3.33g-j	134.8j	14.00o	1.43b	0.83a-d	14.33f	1.31kl
G15	5.50o	29.10gh	3.26ij	102.18o	28.00f	1.37b-d	0.76d-f	16.33cd	2.33ef
G16	11.40e	26.23i	3.46f-i	92.25q	38.00c	1.30d-g	0.80b-e	17.00bc	1.49j-l
G17	5.77no	22.13k	2.53no	83.83r	30.66e	1.33c-e	0.83a-d	15.66de	1.61jk

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

Table 5 (Cont.) Mean performance of 17 characters of 30 genotypes of ridge gourd

Genotypes	PeL	FL	FB	FW	NFP	SL	SB	HSW	FYP
G18	8.37j	32.83e	2.43o	68.10v	18.33mn	1.40bc	0.80b-e	15.00ef	1.46j-l
G19	13.33c	40.27b	3.83b-d	164.47e	22.33hi	1.23gh	0.70f	14.33f	3.34c
G20	9.03i	32.50e	3.53e-g	110.92l	23.66h	1.32c-f	0.83a-d	16.66cd	2.04f-h
G21	7.57k	28.40h	3.93b	118.83k	35.66d	1.86a	0.89a	14.33f	2.89d
G22	5.80no	28.73h	3.23j	77.67t	21.33i-k	1.34c-e	0.77d-f	15.66de	1.71h-j
G23	9.93g	27.07i	4.47a	81.72s	12.00p	1.40bc	0.89a	15.00ef	0.82m
G24	14.00b	32.43e	4.30a	148.25h	35.00d	1.33c-e	0.80b-e	15.00ef	3.85b
G25	13.46c	34.53d	3.70c-e	222.11b	23.33h	1.39bc	0.70f	15.00ef	2.35ef
G26	5.93mn	33.93d	3.30h-j	111.43l	23.33h	1.26e-h	0.73ef	14.00fg	2.18e-g
G27	5.86no	34.53d	2.66mn	106.50n	23.33h	1.23gh	0.77d-f	18.00ab	2.31ef
G28	5.83no	26.56i	2.90kl	96.33p	17.66n	1.80a	0.70f	13.00g	1.21l
G29	8.50j	29.83fg	2.76lm	145.58i	19.33l-n	1.30d-g	0.86a-c	19.00a	1.66i-k
G30	6.60l	30.16fg	3.36g-j	118.58k	29.66ef	1.24f-h	0.85a-c	16.66cd	2.96d
Mean	8.37	30.05	3.41	122.20	24.10	1.36	0.79	15.37	2.09
Min	3.87	12.87	2.43	52.36	8.33	1.13	0.5	13.00	0.59
Max	15.70	42.50	4.47	258.42	54.33	1.86	0.90	19.00	4.65
SE	0.18	0.54	0.10	0.89	0.94	0.04	0.04	0.55	0.19
LSD	0.37	1.09	0.21	1.79	1.87	0.09	0.07	1.10	0.37

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg

4.2.12 Fruit weight (g)

In respect of average fruit weight, significant differences were observed among 30 ridge gourd accessions (Table 4) and ranged from 52.36 g to 258.42 g. The mean value was 122.20 g. The highest value was observed in G1 and the lowest value was in G7 (Table 5). These findings are in agreement with Quamruzzaman *et al.* (2008) in ridge gourd. Zaman *et al.* (2004) in snake gourd and Mannan (1992) and Varghese (1991) also reported similar results in bitter gourd and snake gourd, respectively.

4.2.13 Number of fruits per plant

Significant differences were found among the accessions in this yield contributing traits (Table 5). Number of fruit per plant varied from 8.33 to 54.33. The mean value was observed as 24.10 fruits per plant. The highest number of fruit was recorded in G5 and the lowest number was recorded in G3 (Table 5).

4.2.14 Seed length (cm)

The meaningful differences were observed among the accessions of 30 ridge gourd genotypes in seed length traits (Table 5). The length ranged from 1.13 cm to 1.86 cm. The highest seed length was recorded in G21 and the lowest seed length obtained in G3 (Table 4). The mean value for seed length trait among the accession was 1.36 cm. Guffar (2008) were found significant differences in seed length of snake gourd.

4.2.15 Seed breadth (cm)

Significant differences were existed among the accessions in this trait (Table 5). The highest seed breadth was obtained in G13 (0.90 cm) and G3 (0.50 cm) showed lowest seed breadth among the accession (Table 5). While the mean value of seed breadth was 0.79. Guffar (2008) were found significant differences in seed breadth of snake gourd.

4.2.16 Hundred seed weight (g)

Significant differences were found in respect of hundred (100) seed weight among the 30 ridge gourd accessions (Table 5). Hundred seed weight varied from 13.00 g to 19.00 g. The highest value was observed in G29 and the lowest value was obtained from G28 (Table 5). Khan *et al.* (2008) reported almost similar result in 64 genotypes of pointed gourd.

4.2.17 Fruit yield per plant (kg)

Significant differences were obtained among the accessions in the yield per plant trait (Table 5). The highest yield per plant was found in G5 (4.65 kg), similarly in G4 (4.57 kg) and the lowest yield per plant was observed in G3 (0.59 kg), followed by G7 (0.74 kg) (Table 5). The mean value of 30 ridge gourd genotypes in respect of this trait was 2.09 kg. Quamruzzaman *et al.* and Guffar (2008) and Khan *et al.* (2008) were found significant differences in number of fruits per plant of ridge gourd and pointed gourd respectively.

4.3 Variability, heritability and genetic advance

The 30 genotypes varied significantly measured for all the characters (Table 6). Estimate of genotypic variance (σ^2g), phenotypic variance (σ^2p), environmental variance (σ^2e), genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV), heritability (h^2), genetic advance (GA) and Genetic advance in percentage of mean are presented in Table 6.

4.3.1 Variability of ridge gourd on the basis of yield and yield contributing characters

4.3.1.1 Days to emergence

The phenotypic variance (1.73) was slightly different from genotypic variance (1.72) that certified slight environmental effect over the trait. Least difference between PCV (18.52%) and GCV (18.46%) values which indicated moderate variability exist for this trait (Table 6) among the germplasms.

4.3.1.2 Days to first male flower appearing

The phenotypic and genotypic variances for days to first male flowers were 10.68 and 4.44, respectively. The phenotypic variance was higher than the genotypic variance suggested that higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 9.16% and 5.91%, respectively for first male flower appearing which indicating that less variation exists among different genotypes for this trait (Table 6). The less GCV values of this characters suggest that the less possibility of improving this trait through selection.

4.3.1.3 Days to first female flower appearing

The value of phenotypic variance (28.43) was higher than the genotypic (26.12) variance for first female flower appearing suggests that role of environment was negligible on expression of the character. The difference between phenotypic (12.87%) and genotypic (12.33%) coefficient of variances was low for this trait which indicates the existence of lower variation among the genotype (Table 6).

4.3.1.4 Internode length

The phenotypic variance (10.99) was slightly different from genotypic variance (10.63) that indicated slight environmental effect over the trait. The difference between PCV (26.81%) and GCV (26.37%) values were least which exhibited considerable variability on the expression of this trait (Table 6).

4.3.1.5 Number of primary branch

The value of phenotypic (3.50) was higher than the value of genotypic (2.60) variance for no. of primary branch suggests role of environment on the character. The difference between phenotypic (32.63%) and genotypic (28.12%) coefficient of variances were high for this trait which indicates the existence of adequate variation among the genotype (Table 6).

4.3.1.6 Leaf length

The difference between phenotypic (5.63) and genotypic (5.29) variance for length of leaf was less suggests that role of environment on the character. Again, the difference between phenotypic (11.69%) and genotypic (11.33%) coefficient of variances were low for this trait which indicates the existence of less variation among the genotype (Table 6).

4.3.1.7 Leaf breadth

The phenotypic and genotypic variances for leaf breadth were 8.70 and 8.47, respectively. The phenotypic variance was higher than the genotypic variance suggested influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 13.39% and 13.22%, respectively for leaf breadth which indicating that minimum variation exists among different genotypes (Table 6). The moderate GCV values of this characters suggest that the possibility of improving this trait through selection.

4.3.1.8 Petiole length

The value of phenotypic (5.84) was higher than the value of genotypic (5.33) variance for no. of primary branch suggests role of environment on this character. The difference between phenotypic (20.37%) and genotypic (19.47%) coefficient of variances was comparatively low for this trait which indicates the existence of little variation among the genotype (Table 6).

4.3.1.9 Peduncle length

The phenotypic variance (9.08) was slightly different from genotypic variance (9.03) that indicated minute environmental effect over the trait. The difference between PCV (36.01%) and GCV (35.91%) values were least which existed less variability on the expression of this trait (Table 6).

4.3.1.10 Fruit length

The phenotypic and genotypic variances for fruit length were 36.06 and 35.62, respectively. The phenotypic variance was higher than the genotypic variance suggested influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 19.98% and 19.86%, respectively for fruit length which indicating that minimum variation exists among different genotypes (Table 6).

4.2.2.11 Fruit breadth

The phenotypic variance (0.29) was minutely different from genotypic variance (0.27) that indicated very least environmental effect over the trait. The difference between PCV (15.75%) and GCV (15.30%) values were least which existed less variability on the expression of this trait (Table 6).

4.3.1.12 Fruit weight

The value of phenotypic (2157.04) was higher than the genotypic (2155.84) variance for weight of fruit suggests that role of environment on the character. The difference between phenotypic (38.01%) and genotypic (38%) coefficient of variances were minute for weight of fruit which indicates the existence of less variation among the genotype (Table 6).

4.3.1.13 Number of fruits per plant

The phenotypic and genotypic variances for no. of fruit per plant were 94.47 and 93.16, respectively. The phenotypic variance was higher than the genotypic variance suggested influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 40.33% and 40.05%, respectively for number of fruits per plant which indicating that minimum variation exists among different genotypes (Table 6).

4.3.1.14 Seed length

Phenotypic variance and the genotypic variance were same (0.03). Least difference between PCV (13%) and GCV (12.41%) values indicated that no influence of environment and moderate variability present on this character (Table 6).

4.3.1.15 Seed breadth

Phenotypic variance and the genotypic variance were same (0.01). Medium difference between PCV (11.21%) and GCV (9.66%) values indicated that no influence of environment and moderate variability present on this character (Table 6).

4.3.1.16 Hundred seed weight

The value of phenotypic (2.01) was higher than the genotypic (1.56) variance for weight of hundred seed suggests the role of environment on this character. The difference between phenotypic (9.23%) and genotypic (8.13%) coefficient of variances was lower for weight of hundred seed which indicates the existence of less variation among the genotype (Table 6).

4.3.1.17 Fruit yield per plant

The phenotypic variance (1.04) was slightly different from genotypic variance (0.99) that indicated minute environmental effect over the trait. The difference between PCV (48.80%) and GCV (47.56%) values indicate least influence of environment on the expression of this trait (Table 6) but high level of variability present among the germplasms for this trait.

Table 6. Genetic component of variation for seventeen yield and yield contributing characters of thirty ridge gourd germplasms

Traits	**σ^2g**	**σ^2e**	**σ^2p**	**GCV**	**PCV**	**h^2b**	**GA**	**GAPM**
DE	1.72	0.01	1.73	18.46	18.52	99.36	2.69	37.83
DMF	4.44	6.24	10.68	5.91	9.16	41.60	2.79	7.83
DFF	26.12	2.31	28.43	12.33	12.87	91.87	10.07	24.31
IL	10.63	0.36	10.99	26.37	26.81	96.75	6.59	53.33
NPB	2.60	0.90	3.50	28.12	32.63	74.26	2.86	49.82
LL	5.29	0.34	5.63	11.33	11.69	93.96	4.58	22.59
LB	8.47	0.23	8.70	13.22	13.39	97.38	5.91	26.82
PL	5.33	0.50	5.84	19.47	20.37	91.38	4.54	38.26
PeL	9.03	0.05	9.08	35.91	36.01	99.44	6.16	73.63
FL	35.62	0.44	36.06	19.86	19.98	98.77	12.20	40.58
FB	0.27	0.02	0.29	15.30	15.75	94.35	1.04	30.55
FW	2155.84	1.20	2157.04	38.00	38.01	99.94	95.44	78.10
NFP	93.16	1.31	94.47	40.05	40.33	98.61	19.71	81.77
SL	0.03	0.00	0.03	12.41	13.00	91.08	0.33	24.34
SB	0.01	0.00	0.01	9.66	11.21	74.24	0.14	17.11
HSW	1.56	0.45	2.01	8.13	9.23	77.60	2.26	14.73
FYP	0.99	0.05	1.04	47.56	48.80	94.97	1.99	95.29

Here, DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant, σ^2g = genotypic variance, σ^2e = environmental variance, σ^2p = phenotypic variance, h^2b = heritability, GA = Genetic advance, GAPM = genetic advance in percent of mean

4.3.2 Heritablity and genetic advance

4.3.2.1 Days to emergence

Days to emergence showed high heritability (99.36%) coupled with low genetic advance (2.69) and moderate genetic advance in percentage of mean (37.83%) (Table 6). This result revealed that the character was controlled by non-additive genes and the selection based on this character would not be effective.

4.3.2.2 Days to first male flower appearance

Moderate heritability (41.60%) accompanied with low genetic advance (2.79) and low genetic advance in percentage of mean (7.83%) was calculated in respect of days to first male flower appearance (Table 6). These findings discovered the action of non-additive gene effects on the expression of this trait. Selection would not be effective based on such character.

4.3.2.3 Days to first female flower appearance

Days to first female flower appearance showed high heritability (91.87%) coupled with moderate genetic advance (10.07) and high genetic advance in percentage of mean (24.31%) (Table 6). These finding exposed the predominance of additive genes for controlling this trait. Thus, selection based on this character will be rewarding for improvement.

4.3.2.4 Internode length

The magnitude of heritability in broad sense of internode length was high (96.75%) with low genetic advance (6.59) and high genetic advance in percentage of mean (53.33%) (Table 6). These findings revealed that this trait was controlled by non-additive gene and selection for this character would not be effective.

4.3.2.5 Number of primary branch

High heritability (74.26%) along with low genetic advance (2.86) and high genetic advance in percentage of mean (49.82%) was calculated for number of primary branches per plant (Table 6). It is indicated that presence of non-additive gene action and selection for further improvement of the trait might not be effective.

4.3.2.6 Leaf length

Leaf length showed high heritability (93.96%) coupled with low genetic advance (4.58) and high genetic advance in percentage of mean (22.59%) (Table 6). Genetic advances in percent of mean were higher which is in accordance with the findings of Singh *et al.*, (1977).

4.3.2.7 Leaf breadth

High heritability (97.38%) accompanied with low genetic advance (5.91) and high genetic advance in percentage of mean (26.82%) was calculated in respect of leaf breadth (Table 6). These findings discovered the action of non-additive gene effects on the expression of this trait. Selection may not be effective in such character.

4.3.2.8 Petiole length

Length of petiole showed high heritability (91.38%) coupled with low genetic advance (4.54) and high genetic advance in percentage of mean (38.26%) (Table 6). These finding exposed the predominance of no additive genes for controlling length of petiole. Thus, selection based on this character will not be rewarding for improvement.

4.3.2.9 Peduncle length

The magnitude of heritability in broad sense of length of peduncle leaf was high (99.44%) with low genetic advance (6.16) and high genetic advance in percentage of mean (73.63%) (Table 6). These findings revealed that this trait was controlled by nonadditive gene and selection for this character would not be effective.

4.3.2.10 Fruit length

High heritability (98.77%) along with moderate genetic advance (12.20) and high genetic advance in percentage of mean (40.58%) was calculated of fruit length (Table 6). It is indicated that presence of additive gene action and selection for further improvement of the trait might be effective.

4.3.2.11 Fruit breadth

Fruit breadth showed high heritability (94.35%) coupled with low genetic advance (1.04) and high genetic advance in percentage of mean (30.55%) (Table 6). The result showed that due to presence of no additive gene effect and thus no scope of selection of this trait.

4.3.2.12 Fruit weight

High heritability (99.94%) accompanied with high genetic advance (95.44) and high genetic advance in percentage of mean (78.10%) was calculated in respect of fruit weight (Table 6). These findings discovered the action of additive gene effects on the expression of this trait. Selection would be effective in such character.

4.3.2.13 Number of fruits per plant

No. of fruits per plant showed high heritability (98.61%) coupled with high genetic advance (19.71) and high genetic advance in percentage of mean (81.77%) (Table 6). These finding exposed the predominance of additive genes for controlling no. of fruit per plant. Thus, selection based on this character would be rewarding for improvement.

4.3.2.14 Seed length

The magnitude of heritability in broad sense of seed length was high (91.08%) with low genetic advance (0.33) and high genetic advance in percentage of mean (24.34%) (Table 6). These findings revealed that this trait was controlled by nonadditive gene and selection for this character would not be effective.

4.3.2.15 Seed breadth

High heritability (74.24%) along with low genetic advance (0.14) and moderate genetic advance in percentage of mean (17.11%) was calculated in seed breadth (Table 6). It is indicated that presence of non-additive gene action and selection for further improvement of the trait might not be effective.

4.3.2.16 Hundred seed weight

High heritability (77.60%) accompanied with low genetic advance (2.26) and moderate genetic advance in percentage of mean (14.73%) was calculated in respect of 100 seed weight (Table 6). These findings discovered the action of non-additive gene effects on the expression of this trait.

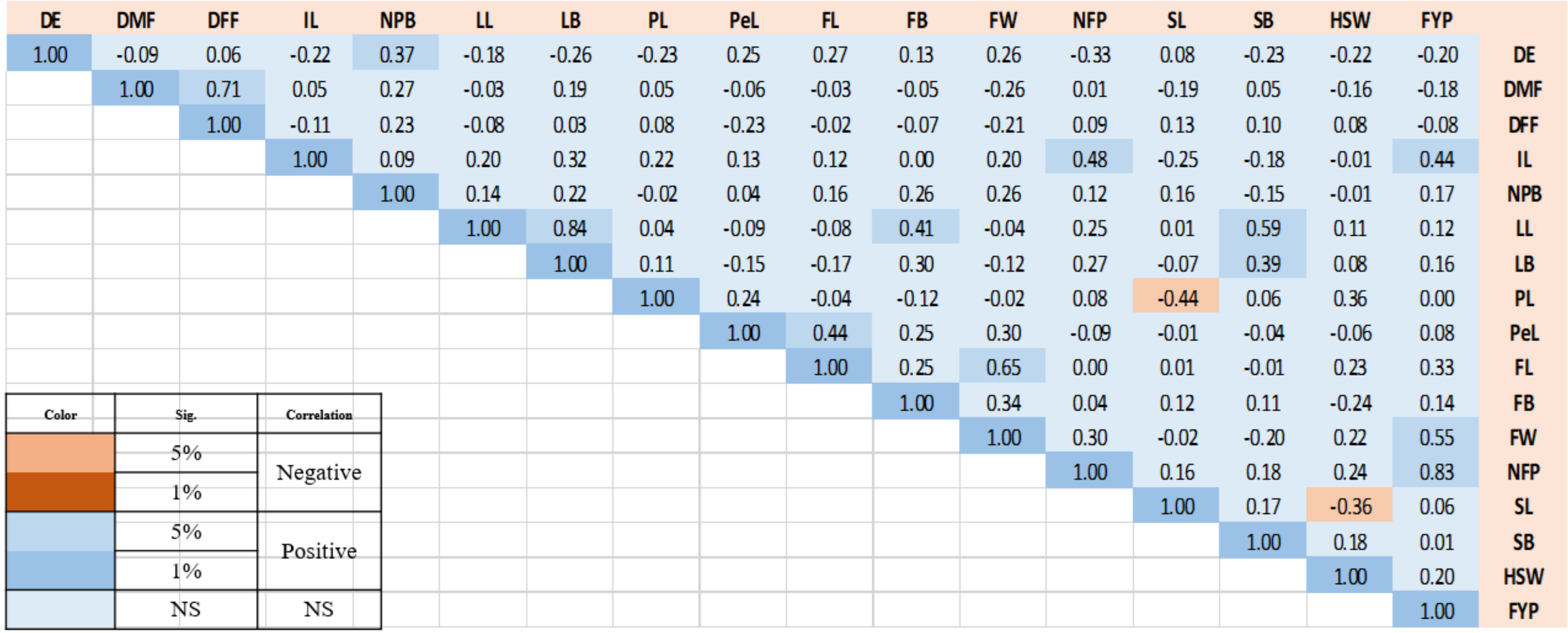
4.3.2.17 Fruit yield per plant

Fruit yield per plant showed high heritability (94.97%) coupled with low genetic advance (1.99) and high genetic advance in percentage of mean (95.29%) (Table 6). These finding exposed the predominance of non-additive genes for controlling fruit yield per plant. Thus, selection based on this character will not be rewarding for improvement.

4.4 Correlation coefficient analysis

Improvement of a particular character in the breeding programs can be achieved by indirect selection via different characters. This wants a good understanding of the association of various characters with the target character and among the different characters themselves. It’s necessary to have the estimates of correlation of yield with different characters that the genotype might be assessed visually. The makeup and constitution correlation reveals the extent of association between completely different characters, thus, it helps to base choice procedure to a needed balance. Once two opposite fascinating characters moving the principal characters are being selected. A positive correlation happens because of coupling section of linkage and negative correlation arises because of repulsion section of linkage of genes dominant completely different traits. No correlation indicates that genes involved are situated so much apart on identical chromosome or they are situated on completely different bodies. Yield being a fancy character is governed by an outsized range of genes. The influence of every character on yield might be well-known through correlation studies with a view to see the extent and nature of relationships prevailing among yield and yield attributing characters. Hence, the constitution of genotypic and phenotypic correlation coefficient values for seventeen characters in ridge gourd germplasms studied are given in Table (7 and 8).

Table 7. Genotypic (r_g) correlation coefficient among different pairs of yield and yield contributing characters in ridge gourd germplasms

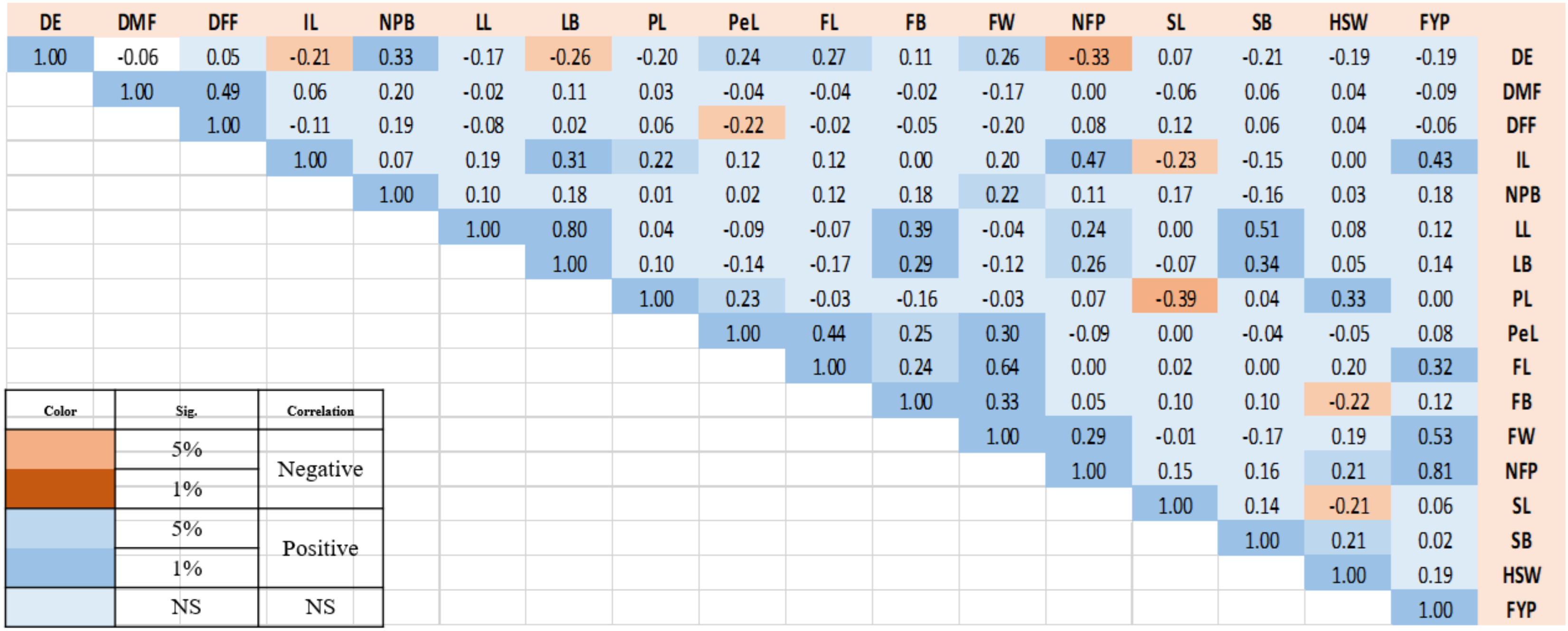


DE	DMF	DFF	IL	NPB	LL	LB	PL	PeL	FL	FB	FW	NFP	SL	SB	HSW	FYP	
1.00	-0.09	0.06	-0.22	0.37	-0.18	-0.26	-0.23	0.25	0.27	0.13	0.26	-0.33	0.08	-0.23	-0.22	-0.20	**DE**
	1.00	0.71	0.05	0.27	-0.03	0.19	0.05	-0.06	-0.03	-0.05	-0.26	0.01	-0.19	0.05	-0.16	-0.18	**DMF**
		1.00	-0.11	0.23	-0.08	0.03	0.08	-0.23	-0.02	-0.07	-0.21	0.09	0.13	0.10	0.08	-0.08	**DFF**
			1.00	0.09	0.20	0.32	0.22	0.13	0.12	0.00	0.20	0.48	-0.25	-0.18	-0.01	0.44	**IL**
				1.00	0.14	0.22	-0.02	0.04	0.16	0.26	0.26	0.12	0.16	-0.15	-0.01	0.17	**NPB**
					1.00	0.84	0.04	-0.09	-0.08	0.41	-0.04	0.25	0.01	0.59	0.11	0.12	**LL**
						1.00	0.11	-0.15	-0.17	0.30	-0.12	0.27	-0.07	0.39	0.08	0.16	**LB**
							1.00	0.24	-0.04	-0.12	-0.02	0.08	-0.44	0.06	0.36	0.00	**PL**
								1.00	0.44	0.25	0.30	-0.09	-0.01	-0.04	-0.06	0.08	**PeL**
									1.00	0.25	0.65	0.00	0.01	-0.01	0.23	0.33	**FL**
										1.00	0.34	0.04	0.12	0.11	-0.24	0.14	**FB**
											1.00	0.30	-0.02	-0.20	0.22	0.55	**FW**
												1.00	0.16	0.18	0.24	0.83	**NFP**
													1.00	0.17	-0.36	0.06	**SL**
														1.00	0.18	0.01	**SB**
															1.00	0.20	**HSW**
																1.00	**FYP**

Color	**Sig.**	**Correlation**
🟧	5%	Negative
🟫	1%	
🟦	5%	Positive
🟦	1%	
⬜	NS	NS

Here, DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

Table 8. Phenotypic (r_p) correlation coefficient among different pairs of yield and yield contributing characters in ridge gourd germplasms



DE	DMF	DFF	IL	NPB	LL	LB	PL	PeL	FL	FB	FW	NFP	SL	SB	HSW	FYP	
1.00	-0.06	0.05	-0.21	0.33	-0.17	-0.26	-0.20	0.24	0.27	0.11	0.26	-0.33	0.07	-0.21	-0.19	-0.19	DE
	1.00	0.49	0.06	0.20	-0.02	0.11	0.03	-0.04	-0.04	-0.02	-0.17	0.00	-0.06	0.06	0.04	-0.09	DMF
		1.00	-0.11	0.19	-0.08	0.02	0.06	-0.22	-0.02	-0.05	-0.20	0.08	0.12	0.06	0.04	-0.06	DFF
			1.00	0.07	0.19	0.31	0.22	0.12	0.12	0.00	0.20	0.47	-0.23	-0.15	0.00	0.43	IL
				1.00	0.10	0.18	0.01	0.02	0.12	0.18	0.22	0.11	0.17	-0.16	0.03	0.18	NPB
					1.00	0.80	0.04	-0.09	-0.07	0.39	-0.04	0.24	0.00	0.51	0.08	0.12	LL
						1.00	0.10	-0.14	-0.17	0.29	-0.12	0.26	-0.07	0.34	0.05	0.14	LB
							1.00	0.23	-0.03	-0.16	-0.03	0.07	-0.39	0.04	0.33	0.00	PL
								1.00	0.44	0.25	0.30	-0.09	0.00	-0.04	-0.05	0.08	PeL
									1.00	0.24	0.64	0.00	0.02	0.00	0.20	0.32	FL
										1.00	0.33	0.05	0.10	0.10	-0.22	0.12	FB
											1.00	0.29	-0.01	-0.17	0.19	0.53	FW
												1.00	0.15	0.16	0.21	0.81	NFP
													1.00	0.14	-0.21	0.06	SL
														1.00	0.21	0.02	SB
															1.00	0.19	HSW
																1.00	FYP

Color	Sig.	Correlation
🟧	5%	Negative
🟫	1%	
🟦	5%	Positive
🟦	1%	
⬜	NS	NS

Here, DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg)

4.4.1 Days to emergence

Days to emergence showed highly significant and positive correlation (r_g = 0.37, r_p = 0.33) with number of primary branches per plant. Significant and positive correlation of days to emergence was observed with peduncle length (r_g = 0.25, r_p = 0.24), fruit length (r_g = 0.27, r_p = 0.27), fruit weight (r_g = 0.26, r_p = 0.26). Highly significant negative correlation was observed with number of fruit per plant (r_g = -0.33, r_p = -0.33). Significant negative correlation was observed with internode length (r_g = -0.22, r_p = -0.21) and leaf breath (r_g = -0.26, r_p = -0.26). Non-significant differences were observed for the other traits.

4.4.2 Days to first male flower appearance

Days to first male flower appearance showed highly significant and positive correlation (r_g = 0.71, r_p = 0.49) with days to first male flower appearance. Non-significant differences were observed for the other traits.

4.4.3 Days to first female flower appearance

Days to first female flower appearance showed significant negative correlation (r_g = -0.23, r_p = -0.22) with peduncle length. Non-significant differences were observed for the other traits.

4.4.4 Internode length

Internode length showed highly significant and positive correlation with number of fruit per plant (r_g = 0.48, r_p = 0.47), fruit yield per plant (r_g = 0.44, r_p = 0.43) and leaf breadth (r_g = 0.32, r_p = 0.31). Significant and positive correlation was observed with petiole length (r_g = 0.22, r_p = 0.22). Significant negative correlation was observed with seed length (r_g = -0.25, r_p = -0.23). Non-significant differences were observed for the other traits.

4.4.5 Number of primary branch

Number of primary branch showed significant and positive correlation with fruit weight (r_g =0.26, r_p = 0.22). Non-significant differences were observed for the other traits.

4.4.6 Leaf length

Leaf length (cm) showed highly significant and positive correlation with leaf breath (r_g = 0.84, r_p = 0.80), seed breadth (r_g = 0.59, r_p = 0.51) and fruit breadth (r_g = 0.41, r_p =

0.39). Significant and positive correlation was observed with number of fruit per plant ($r_g = 0.25$, $r_p = 0.24$). Non-significant differences were observed for the other traits.

4.4.7 Leaf breadth

Leaf breadth showed highly significant and positive correlation with seed breath ($r_g = 0.39$, $r_p = 0.34$) and fruit breath ($r_g = 0.30$, $r_p = 0.29$). Significant and positive correlation was observed with number of fruit per plant ($r_g = 0.27$, $r_p = 0.26$). Non-significant differences were observed for the other traits.

4.4.8 Petiole length

Petiole length showed highly significant and positive correlation with hundred seed weight ($r_g = 0.36$, $r_p = 0.33$). Significant and positive correlation was observed with peduncle length ($r_g = 0.24$, $r_p = 0.23$). Highly significant negative correlation was observed with seed length ($r_g = -0.44$, $r_p = -0.39$). Non-significant differences were observed for the other traits.

4.4.9 Peduncle length

Peduncle length (cm) showed highly significant and positive correlation with fruit length ($r_g = 0.44$, $r_p = 0.44$) and fruit weight ($r_g = 0.30$, $r_p = 0.30$). Significant and positive correlation was observed with fruit breadth ($r_g = 0.25$, $r_p = 0.25$). Non-significant differences were observed for the other traits.

4.4.10 Fruit length

Fruit length (cm) showed highly significant and positive correlation with fruit weight ($r_g = 0.65$, $r_p = 0.64$) and fruit yield per plant ($r_g = 0.33$, $r_p = 0.32$). Significant and positive correlation was observed with fruit breadth ($r_g = 0.25$, $r_p = 0.24$). Non-significant differences were observed for the other traits.

4.4.11 Fruit breadth

Fruit breadth (cm) showed highly significant and positive correlation with fruit weight ($r_g = 0.34$, $r_p = 0.33$). Significant negative correlation was observed with hundred deed weight ($r_g = -0.24$, $r_p = -0.22$). Non-significant differences were observed for the other traits.

4.4.12 Fruit weight

Fruit weight (g) showed highly significant and positive correlation with fruit yield per plant (r_g = 0.55, r_p = 0.53) and number of fruit per plant (r_g = 0.30, r_p = 0.29). Non-significant differences were observed for the other traits.

4.4.13 Number of fruit per plant

Number of fruit per plant showed highly significant and positive correlation with fruit yield per plant (r_g = 0.83, r_p = 0.81). Significant and positive correlation was observed with hundred seed weight (r_g = 0.24, r_p = 0.21). Non-significant differences were observed for the other traits.

4.4.14 Seed length

Seed length (cm) showed significant negative correlation with hundred deed weight (r_g = -0.36, r_p = -0.21). Non-significant differences were observed for the other traits.

4.4.15 Seed breadth

Seed breadth (cm) showed significant and positive correlation with hundred seed weight (r_g = 0.18, r_p = 0.21). Non-significant differences were observed for the other traits.

4.4.16 Hundred seed weight

Hundred seed weight showed significant and positive correlation with fruit yield per plant (r_g = 0.20, r_p = 0.19). Non-significant differences were observed for the other traits.

4.5 Path coefficient analysis

Correlation analysis indicates the association pattern of component traits with yield, they merely represent the influence of a selected attribute on yield instead of providing cause and impact relationship. The path coefficient analysis technique was developed by Wright (1923) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It's standardized partial parametric statistical analysis. As such, it measures the direct influence of one variable upon another. Such data would be of good value in enabling the breeder to specifically determine the necessary component traits of yield and utilize the genetic stock for improvement in a planned way. The direct and indirect effects of yield contributing characters on yield were found out by using path analysis.

Here fruit yield per plant was considered as effect (dependent variable) and other parameters were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of ridge gourd in (Table 9).

4.5.1 Days to emergence

Path co-efficient analysis revealed that days to emergence had a positive direct effect (27.14) on fruit yield per plant. For improvement direct selection based on days to emergence could be rewarding. Indirect selection could be performed via leaf breadth, fruit breadth, number of fruits per plant, seed length and seed breadth. Days to emergence had significant and negative genotypic correlation (-0.21) with fruit yield per plant via positive indirect effect on leaf breadth (4.53), fruit breadth (2.64), number of fruit per plant (3.24), seed length (3.33) and seed breadth (1.38) and negative indirect effect of days to first male flower emergence (-5.12), days to first female flower emergence (-2.76), internode length (-4.46), number of primary branches (-8.18), leaf length (-1.04), petiole length (-3.65), peduncle length (-4.43), fruit length (-3.78) and fruit weight (-0.05)(Table 9).

4.5.2 Days to first male flower appearance

Path coefficient analysis revealed that days to first male flower appearance had a positive direct effect (56.35) on fruit yield per plant. Days to first male flower appearance had positive and indirect effect on internode length (0.92), petiole length (0.86), peduncle length (1.17), fruit length (0.39) and fruit weight (0.05) while negative indirect effect on days to emergence (-2.46), days to first female flower emergence (-31.85), number of primary branch (-6.04), leaf length (-0.17), leaf breadth (-3.40), fruit breadth (-1.08), number of fruit per plant (-0.14), seed length (-8.14), seed breadth (-0.30) and hundred seed weight (-6.33). It showed that non-significant and negative genotypic correlation (-0.17) with fruit yield per plant (Table 9).

4.5.3 Days to first female flower appearance

Path coefficient analysis revealed that days to first female flower appearance had a negative and direct effect (-45.14) on fruit yield per plant. Days to first female flower appearance had positive and indirect effect on days to emergence (1.66), days to first male flower appearance (39.77), petiole length (1.33), peduncle length (4.11), fruit length (0.31), fruit weight (0.04), seed length (5.80) and hundred seed weight (3.19) while negative indirect effect on internode length (-2.29), number of primary branch (-5.16), leaf length (-0.48), leaf breadth (-0.48), fruit breadth (-1.35), number of fruit per plant (-0.83) and seed breadth (-0.57). It showed non-significant and negative genotypic correlation (-0.09) with fruit yield per plant (Table 9).

4.5.4 Internode length

Path coefficient analysis revealed that internode length had a positive and direct effect (20.16) on fruit yield per plant. Internode length had positive and indirect effect on days to first male flower appearance (2.59), days to first female flower appearance (5.12), leaf length (1.19), petiole length (3.58), fruit breadth (0.10) and seed breadth (1.07) while negative indirect effect on days to emergence (-6.00), number of primary branch (-1.95), leaf breadth (-5.57), peduncle length (-2.29), fruit length (-1.66), fruit weight (-0.04), number of fruits per plant (-4.63), seed length (-10.95) and hundred seed weight (-0.28). It showed highly significant and positive genotypic correlation (0.44) with fruit yield per plant (Table 9).

4.5.5 Number of primary branch

Path coefficient analysis revealed that number of primary branch had a negative and direct effect (-22.05) on fruit yield per plant. Number of primary branch had positive and indirect effect on days to emergence (10.07), days to first male flower appearance (15.43), internode length (1.79), leaf length (0.79), fruit breadth (5.49), seed length (7.07) and seed breadth (0.90) while negative indirect effect on days to first female flower appearance (-10.56), leaf breadth (-3.77), petiole length (-0.30), peduncle length (-0.74), fruit length (-2.22), fruit weight (-0.05), number of fruit per plant (-1.18), and hundred seed weight (-0.51). It showed non-significant and positive genotypic correlation (0.16) with fruit yield per plant (Table 9).

4.5.6 Leaf length

Path coefficient analysis revealed that leaf length had a positive and direct effect (5.81) on fruit yield per plant. Leaf length had positive and indirect effect on days to first female flower appearance (3.69), internode length (4.12), petiole length (0.63), peduncle length (1.60), fruit length (1.06), fruit breadth (8.53), fruit weight (0.01), seed length (0.35) and hundred seed weight (4.39) while negative indirect effect on days to emergence (-4.86), days to first male flower appearance (-1.70), number of primary branch (-3.00), leaf breadth (-14.62), number of fruit per plant (-2.39), and seed breadth (-3.50). It showed non-significant and positive genotypic correlation (0.12) with fruit yield per plant (Table 9).

4.5.7 Leaf breadth

Path coefficient analysis revealed that leaf breadth had a negative and direct effect (-17.45) on fruit yield per plant. Leaf breadth had positive and indirect effect on days to first male flower appearance (10.98), internode length (6.43), leaf length (4.86), petiole length (1.85), peduncle length (2.62), fruit length (2.40), fruit breadth (6.14), fruit weight (0.03), and hundred seed weight (3.16) while negative indirect effect on days to emergence (-7.05), days to first female flower appearance (-1.25), number of primary branch (-4.76), number of fruit per plant (-2.39), seed length (-2.88) and seed breadth (-2.32). It showed non-significant and positive genotypic correlation (0.17) with fruit yield per plant (Table 9).

4.5.8 Petiole length

Path coefficient analysis revealed that petiole length had a positive and direct effect (16.07) on fruit yield per plant. Petiole length had positive and indirect effect on days to first male flower appearance (3.00), internode length (4.49), number of primary branch (0.41), leaf length (0.23), fruit length (0.53), fruit weight (0.00), and hundred seed weight (14.24) while negative indirect effect on days to emergence (-6.16), days to first female flower appearance (-3.75), leaf breadth (-2.00), peduncle length (-4.34), fruit breadth (-2.45), number of fruit per plant (-0.78), seed length (-19.15) and seed breadth (-0.35). It showed non-significant and negative genotypic correlation (-0.01) with fruit yield per plant (Table 9).

4.5.9 Peduncle length

Path coefficient analysis revealed that peduncle length had a negative and direct effect (-18.06) on fruit yield per plant. Peduncle length had positive and indirect effect on days to emergence (6.65), days to first female flower appearance (10.27), internode length (2.55), leaf breadth (2.53), petiole length (3.86), fruit breadth (5.26), number of fruit per plant (0.86) and seed breadth (0.26) while negative indirect effect on days to first male flower appearance (-3.65), number of primary branch (-0.90), leaf length (-0.51), fruit length (-6.21), fruit weight (-0.06), seed length (-0.45) and hundred seed weight (-2.32). It showed non-significant and positive genotypic correlation (0.08) with fruit yield per plant (Table 9).

4.5.10 Fruit length

Path coefficient analysis revealed that fruit length had a negative and direct effect (-14.08) on fruit yield per plant. Fruit length had positive and indirect effect on days to emergence (7.28), days to first female flower appearance (1.01), internode length (2.37), leaf breadth (2.97), fruit breadth (5.23), seed length (0.64), seed breadth (0.05) and hundred seed weight (9.07) while negative indirect effect on days to first male flower appearance (-1.57), number of primary branch (-3.47), leaf length (-0.44), petiole length (-0.60), fruit weight (-0.13) and number of fruit per plant (-0.03). It showed highly significant and positive genotypic correlation (0.34) with fruit yield per plant (Table 9).

4.15.11 Fruit breadth

Path coefficient analysis revealed that fruit breadth had a positive and direct effect (20.80) on fruit yield per plant. Fruit breadth had positive and indirect effect on days to emergence (3.44), days to first female flower appearance (2.94), internode length (0.10), leaf length (2.38) and seed length (5.17) while negative indirect effect on days to first male flower appearance (-2.92), number of primary branch (-5.82), leaf breadth (-5.15), petiole length (-1.89), fruit weight (-0.07), number of fruit per plant (-0.39), seed breadth (-0.68) and hundred seed weight (-9.64). It showed non-significant and positive genotypic correlation (0.16) with fruit yield per plant (Table 9).

4.5.12 Fruit weight

Path coefficient analysis revealed that fruit weight had a negative and direct effect (-0.21) on fruit yield per plant. Fruit weight had positive and indirect effect on days to emergence (7.13), days to first female flower appearance (9.25), internode length (4.03), leaf breadth (2.16), fruit breadth (7.12), seed breadth (1.16) and hundred seed weight (8.85) while negative indirect effect on days to first male flower appearance (-14.57), number of primary branch (-5.66), leaf length (-0.23), petiole length (-0.39), peduncle length(-5.47), fruit length(-9.08), number of fruit per plant (-2.88) and seed length (-0.67). It showed highly significant and positive genotypic correlation (0.54) with fruit yield per plant (Table 9).

4.5.13 Number of fruit per plant

Path coefficient analysis revealed that number of fruit per plant had a negative and direct effect (-9.71) on fruit yield per plant. Number of fruit per plant had positive and indirect effect on days to first male flower appearance (0.82), internode length (9.61), leaf length (1.43), petiole length (1.30), peduncle length(1.60), fruit breadth (0.83), seed length (6.88) and hundred seed weight (9.53) while negative indirect effect on days to emergence (-9.06), days to first female flower appearance (-3.88), number of primary branch (-2.68), leaf breadth (-4.66), fruit length (-0.04), fruit weight (-0.06), and seed breadth (-1.08). It showed highly significant and positive genotypic correlation (0.83) with fruit yield per plant (Table 9).

4.5.14 Seed length

Path coefficient analysis revealed that seed length had a positive and direct effect (43.06) on fruit yield per plant. Seed length had positive and indirect effect on days to emergence (2.07), leaf length (0.05), leaf breadth (1.15), peduncle length (0.19), fruit breadth (2.47) and fruit weight (0.00) while negative indirect effect on days to first male flower appearance (-10.53), days to first female flower appearance (-6.01), internode length (-5.06), number of primary branch (-3.58), petiole length (-7.06), fruit length (-0.21), number of fruit per plant (-1.53), seed breadth (-1.02) and hundred seed weight (-14.48). It showed non-significant and positive genotypic correlation (0.05) with fruit yield per plant (Table 9).

4.5.15 Seed breadth

Path coefficient analysis revealed that seed breadth had a negative and direct effect (-5.93) on fruit yield per plant. Seed breadth had positive and indirect effect on days to emergence (2.07), leaf length (0.05), leaf breadth (1.15), peduncle length (0.19), fruit breadth (2.47) and fruit weight (0.00) while negative indirect effect on days to first male flower appearance (-10.53), days to first female flower appearance (-6.01), internode length (-5.06), number of primary branch (-3.58), petiole length (-7.06), fruit length (-0.21), number of fruit per plant (-1.53), and hundred seed weight (-14.48). It showed non-significant and positive genotypic correlation (0) with fruit yield per plant (Table 9).

4.5.16 Hundred seed weight

Path coefficient analysis revealed that hundred seed weight had a positive and direct effect (40.04) on fruit yield per plant. Hundred seed weight had positive and indirect effect on number of primary branch (0.28), leaf length (0.64), petiole length (5.72) and peduncle length (1.05) while negative indirect effect on days to emergence (-6.10), days to first male flower appearance (-8.90), days to first female flower appearance (-3.59), internode length (-0.14), leaf breadth (-1.38), fruit length (-3.19), fruit breadth (-5.00), fruit weight (-0.05), number of fruit per plant (-2.31), seed length (-15.77) and seed breadth (1.09)It showed non-significant and positive genotypic correlation (0.21) with fruit yield per plant (Table 9).

Table 9. Path analysis showing direct and indirect effects of different characters on fruit yield per plant of thirty ridge gourd germplasms.

Traits	DE	DMF	DFF	IL	NPB	LL	LB	PL	PeL	FL	FB	FW	NFP	SL	SB	HSW	Genotypic correlation with FYP
DE	**27.14**	-5.12	-2.76	-4.46	-8.18	-1.04	4.53	-3.65	-4.43	-3.78	2.64	-0.05	3.24	3.33	1.38	-9.00	**-0.21***
DMF	-2.46	**56.35**	-31.85	0.92	-6.04	-0.17	-3.40	0.86	1.17	0.39	-1.08	0.05	-0.14	-8.14	-0.30	-6.33	**-0.17ns**
DFF	1.66	39.77	**-45.14**	-2.29	-5.16	-0.48	-0.48	1.33	4.11	0.31	-1.35	0.04	-0.83	5.80	-0.57	3.19	**-0.09ns**
IL	-6.00	2.59	5.12	**20.16**	-1.95	1.19	-5.57	3.58	-2.29	-1.66	0.10	-0.04	-4.63	-10.95	1.07	-0.28	**0.44****
NPB	10.07	15.43	-10.56	1.79	**-22.05**	0.79	-3.77	-0.30	-0.74	-2.22	5.49	-0.05	-1.18	7.07	0.90	-0.51	**0.16ns**
LL	-4.86	-1.70	3.69	4.12	-3.00	**5.81**	-14.62	0.63	1.60	1.06	8.53	0.01	-2.39	0.35	-3.50	4.39	**0.12ns**
LB	-7.05	10.98	-1.25	6.43	-4.76	4.86	**-17.45**	1.85	2.62	2.40	6.14	0.03	-2.59	-2.88	-2.32	3.16	**0.17ns**
PL	-6.16	3.00	-3.75	4.49	0.41	0.23	-2.00	**16.07**	-4.34	0.53	-2.45	0.00	-0.78	-19.15	-0.35	14.24	**-0.01ns**
PeL	6.65	-3.65	10.27	2.55	-0.90	-0.51	2.53	3.86	**-18.06**	-6.21	5.26	-0.06	0.86	-0.45	0.26	-2.32	**0.08ns**
FL	7.28	-1.57	1.01	2.37	-3.47	-0.44	2.97	-0.60	-7.96	**-14.08**	5.23	-0.13	-0.03	0.64	0.05	9.07	**0.34****
FB	3.44	-2.92	2.94	0.10	-5.82	2.38	-5.15	-1.89	-4.57	-3.54	**20.8**	-0.07	-0.39	5.17	-0.68	-9.64	**0.16ns**
FW	7.13	-14.57	9.25	4.03	-5.66	-0.23	2.16	-0.39	-5.47	-9.08	7.12	**-0.21**	-2.88	-0.67	1.16	8.85	**0.54****
NFP	-9.06	0.82	-3.88	9.61	-2.68	1.43	-4.66	1.30	1.60	-0.04	0.83	-0.06	**-9.71**	6.88	-1.08	9.53	**0.83****
SL	2.07	-10.53	-6.01	-5.06	-3.58	0.05	1.15	-7.06	0.19	-0.21	2.47	0.00	-1.53	**43.6**	-1.02	-14.48	**0.05ns**
SB	-6.34	2.89	-4.31	-3.64	3.34	3.43	-6.82	0.94	0.81	0.11	2.39	0.04	-1.77	7.52	**-5.93**	7.34	**0ns**
HSW	-6.10	-8.90	-3.59	-0.14	0.28	0.64	-1.38	5.72	1.05	-3.19	-5.00	-0.05	-2.31	-15.77	-1.09	**40.04**	**0.21**

Here, DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant

***= 5% level of significant, **= 1% level of significant, ns= Non-significant. The diagnoal elements are direct effects while off-diagonal elements are indirect effects. Residual effect 10.80%**

4.6 Genetic Diversity

4.6.1 Principal component analysis

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. The Principal Components analysis yielded eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 18.33% of the total variation among the genotypes, whereas five of these eigen values above unity accounted for 66.62%. The first four principal axes accounted for 57.1% of the total variation among the 17 characters describing in 30 different ridge gourd genotypes (Table 10). In the principal component analysis; the second, third, fourth and fifth components accounted for 16.46%, 12.02%, 10.29%, and 9.52% of the total variation, respectively. The rest of the components accounted for only 33.38% of the total variation (Table 10). Based on principal component axis I and II, a two-dimensional chart (Z1-Z2) of the genotypes are presented in Figure 4. The scatter diagram (Figure 4) represented that apparently there were mainly five clusters, and the genotypes were distantly located from each other.

4.6.2 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two-dimensional (Z1-Z2) scatter diagram was constructed, using component score 1 as X-axis and component score 2 as Y-axis, which is presented in figure 4. The positions of the genotypes in the scatter diagram were random, which indicated the considerable diversity among the genotypes included in the cluster.

Scree Plot: Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 18.3 % variability with eigen value 3.11 which then declined gradually and semi curve line is obtained (Table 10). From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other 10 PCs. So, selection of lines from this PC will be useful (Fig.2). Those principal components having more than one eigen value that showed more variation among the ridge gourd genotypes for the selection of the diverse parents.

Table 10. Eigen values and yield percent contribution of 17 characters of 30 different ridge gourd germplasms

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
GI	3.11	18.33	18.33
GII	2.79	16.46	34.79
GIII	2.04	12.02	46.81
GIV	1.74	10.29	57.11
GV	1.61	9.52	66.63
GVI	1.29	7.60	74.24
GVII	0.97	5.74	79.98
GVIII	0.77	5.45	84.52
GIX	0.61	3.62	88.14
GX	0.48	2.84	90.99
GXI	0.43	2.56	93.56
GXII	0.30	1.77	95.33
GXIII	0.25	1.48	96.81
GXIV	0.23	1.38	98.20
GXV	0.14	0.82	99.02
GXVI	0.12	0.72	99.74
GXVII	0.04	0.25	100.00

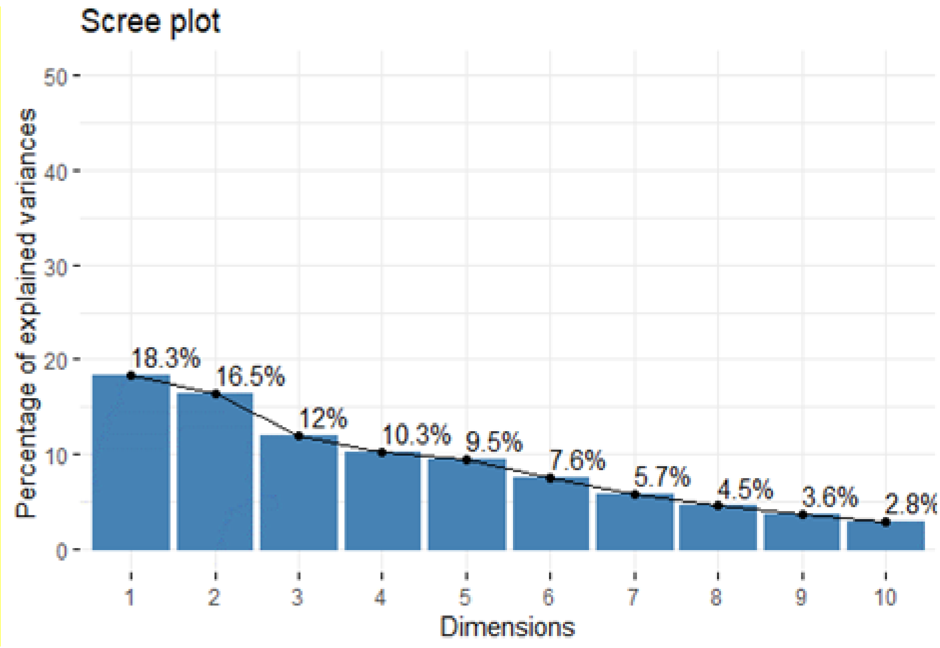


Figure 2. Scree plot showing percentages of explained variances of different genotypes

Principal component biplot

The genotypes by traits biplot were constructed from a two-way matrix of 17 morpho-physiological traits and 30 ridge gourd genotypes using the relative value of the trait (Figure 2). Again, biplot analysis showed the trait profiles of the the genotypes, especially, those genotypes positioned far away from the origin and the results indicated a correlation between traits with genotypes. Again, traits on opposite sides of the origin are negatively correlated and traits near each other are positively correlated. Moreover, traits at 90° to each other are not correlated, concerning the origin.

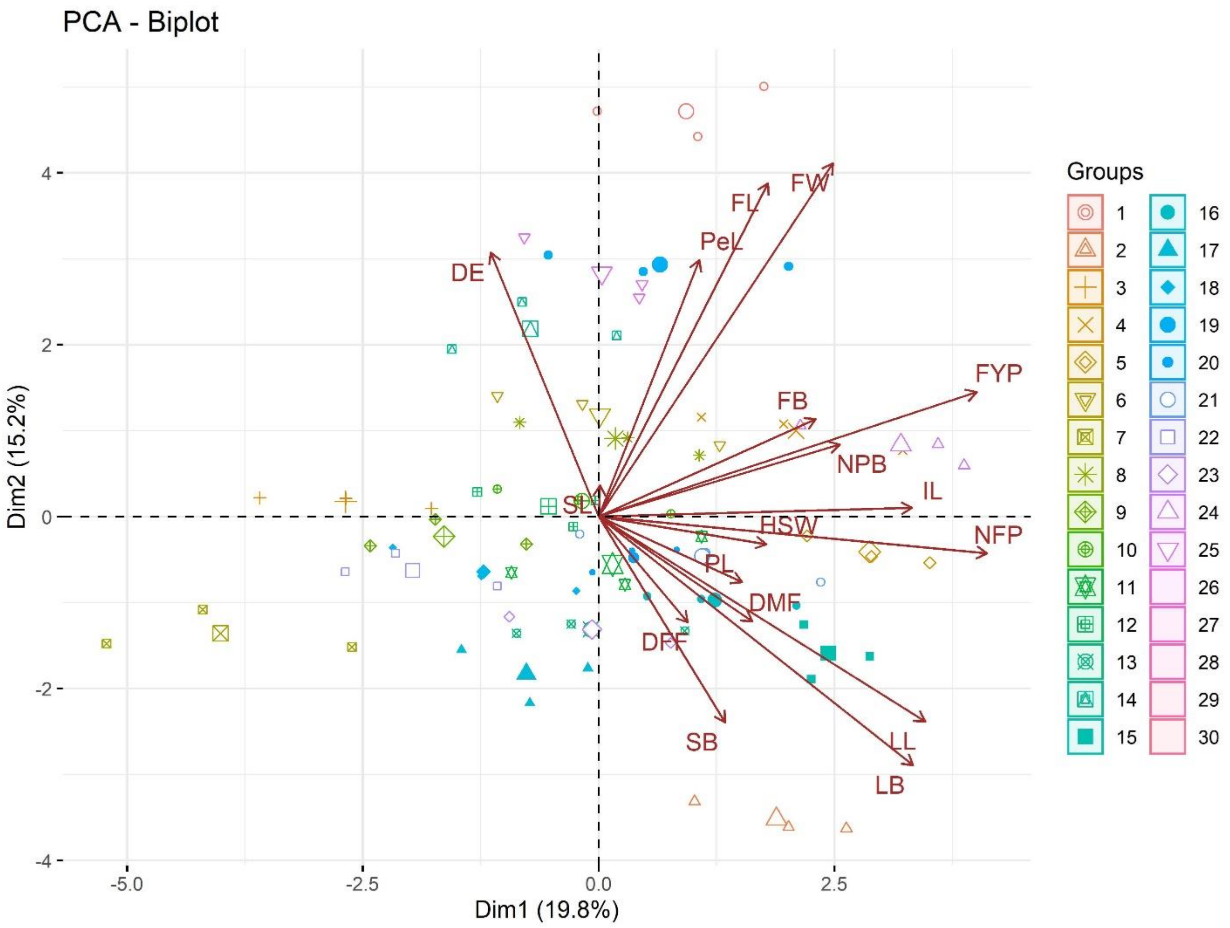


Figure 3. Genotypes by traits (G×T) biplot based on 30 germplasms and 17 quantitative traits of ridge gourd.

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruits per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg).

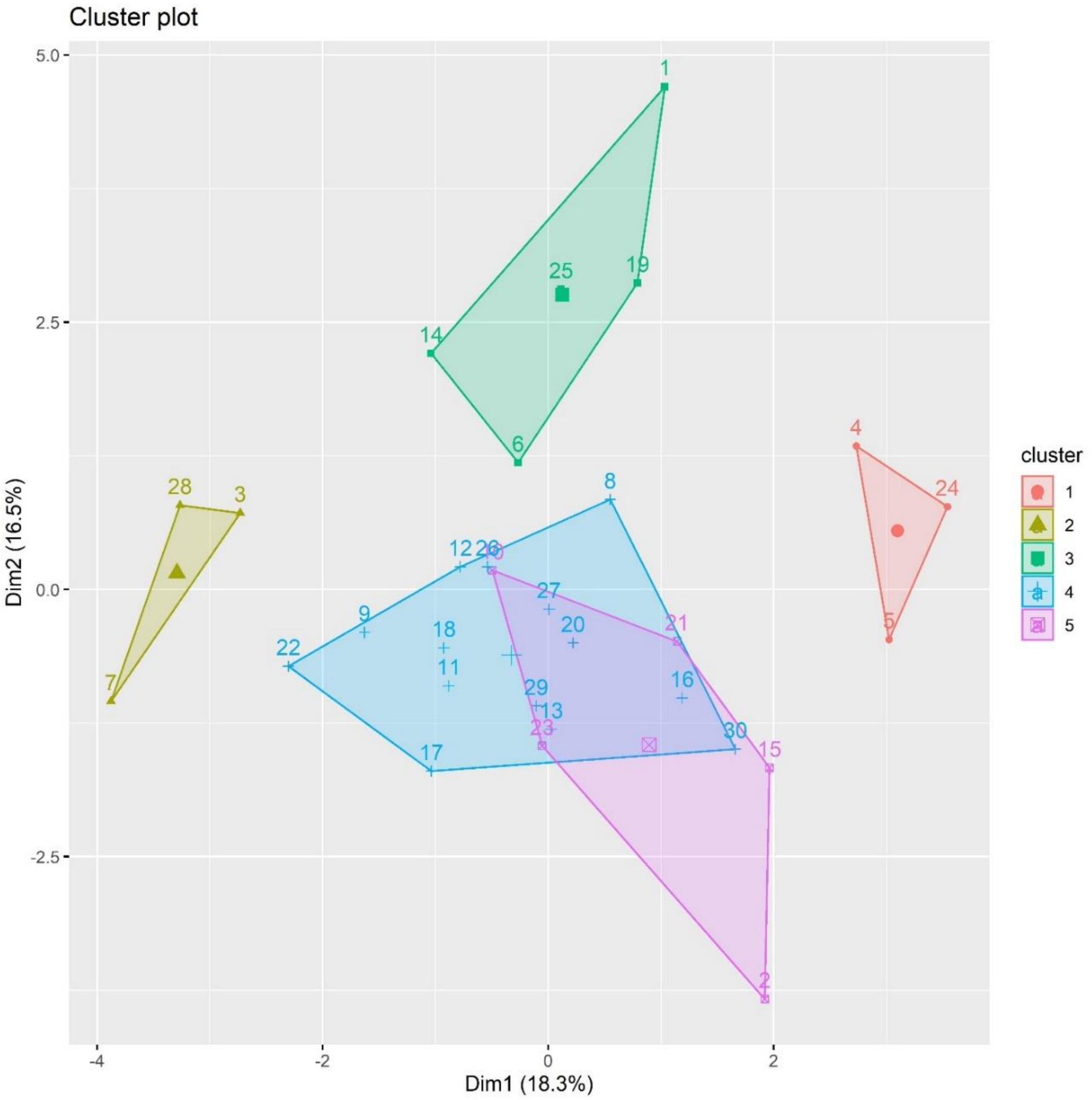


Figure 4. Scatter distribution of 30 ridge gourd genotypes based on their principal component scores superimposed with clustering

Table 11. Distribution of 30 ridge gourd genotypes in five different clusters

Cluster no.	Genotypes	No. of genotypes
I	G4, G5, G24	3
II	G3, G7, G28	3
III	G1, G6, G14, G19, G25	5
IV	G8, G9, G11, G12, G13, G16, G17, G18, G20, G22, G26, G27, G29, G30	14
V	G2, G10, G15, G21, G23	5
Total		**30**

Table 12. Cluster mean values of 17 different traits of 30 different ridge gourd germplasms

Traits	I	II	III	IV	V
DE	-0.59	0.42	1.28	-0.39	-0.08
DMF	-0.65	-0.84	-0.13	0.31	0.14
DFF	-0.61	-0.44	-0.09	0.16	0.27
IL	1.33	-0.59	-0.32	0.05	-0.26
NPB	0.22	-0.23	0.50	-0.48	0.86
LL	0.24	-1.17	-0.47	-0.10	1.33
LB	0.42	-0.59	-0.39	0.38	-0.59
PL	0.32	-0.69	1.10	-0.13	-0.50
PeL	-0.14	-1.65	1.44	-0.002	-0.35
FL	0.18	-0.57	0.55	-0.42	0.85
FB	0.84	-0.96	1.41	-0.35	-0.34
FW	2.06	-1.21	-0.37	-0.08	0.09
NFP	-0.07	0.10	-0.25	-0.29	1.05
SL	-0.30	-1.45	-0.61	0.32	0.76
HSW	0.05	-1.21	-0.03	0.32	-0.18
FYP	2.28	-1.23	0.25	-0.27	-0.12

4.6.3 Cluster analysis

The experiment was conducted to investigate the genetic diversity of thirty genotypes of ridge gourd. The genotypes were divided into five different clusters (Table 11). The cluster IV had (G8, G9, G11, G12, G13, G16, G17, G18, G20, G22, G26, G27, G29, G30) maximum number of genotypes (14) followed by cluster III and V which had 5 genotypes. Cluster I and II had 3 genotypes each respectively. Remarkably cluster III had five (G1, G6, G14, G19, G25) and cluster V had five (G2, G10, G15, G21, G23) genotype. Where, cluster I and II carried the lowest number (3) of genotypes. Cluster I contained (G4, G5, G24) and cluster II had (G3, G7, G28). Two genotypes each clustering was done at random that indicate a broad genetic base of the genotypes.

4.6.4 Non-hierarchical clustering

By using covariance matrix with the application of non-hierarchical clustering, the 30 ridge gourd genotypes were grouped into five different clusters. These results confined the clustering pattern of the genotype according to the principal component analysis. Compositions of different clusters with their corresponding genotypes in each cluster were presented in (Table 11). These results confirmed the clustering pattern of the genotypes according to the principal component analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering.

4.6.4.1 Cluster I

Cluster I had three genotypes namely G4, G5, G24 (Table 11). From the clustering mean values (Table 12), it was observed that cluster I produced the highest mean for fruit yield per plant (2.28) followed by fruit weight (2.06), internode length (1.33) and others.

4.6.4.2 Cluster II

Cluster II was composed of three genotypes namely G3, G7, G28 (Table 11). These genotypes produced the highest mean for days to emergence (0.42) followed by number of fruit per plant (0.10) and others.

4.6.4.3 Cluster III

Cluster III consists of five genotypes (G1, G6, G14, G19, G25) (Table 11). From the clustering mean values (Table 12), it was observed that cluster III produced the highest mean values for peduncle length (1.44) followed by fruit breadth (1.41), days to emergence (1.28), petiole length (1.10), fruit length (0.55) and others.

4.6.4.4 Cluster IV

Cluster IV had maximum number (14) of genotypes namely (G8, G9, G11, G12, G13, G16, G17, G18, G20, G22, G26, G27, G29, G30) (Table 11). From the clustering mean values (Table12), it was observed that cluster IV produced the highest mean values for leaf breadth (0.38) followed by seed length (0.32), hundred seed weight (0.32), days to first male flower appearance (0.31) and others.

4.6.4.5 Cluster V

Cluster V consists of five genotypes namely G2, G10, G15, G21, G23 (Table 11). From the clustering mean values (Table 12), it was observed that cluster I produced the highest mean for leaf length (1.33) followed by number of fruit per plant (1.05), number of primary branch (0.86), fruit length (0.85) and others. The lowest mean value for cluster V (-0.59) was the leaf breadth.

4.6.5 Heatmap Analysis

The heatmap represented the overall performance of 17 observable traits among the 30 germplasms. A heatmap is a two-dimensional data visualization technique that uses color to show the scope of a phenomenon. Color variation by hue or intensity provides the reader with a visual representation of how the phenomenon is grouped or varies over space. It depicts the relative patterns of highly abundant features against a background of mostly low-abundance features (Figure 5). Heatmap displaying the relationship matrix among ridge gourd genotypes. The yellow diagonal represents a perfect relationship of each accession with itself. The symmetric off diagonal elements represent the relationship measures for pairs of genotypes. The sky blue colors on the diagonal show clusters of closely related genotypes.

A heatmap analysis of characteristics was performed to demonstrate a chromatic examination of the genotypes. The heatmap analysis produced two dendrograms: one in the vertical direction, representing the traits that caused the diffusion, and one in the horizontal direction, representing the germplasm. The yellow diagonal depicts each accession’s perfect connection to itself. The relationship measurements for pairs of germplasm are represented by the symmetric off-diagonal elements. Based on the morpho-physiological properties of the germplasm studied, five clusters emerged through hierarchical clustering (Figure 5). Group (a) included 18 germplasm from clusters III (2 germplasms), IV (12germplasms) and IV (4 germplasms) while group (b) included the remaining 12 germplasms from two clusters. Out of a total of 12 germplasm, cluster I received 3 germplasms and cluster II received 9 germplasms (Figure 5). Dendrogram two also revealed two significant groups: group (a) is associated with seven traits (FB, PeL, FL, FW, SL, DE, and NPB), while group (b) is associated with three traits (IL, NFP, FYP, DMF, DFF, SB, LL, LB, PL and HSW). Surprisingly, the dendrogram two groups and sub-groups revealed the disparity effects of different ridge gourds.

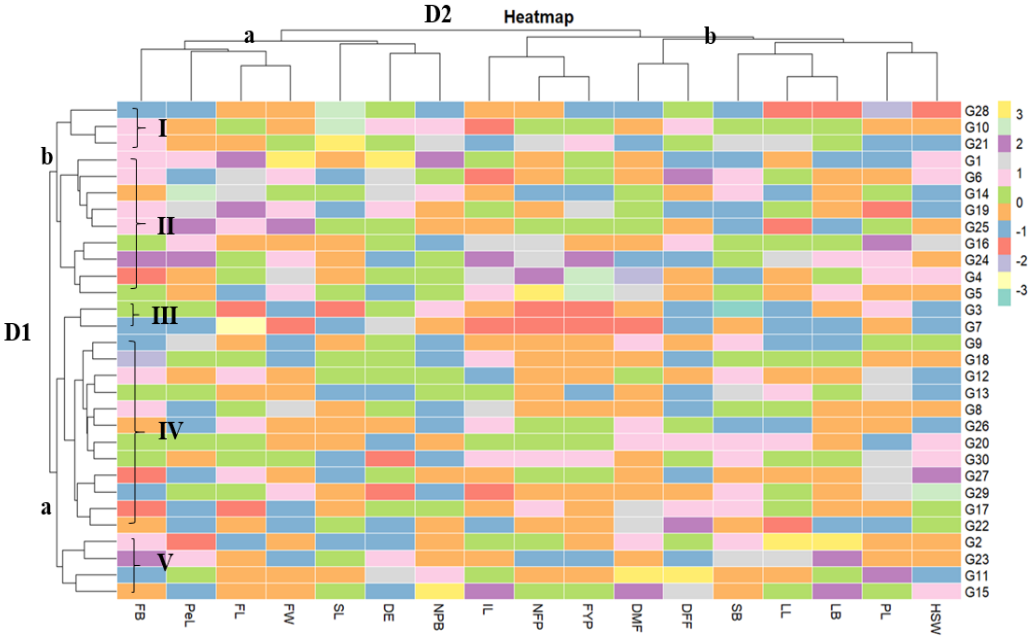


Figure 5. Heatmap showing the clustering pattern of 30 ridge gourd genotypes with 17 morpho physiological traits.

DE = Days to emergence, DMF = Days to first male flower appearance, DFF = Days to first female flower appearance, IL = Internode length (cm), NPB = Number of primary branch, LL = Leaf length (cm), LB = Leaf breadth (cm), PL = Petiole length (cm), PeL = Peduncle length (cm), FL = Fruit length (cm), FB = Fruit breadth (cm), FW = Fruit weight (g), NFP = Number of fruit per plant, SL = Seed length (cm), SB = Seed breadth (cm), HSW = Hundred seed weight (g), FYP = Fruit yield per plant (kg).

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was undertaken to evaluate a set of genotypes for variability in morphological characters, extent of character association and genetic diversity to find out the variability regarding yield and some yield contributing characters, the degrees of association among the characters under study and their indirect and direct effects. The material for this study comprised of 32 rice genotypes at the experimental plot of Sher-E-Bangla Agricultural University farm, Dhaka, during July to October 2021.

The experiment was laid out in randomized complete block design with three replications. Days to emergence, days to first male flower appearance, days to first female flower appearance, internode length (cm), number of primary branch, leaf length (cm), leaf breadth (cm), petiole length (cm), peduncle length (cm), fruit length (cm), fruit breadth (cm), fruit weight (g), number of fruit per plant, seed length (cm), seed breadth (cm), hundred seed weight (g), fruit yield per plant (kg) were recorded. The most important findings of the present study have been summarized on the basis of the characters under study. In case of days to emergence, the highest value was recorded in G1 (11 days) whereas the minimum days to emergence was recorded in G29 and g30 (5 days). The days to first male flower was maximum in G11 (43 days) and minimum was observed in G4 (29.67 days). The days to first female flower appearance were highest in G11 (57.67 days) and lowest was observed in G18 (35 days). In respect of internode length, the maximum value was observed in G15 (18.33 cm) and minimum was in G29 (7.00 cm). The no. of primary branches per plant was maximum in G15 (11.33) and minimum was observed in G28 (3.67). In case of leaf length,it was found that the maximum value was in G2 (27.13 cm) and minimum was in G22 (16.10 cm). The leaf breadth was maximum in G2 (32 cm) and minimum was observed in G28 (17.23 cm). In respect of petiole length, the highest value was in G16 (16 cm) and lowest was in G28 (7.33 cm). The peduncle length was maximum in G14 (15.70 cm) and minimum was observed in G2 (3.87 cm). The fruit length was maximum in G26 (42.50 cm) and minimum was observed in G7 (12.87 cm). The fruit breadth was maximum in G23 (4.47 cm) and minimum was observed in G18 (2.43 cm). The highest fruit weight was found in G1 (258.42 g) and lowest was G7 (52.36 g). In case of fruit per plant, the maximum value was observed in G5 (54.) and minimum was in G3 (1.13). The highest seed length was recorded maximum in G21 (1.86 cm) and minimum was in G3 (1.13 cm). The highest seed breadth was found in G13 (0.90 cm) and the lowest was in G3 (0.50 cm). The hundred seed weight was maximum in G29 (19.00 g) and minimum was observed in G28 (13.00 g). The fruit yield per plant was recorded maximum in G5 (4.65 g) and minimum was observed in G3 (0.59 g). The phenotypic variance was higher than genotypic variance in all the characters under study. Phenotypic coefficients of variation were also near to genotypic coefficients of variation for all the characters under study.

The high heritability coupled with high genetic advance observe in fruit weight and no. of fruit per plant. High heritability coupled with low genetic advance was found in days to emergence, internode length, number of primary branch, leaf length, leaf breadth, petiole length, peduncle length, fruit breadth, seed length, seed breadth, hundred seed weight, fruit yield/plant. High heritability and moderate genetic advance was observed in fruit length and days to first female flower. Moderate heritability with low genetic advance was found in days to first male flower.

Correlation revealed that highly significant positive association of fruit yield per plant with internode length, leaf length, fruit length, fruit weight and number of fruit per plant at both genotypic and phenotypic level. Genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient. This indicates greater contribution of genetic factor in the development of the association.

The path coefficient analysis revealed the positive direct effect on yield per plant by days to emergence, days to first male flower, internode length, leaf length, petiole length, fruit breadth, seed length and hundred seed weight.

Multivariate analysis was performed through Principal component analysis, Principal coordinate analysis, Cluster analysis and canonical variety analysis. The PCA showed 66.62% variation against first five values. Based on the PCA and cluster analysis thirty genotypes were grouped into five different clusters.

Cluster I showed maximum performance for fruit yield per plant (2.28). Cluster II showed maximum performance for days to emergence (0.42), and number of fruit/plant (0.10). Cluster III recorded highest mean performance for peduncle length (1.44), fruit breadth (1.41), days to emergence (1.28), and petiole length (1.10). Cluster IV showed maximum performance for leaf breadth (0.38), seed length and seed weight both are (0.32). Cluster V show maximum performance for leaf length (1.33) and number of fruits per plant (1.05).

Considering the degree of variability, heritability, genetic advance in percent of mean, correlation with grain yield, path analysis, magnitude of distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and performance, the genotypes G4, G5 and G24 for yield per plant from cluster I; G1 and G19 for fruit length from cluster III might be considered better parents for efficient hybridization program.

The result of the present study revealed that a wide variability exists among the collected ridge gourd genotypes. In addition, there was also association of different yield 88 contributing characters with yield of ridge gourd. From the findings of the present study. The following conclusions could be drawn:

i. Wide range of genetic diversity existed among the ridge gourd genotypes. That variability could be used for future breeding programme of' ridge gourd in Bangladesh.

ii. Selection procedure would be applied for desired characters such as lowest days to first male flower, first female flower, fruit length, fruit breadth, number of fruits per plant to develop high yielding varieties.

iii. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like average fruit weight, number of fruits per plant, yield per plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

iv. Further collection of ridge gourd germplasm would be continued for getting more variability and desired traits in ridge gourd.

CHAPTER VI

REFERENCES

Abusaleha and Dutta, O.P. (1990). Studies on variability, heritability and scope of improvement in cucumber. *Haryana J. Hort. Sci.* **19**(3-4):349-352.

Abusaleha and Dutta, O.P. (1989). Interrelationship of yield components in cucumber. Veg. Sci. **15**(1):75-85.

Allard, R.W. (1960) Principles of Plant Breeding. John Wiley and Sons. New York. p.36.

Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agro. J.* **50**(10): 633–636.

Ananda, I.J. and Rawat, D.S. (1984). Genetic diversity, combining ability and heterosis in brown mustard. *Indian J. Genet.* **44**: 226-234.

Ananthan, M. and Pappoah, C.M. (1997). Combining ability and correlation studies in cucumber *(Cucumis sativus L.). South Indian Hort.* **45** (1 &2): 57-58.

Ansari, N. M., Houlihan, L., Hussain, B. and Pieroni, A. (2005). Antioxidant activity of five vegetables traditionally consumed by South-Asian migrants in Bradford, Yorkshire, UK. Phytother. Res. **19**(10): 907–911.

Apu, M.M.R.B., Hossain, P.D.M.I and Saha, D.S.R. (2013). Variability characters association and path co-efficient analysis of ridge gourd. M.S.Thesis Dept. Of Horticulture, SAU, Dhaka.

Ashok, P. and Rajan, S. (2002). Principal component analysis of growth, yield and seed characters of snake gourd *(Trichosanthes anguina L.). Veg. Sci.* **29**(2):137-141.

Badade, D.S., Warade, S.D. and Gaikwad, S.K. (2001). Genetic divergence in bottle gourd. *J. Maharashtra Agric. Univ.* **26** (1-3): 137-139.

Banik, B.R. (2003). In nheritance pattern in snake gourd *(Trichosanthes anguina L.).* Ph, D Thesis. Department of Genetics and Plant Breeding. Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. pp. 1-60.

BBS. (2016). Bangladesh Bureau of Statistics, Year book of Agricultural Statistics, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka. p.207.

BBS. (2008). Monthly Statistical Bulletin, Bangladesh (August). Bangladesh Bureau of Statistics, Planning Division, Ministry of Planning, Government of Bangladesh. p. 66.

Belaj, A., Satovic, Z., Rallo, L. and Trusillo. (2002). Genetic diversity and relationship in olive (*Olea europea* L.) germplasm collection as determined by RAPD. Theor. *Appl. Genet.* **105**(4): 638-644.

Bijalwan, P., Singh, M. and Madhavi, N. (2018). Assessment of Genetic Divergence in Chilli (Capsicum annuum L.) Genotypes. *Int. J. of Current Microbiology and Applied Sci.* **7:** 1585–1590.

Bora, G.C., Bordoloi, S.P., Gogoi, S. Das, R. M., Phukan, M., Kachari, Deka, N.C. and Pau, S.K. (2015). Direct *Res. J. of Agric. and Food Sci*. **3**(1): pp.7-9.

Carreira, J.C.A., Brazil, R.P., Carvalho, B.S. and Silva, A.V.M. (2018). Breeding—A Probable Breeding Substrate in Nature. *Open J. of Animal Sci.* **8**(4): 370–380.

Chen, J.F., Staub, J., Adelberg, J., Lewis, S. and Kunkle, B. (2002). Synthesis and preliminary characterization of a new species in *Cucumis. Euphytica***, 123**(3): 315-322.

Chetariya, C. and Vaddoria, M. (2017). Genetic divergence analysis in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.]. *J. of Applied and Natural Sci.* **9**:1949–1953.

Choudhury, B.D., Bhat, P.N. and Singh, V.P. (1975). Genetic diversity in cluster beans. *Indian J. Agric. Sci.* **45**: 510-535.

Choudhary, B. R., Pandey, S., Bhardwaj, D. R., Yadav, D. S. and Rai, M. (2008). Component analysis for qualitative traits in ridge gourd (*Luffa acutangula* (Roxb. L.). Vegetable Sci. **35**(2): 144-147.

Choudhary, M.I. and Mandal, G. (1987). Correlation and path analysis in cucumber *(Cucumis sativus L.). Haryana J. Hort. Sci.* **16** (3&4): 269-273.

Chowdhury, D. and Sharma, K.C. (2002). Studies on variability, heritability, genetic advance and correlations in ridge gourd (*Luffa acutangula* L.). *Hort. J.* **15** (3): 53-8.

Comstock, K. and Robinson, P.R. (1952). Estimation of genetic advance. *Indian J.* Hill. **6**(2): 171-174.

Crossa, J., Hernandez, C.M., Bretting, P., Eberhart, S.A. and Taba, S. (1993). Statistical genetic considerations for maintaining germplasm collections. *TAG. Theor. and App. Gen. Theoretische Und Angewandte Genetik*. **86**(6): 673–678.

Devmore J.P., Dhonukshe B.L., Thaware, B.L., Bendale, V.W., Jadhav, B.B., and Thprat, T.N. (2010). Genetic variability and heritability studies in ridge gourd. *J.* of *Maharashtra Agri. Uni.* **35**(1): 163-165.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agro. J.* **51:** 515-518.

Dora, D.K., Behera, T.K., Acharya. G.C., Das, S., Mahapatra, P. and Mishra, B. (2003). Genetic variability and character association in pointed gourd *(Trichosanthes dioica Roxb.). Indian J. Hort.* **60**(2): 163-166.

El-Sharkawy, M.A. (2012). Stress-Tolerant Cassava: The Role of Integrative Ecophysiology-Breeding Research in Crop Improvement. *Open J. of Soil Sci.* **2**(2): 162–186.

Ferdous, F., Nath, U. and Islam, A. (2011). Genetic divergence and genetic gain in bread wheat through selection practices. *J. of the Bang. Agri. Uni*. p. 150.

Gaur, P., Gupta, C. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica.* **27**:361 -368.

Gautam, A., Suresh, J. and Sheshu M. (2016). Study of genetic variability in genotypes of rice (*Oryza sativa* L.). *Res. J. of Agric. Sci.* **(7):**235–236.

Girgis, P. and Said, F. (1968). Lesser known Nigerian edible oils and fat characteristics of melon seeds. *J. Sci. Food Agric*. **19**(10): pp. 615-616.

Gomez, K.A. and Gomez, A.A. (1984). Statistical procedure for Agricultural Research (2nd edn.). Int. Rice Res. Inst., A Willey Int. Sci. pp. 28-192.

Gowda, H. (2011). Genetic variability studies in ridge gourd (*Luffa acutangula* L.). An M.Sc thesis. University of Horticultural Sciences, Bagalkot, India. p.148.

Guffar, A. (2008). Characterization and genetic diversity of sponge gourd *(Luffa cylindrica L.).* M. Sc. Thesis. Dept. Genetics and Plant Breeding, SAU, Dhaka.

Hedau, N.K. and Sirohi, P.S. (2004). Combining ability for yield and its contributing characters in ridge gourd. *Prog Hort.* **36**(1):91–93.

Hossain, M.S. (1996). Floral biology of ridge gourd. M. Sc. Thesis. Dept. of Genetics A and Plant Breeding, IPSA, Salna, Gazipur.

Islam, M.N. (1993). Studies on heterosis and combining ability in bottle gourd. M. Sc. Thesis. Dept. Genetics and Plant Breeding, BSMRAU Gazipur.

Jahan, T., Islam, M., Begum, A. and Rahman, MS. (2019). Characterization of ridge gourd germplasm. pp. 300-312.

Jain, S. K., Qualset, C. O., Bhatt, G. M. and Wu, K. K. (1975). Geographical patterns of phenotypic diversity in a world collection of Durum Wheat. *Crop Sci.* **15**: 700-704.

Johnson, H.W., Robinson, H.F. and Comstock. R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-318.

Joseph, S. (1978). Genetic variability and correlation studies in snake gourd *(Trichosanthes anguina L.)* M. Sc. Thesis. Kerala Agricultural University. Trissur, Kerala. India. p.120.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement of yield with special reference to self fertlilization. *Crop Ind. J. Genet. Plant Breed*. **26**: 101-113.

Kamel, B. S. and Blackman, B. (1982). Nutritional and oil characteristics of the seeds of angled *Luffa acutangula* [cucurbit vegetable]. Food Chemistry (UK). pp. 102-103.

Karuppaiah, P., Kavitha. R. and Senthilkumar, P. (2005). Divergent analysis in ridge gourd (*Luffa)*. India: Palani paramount publications. pp. 123-125.

Kumar, S., Singh, R. and Pal, A.K. (2007). Genetic variability, heritability, genetic advance, correlation coefficient and path analysis in bottle gourd. *Indian J. Hort.* **64**(2): 163-168.

Kumaran, S.S., Natarajan, S. and Thamburoj, S. (1998). Correlation and path analysis studies in pumpkin *(Cucurbita moschata* poir.*). South Indian Hort.* **46**(3&6): 138-142.

Levy, S.G. (2017). Erratum to the faraday isolator, detailed balance and the second law. *J. of Applied Mathematics and Physics*, **5**(8): 1537–1539.

Li, J.W., Sun, S.R. and Rer, Y.H. (1997). Study on genetic correlation, path analysis of the main agronomic characters of cucumber. Acta. Agricultural University, Henamensis. **31**(3): 244-247.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proc. Nat. Inst. Sci. India. **2**: 49-55.

Mannan, M.A. (1992). Studies on variability, genetic parameters and correlation in bitter gourd. M. Sc. Thesis. Dept. Genetics and Plant Breeding, BAU, Mymensingh. pp. 28-65.

Manoj, Y.B., Lakshmana, D., Shashikala, S.K. And Chandana, B.C. (2018). Assessment of genetic diversity and variability in ridge gourd for growth and yield parameters. Green Farming. **9**(2): 239-243.

Martin, F. W. (1979). Sponge and bottle gourds, *Luffa* and *Lagenaria*. pp. 1-19.

Methela N.J., Islam, M.S., Mitu, N. and Latif, M.A. (2019). Mean performance and heritability studies of some ridge gourd (*Luffa acutangula* L.) genotypes. Research Agriculture, Livestock, Fisheries. **6**(1): 35-45.

Miah, M.A., Rahman, M.M., Uddin, M.S., Ralunan, A.K.M.M.and UIlah, M.H. (2000). Genetic association in bitter gourd. Bangladesh *J. Sci.* Technol. **2**(1):21-25.

Mondal, S.N., Rashid, A., Inove. K., Hossain, A.K.M.A. and Hossain. M.A. (1989). Genetic variability, correlation and path co-efficient analysis in watermelon. *Bangladesh J. Plant Breed. Genet.* **2**(1): 31-35.

Murty, B.R. and Arunachalam, V. (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*. **26**: 188-198.

Ng, T.B., Chan, W.Y. and Yeung, H.W. (1992). Proteins with abortifacient, ribosome inactivating, immunomodulatory, antitumor and anti-AIDS activities from cucurbitaceae plants. General Pharmacology: The Vascular System, **23**(4): 579–590.

Noris, G., Santana, C., Herrán-Aguirre, M., Meraz-Ríos, M.A., Pérez-Martínez, M., Esquivel-Lacroix, C., Acosta-Saavedra, L.C., Rodríguez, E., Paz Juaréz, M., Calderón-Aranda, E.S. and Gómez, R. (2014). Genetic Diversity of great gane Breed. Using Ten Microsatellites: Impact of breeding control over the breeding line. *Open J. of Genet.*, **4**(2): 78–86.

Patil, R.M. (1988). Studies on relative performance of different genotypes of cucumber *(Cucumis sativus L.).* J. Res. Birsal Agricultural University, **49**(1): 62-69.

Prasad, L., Gautam, N.C. and Singh, S.P. (1988). Studies on genetic variability and character association in watermelon *(Citrullus lanatus). Veg. Sci.* **15**(1): 86-94.

Prasanna, S.C., Krishnappa, K.S., and Reddy, N.S. (2002). Correlation and path coefficient analysis studies in ridge gourd. Current Research **31**: 150-2.

Quamruzzaman, A.K.M., Rahman, M.H., Islam, N.M., Rahman, S.M.L. and Sarker, B.C. (2008). Genetic diversity in land races of ridge gourd. *Bangladesh Res. Pub. J.,* **1**(1): 5-12.

Rabbani, M.G. (2007). Annual report: USDA-Bangladesh collaborative research-CVFB. Dept. Of Horticulture, Bangladesh Agricultural University, Mymensingh. p. 35.

Rahinan, M.M., Dey, S.K. and Wazuddin, M. (1990). Yield components and plant clnracters of several bittter gourds. Ribbed gourd, bottle gourd and sweet gourd genotype. BAU Thesis. Progress. **4**: 117-127.

Rahman, M.M., Dey, S.K. and Wazuddin, M. (1991). Study of yield and yield components and vine characters of some cucurbit genotypes. BAU Res. Prog. **5**: 75-85.

Rajput, J.C., Palve, S.B. and Jamadagni, B.M. (1991). Correlation and path analysis studies in cucumber *(Cucumis sativus L.). Maharashtra. J. Hort.,* **5**(2):52-55.

Ram, D., Rai, M., Verma, A. and Singh, Y. (2006). Genetic variability and association analysis in *Luffa sp. Indian J of Hort.* **63**(3): 294–297.

Rana, J., Gautam, N.C.G., Singh, M., Yadav, R., Tripathi, K., Yadav, S., Panwar, N. and Bhardwaj, R. (2016). Genetic resources of pulse crops in India: An overview. *Ind. J. of Gene. and Plant Breed.* **76**: 420–436.

Rao, B.N., Rao, P.V. and Reddy, YN. (2000). Combining ability studies in ridge gourd (*Luffa acutangula* (L.) Roxb.). *Int. J. Trop. Agric.* **18**(2): 141-146.

Rao, B.N., Rao, P.V. and Reddy, B.M.M. (1999). Correlation and path analysis in the segregating population of ridge gourd [*Luffa acutangula* (Roxb.) L.]. *Crop Research (Hisar).* **20**(2): 338–342.

Rao, C.R. (1952). Advanced statistical methods in biometrical research, John Wiley and Sons. New York. 357-369.

Rathore, J.S., Collis, J.P., Singh, G., Rajawat, K.S. and Jat, B.L. (2017). Studies on genetic variability in ridge gourd (*Luffa acutangula* L. (Roxb.) Genotypes in Allahabad agro-climate condition. *Inter. J. of Current Microbiology and Applied Sci.* **6**(2): 317–338.

Rastogi, K.B., Arya, D. and Deep, D. (1990). A note on interrelatiohip between yield and important plant characters of cucumber *(Cucumis sativus L.). Veg. Sci.* **17**(1): 102- 104.

Reddy, K.S. and Rao, M.R. (1984). Studies on heritability, genetic advance and character association in ribbed gourd. *South Indian Hor.* **32**(2): 97-100.

Robinson, H.F. (1966). Quantitative genetics in relation to breeding on the centennial of Mendelism. (The impact of Mendelism on agriculture, biology and medicine.). *Indian J. Genet.*, **26**: 171–187.

Sarkar, S.K., Marity, T.K. and Som, N.G. (1999). Correlation and path coefficient studies in pointed gourd (Trichosanthes dioica Roxb.) *Indian J. Hort.*, **56**(3): 252-255.

Shah, S.R. and Kale, P.N. (2002). Yield component association analysis in ridge gourd. *J. Maharashtra Agril. Univ.* **27**(2): 197-198.

Shaha, S.R. and Kale, P.N. (2003). Diallel analysis for combining ability in ridge gourd. *J Maharashtra Agric. Univ.* **28**(3): 252-254.

Shaha, S.R. and Kale, P.N. (2001). Diallel analysis for combining ability in ridge gourd.*J. Maharastra Agril. Uni.* **28**(3): 252-254.

Shaha, S.R., Kale, P.N.and Narale, P.A. (1999). Combining ability analysis in ridge gourd. *J. Maharashtra Agric. Univ.* **24**(2): 133-135.

Sharma, K., and Chowdhury, D. (2000). Studies on variability, heritability, genetic advance and correlation in ridge gourd (*Luffa acutangula* Roxb.). *Hort. J.* **15**(3):53-58

Shinde, S.J., Nilangekar, R.G., Barkule, S.R., Hingole, D.G., Kadam, A.S. and Sukase, K.A. (2003). Studies on fruit characteristics of different ridge gourd genotypes. *J. Soils Crops.* **13**(1): 52-55.

Singh, B.D. (2000). Plant Breeding-Principles and Methods (6th Edition). Kalyani Publishers, New Delhi, India. p.896.

Singh, D.K. and Ram, H.H. (2003). Correlation among fruit characters in the indigenous germplasm lines of musk melon. Prog. Hort. **35**(1): 69-72

Singh, H.N., Srivastava, J.P. and Prasad, R. (1977). Genetic variability, character association and genetic correlation studies in bitter gourd. *Indian J. Agri. Sci.*, **47**(12): 604-607.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. India. p. 56.

Singh, R.P., Mohan, J. and Singh, D. (2002). Studies on genetic variability and heritability in ridge gourd. Agricultural Science Digest. **22**(4): 279-280.

Singh, R.V., Verman, T.S. and Thakur, P.C. (2002). Characters association in cucumber. *Haryana J. Hort. Sci.* **31**(1 &2): 91-93.

Singh, V.P. Singh, K. and Jaiswal, R.C. (1986). Genetic variability and correlation studies in pointed gourd *(T. dioica Roxb.). Narendra Deva J. Agric. Res.*, **1**(2): 120-124.

Spuhler, J.N. (1954). Advanced statistical methods in biometric research. By C. Radhakrishna Rao. John Wiley & Sons, Inc., New York, N.Y. 1952. 390 pp. *American Journal of Physical Anthropology*, **12**(2): 268–270.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agril. J.* **60**: 1093-1096.

Swetha, M.P., and Muthukumar, S.P. (2016). Characterization of nutrients, amino acids, polyphenols and antioxidant activity of Ridge gourd (*Luffa acutangula*) peel. *Journal of Food Science and Technology*, **53**(7): 3122–3128.

Sych, Z.D. (1990). Results of watermelon breeding material. Ovoshchevodstvo-i-Bakhehevodstvo. **35**: 67-69.

Tian, P. (2022). Where Is Way out of Crop Crossing Breeding? *OALib*. **9**(4): 1-22.

Tindall, H. D. (1987). Vegetables in the tropics. Macmillan international college education. Houndmills, Basingtoke, Hampshire and London. pp. 173-176.

Tindall, H.D. (1983) Vegetables in the Tropics. Macmillan Press Ltd., London. p. 734.

Thakur, P.C. (2002). Characters association in cucumber. *Haryana J. Hort. Sci.,* **31**(1 &2): 91-93.

Tyagi, S.V.S., Sharma, P. Siddiqui, S.A. and Khandelwal, R.C. (2003). Combining ability for yield and fruit quality in *Luffa acutangula* Roxb. *Int. J. Veg. Sci*. **16**: 267-277.

Varghese, P. (1991). Heterosis in snake gourd (Trichosanthes andguina L.). M.S. Thesis, Kerala Agricultural University. Kerala, India. pp. 37-60

Vijay, O.P. (1987). Genetic variability, correlation and path analysis in muskmelon *(Cucumis melon L.). Indian J. Hort.* **44** (3&4): 233-238.

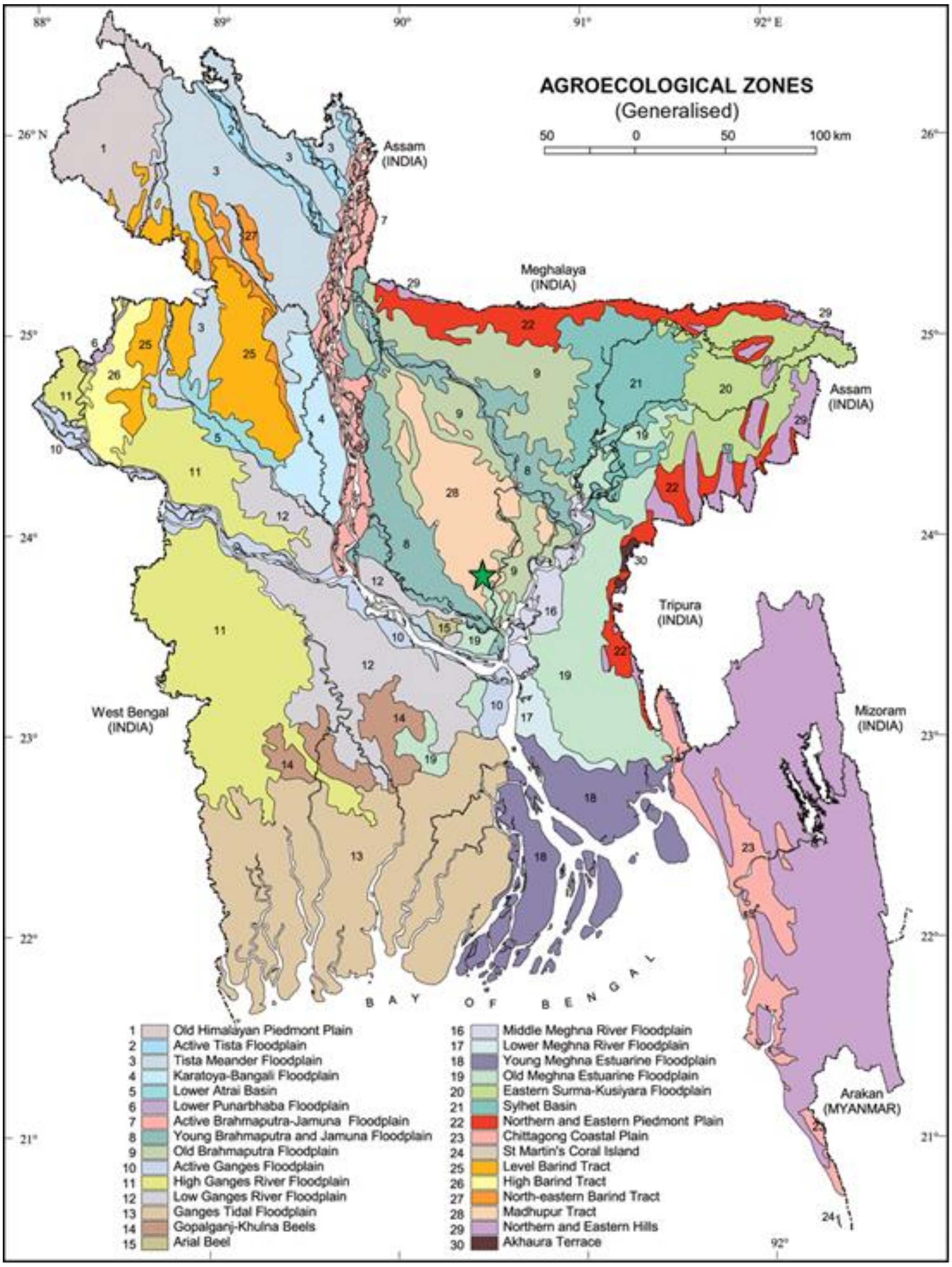
Wright, S. (1923). Theory of path coefficients. Genetics **8**: 239–255**.**

Yawalkar, K.S. (1985). Vegetable crops of India. (3rd Edition). Agric. Horticultural Publishing House. Nagpur. 440010. pp. 166-170.

Zaman, A.K.M., Masud, Q.M.A.T. and Rashid, M. A. (2004). Regional yield trial of sponge gourd. HRC Annual Report. Hort. Res. Cen., BARI, Joydevpur, Gazipur. p.39.

APPENDICES

Appendix I. Map showing the experimental site under the study



★ The experimental site under the study

Appendix II. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Morphological characteristics of the experimental field

Morphological features	**Characteristics**
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	**%**	**Methods employed**
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

Appendix II. (Cont'd): Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

C. Chemical composition of the soil

Sl. No.	**Soil characteristics**	**Analytical data**	**Methods employed**
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Appendix III. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from January 2019 to October 2020

Monthly and yearly average humidity (%):

Year	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Sep.	Oct.	Nov.	Dec.	Annual
2021	71	64	62	71	76	82	83	82	83	78	73	73	74

Monthly average sea level pressure (milliber):

Index	Year	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.
11111	2021	1014.2	1012.3	1009.3	1006.4	1003.5	1000	999.9	1001.4	1004.4	1008.5	1011.5	1013.4

Monthly and yearly Total Rainfall (mm):

Year	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Spt.	Oct.	Nov.	Dec.	Annual
2021	7.7	28.9	65.8	156.3	339.4	340.4	373.1	316.5	300.4	172.3	34.4	12.8	2148

Appendix III. (Cont.): Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from January 2019 to October 2020

Monthly average Dry-bulb temperature (degree Celsius)

Index	**Year**	**Jan.**	**Feb.**	**Mar.**	**Apr.**	**May**	**June**	**July**	**Aug.**	**Sep.**	**Oct.**	**Nov.**	**Dec.**
11111	2021	19.1	21.8	26.4	28.6	28.7	29.1	28.8	28.9	28.8	27.7	24.4	20.2

Month	**Year**	**Monthly average air temperature (^{o} C)**			**Average relative humidity (%)**	**Total rainfall (mm)**	**Total sunshine (hours)**
		Maximum	**Minimum**	**Mean**			
July	2021	31.4	26.2	28.8	83	373.1	225
Aug.	2021	31.6	26.3	28.9	82	316.5	243
Sep.	2021	31.8	25.9	28.8	83	300.4	246
Oct.	2021	31.6	23.8	27.7	78	172.3	237

Source: Bangladesh Meteorological Department (Climate division), Agargaon, Dhaka-1212