GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF YARD LONG BEAN *(Vigna unguiculata* L.)

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CERTIFICATE

*This is to certify that thesis entitled, **"GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF YARD LONG BEAN (Vigna unguiculata L.)"** 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 result of a piece of bona fide research work carried out by **ZAKIA SULTANA**, Registration No. **10-04109** 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: June, 2017
Place: Dhaka, Bangladesh

Dr. Md. Abdur Rahim
Associate Professor
Supervisor

Dedicated To

My Beloved Parents

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GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN YIELD AND YIELD CONTRIBUTING TRAITS OF YARD LONG BEAN (Vigna unguiculata L.)

By

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ABSTRACT

A field experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University with yard long bean genotypes during '*Kharif*' season (June 2016 to September 2016). Ten characters were studied to find out the genetic variability, heritability and genetic advance, correlation coefficient analysis, path coefficient analysis and genetic divergence. The genotypes were significantly variable for all of the characters studied. High genotypic and phenotypic coefficient of variation was observed for number of pods per plant (28.00% and 28.46%) and pod yield per plant (27.87% and 29.37%). Accordingly high heritability accompanied with high genetic advance in percent of mean in number of pod per plant (96.78% and 56.74%), pod yield per plant (90.01% and 54.46%), pod diameter (64.39% and 26.2%) and hundred seed weight (91.21% and 23.37%) suggested that these characters would be considered for varietal selection. The correlation studies revealed that pod yield per plant showed significant positive correlation with no. of seed per pod (0.932 and 0.767), no. of pods per plant (0.974 and 0.970) and significantly negative correlation with dates to marketable harvest (-0.537 and -0.503) at genotypic and phenotypic level. These characters would be considered for the selection a good variety. Path analysis revealed days to first flowering (0.502), days to maturity (1.269), number of pods per plant (0.600), pod weight (0.185) and number of seeds per pod (0.143) had direct positive effect on pod yield per plant, indicating these traits are the main contributors to pod yield per plant. The studied genotypes were clustered into 3 groups with highest of inter-cluster distance between clusters I and III (79.856). This indicates diverse genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III (34.640).

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SOME COMMONLY USED ABBREVIATIONS

Full word	**Abbreviation**
At the Rate	@
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Analysis of Variance	ANOVA
And Others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
By Way of	Via
Cultivars	cv.
Centimeter	Cm
Canonical Variate Analysis	CVA
Degree Celsius	^{0}C
Degrees of Freedom	DF
Days to 50% Flowering	D50%F
Days After Sowing	DAS
Days to Marketable Harvest	DMM
Etcetera	etc.
Environmental Variance	$\sigma^2{}_e$
Genotypic Variance	$\sigma^2{}_g$
Gram	G
Genotype	G
Genetic Advance	GA
Genetic Advance over Mean	GAM
Genotypic coefficient of variation	GCV
Genetic Advance	GA
Harvest Index	HI
Heritability in Broad Sense	$h^2{}_b$
Journal	J.

SOME COMMONLY USED ABBREVIATIONS (*Continued...*)

Full word	Abbreviation
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Murate of Potash	MP
Number	No.
Namely	Viz.
Principal Component Analysis	PCA
Principal Coordinate Analysis	PCO
Phenotypic Coefficient of Variation	PCV
Percent	%
Phenotypic Variance	$\sigma^2{}_p$
Percentage of Coefficient of Variation	CV%
Residual Effect	R
Randomized Complete Block Design	RCBD
Science	Sci.
Standard Error	SE
Pod Length	PL
Pod Diameter	PD
Pod Yield per Plant	PYP
Seeds per Pod	SPP
Square Meter	m^2
Sher-e-Bangla Agricultural University	SAU
Triple Super Phosphate	TSP
The Third Generation of a Cross Between Two Dissimilar Homozygous Parents	F_3
University	Uni.
Variety	var.

CHAPTER I

INTRODUCTION

Yard long bean (*Vigna unguiculata* L.) is one of the most important and popular legume vegetables in Bangladesh. It is well-known as Barboti in Bangladesh. Yard long bean to the class Dicotyledonea, order Fabales, family Fabaceae, subfamily Faboideae, tribe Phaseoleae, subtribe Phaseolinae and genus *Vigna* (Padulosi and Ng, 1997). The cultivated yard long beans are grouped under the species *Vigna unguiculata*, which is subdivided into four cultivar groups: *unguiculata* (the common cowpea), *biflora* (the catjang), *sesquipedalis* (the yard long bean) and *textilis* (used for fibers) (Singh *et al.*, 1997; Reis and Frederico, 2001).

It is widely grown throughout Asia particularly in summer. However, the production is much lower in Bangladesh (3.64 MT/ha) as compared to other Asian countries (Huque *et al.*, 2012**)**. It is grown for its young leaves, immature pods and mature dry seeds (Hall *et al.*, 2003; Hazra *et al*., 2007). Yard long bean grown in summer specifically '*Kharif'* season in our country, when there is a scanty of different vegetable crops. Therefore, it is crucial to improve the yield and quality of this important vegetable.

Like other legume vegetables, yard long bean is also nutritionally rich. It contains high percentage of digestible protein (23.52-26.27%), vitamin A, thiamin, riboflavin, calcium, phosphorus, sodium, potassium, magnesium and (Anon., 2006; Ano and Ubochi, 2008). Besides, the immature pods of yard long bean is a good source of vitamins C, folate and micronutrients 102.69-120.02 mg/kg of iron, 32.58 - 36.66 mg/kg of zinc, 2.92 - 3.34 mg/kg of manganese and 0.33 - 0.57 mg/kg of cobalt (Vaughan and Geissler, 2008). The immature tender pods and fresh seeds of yard long bean are used to prepare delicious dishes. In addition, its dry seeds are also preferred indifferent part of the world (Nielsen *et al.*, 1997; Timko and Singh, 2008). Therefore, this nutritionally rich vegetable can be used to improve the diet of the people in Bangladesh.

Yard long beans can grow in the areas with low rainfall and improves the fertility of soils through biological nitrogen fixation. It is a short duration crop and become an important component of sustainable agriculture. The yield and quality of yard long bean is very low since it grows during the '*Kharif*' season when there the environment is favorable to pests and diseases. Although, it is an important summer vegetable, until now, no commercial cultivar of yard long bean with higher yield is available in Bangladesh. Furthermore, there is a lack of proper breeding strategies for the improvement of this nutritious vegetable.

Yield of yard long bean is a complex and highly variable which is connected to a number of component traits (Ullah *et al.*, 2011). Thus, selection of appropriate cultivars/breeding lines is a key step for commercial cultivation of these vegetables. The information on genetic variability, character association between yield and its contributing traits is essential for improvement of yield via the conventional breeding program (Fraser and Eaton, 1983). Cause-effect analysis also offers an effective means of partitioning the correlation coefficients into direct and indirect effects of the component trait on yield on the basis of which crop improvement program can be logically devised (Rao *et al.*, 1997). Further, the genetic distance between pair of genotypes offers the basis for understanding the structure of the diversity of any intra-species population. It constructs an all-to-all matrix to describe the distance between each sequence pair of genotypes; thereby guiding plant breeder in their selection procedure (Adewale *et al.*, 2011). The multivariate analysis is a valuable tool for selecting parents for hybridization program (Hazra *et al.*, 1992, Rahim *et al.* 2010**)**. Besides, the genetic diversity or genetic similarity could help to get long-term selection gain in plants (Chowdhury *et al.* 2005). Therefore, evaluation of genetic divergence in the available germplasm of the crop is crucial to know the source of genes for a particular character within (Tomooka, 1991).

Objective(s):

Up to now, little is known about the genetic improvement of yard long bean in Bangladesh. Therefore, the proposed study was undertaken with the following objectives:

- to characterize the important traits related to yield and quality of yard long bean
- to determine the genetic diversity of different traits of yard long bean
- to select genetically diverse parent for the hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Proper understanding of the problem requires thorough review of the existing knowledge related to the problem. Keeping in view the objectives of the present investigation, the available literature on genetic variability, genetic divergence, character association and character contribution in yard long bean is presented under the following headings.

2.1 Genetic variability
2.2 Heritability and genetic advance
2.3 Correlation coefficient analysis
2.4 Path coefficient analysis
2.5 Genetic divergence

2.1 GENETIC VARIABILITY

For a successful crop improvement program, data on the nature and magnitude of genetic variability, degree of transmission of the traits is of immense importance. The variability available in the population can be partitioned into heritable and non-heritable components viz., phenotypic and genotypic coefficients of variation, heritability and genetic advance on which selection can be effectively carried out. High heritability alone is not enough to make efficient selection in segregating generations, unless information is accompanied by substantial amount of genetic advance (Johnson *et al.*, 1955). However, such genetic variability studies in yard long bean are limited. Hence, the information available on other legume crops like cowpea, french bean, dolichos bean etc. was also included in the review of literature. The available literature in yard long bean on genetic parameters is reviewed under here.

Sakrajitjana and Das (1983) reported that pod length in the range of 13.5 to 27.0 cm with low GCV and PCV coupled with high heritability (85.46%) and low GA (4.99%) in cowpea. Backiyarani and Nandarajan (2000) demonstrated a wide variation in pod length (10.3 to 18.1cm), low GCV (16.02) and PCV (17.82) with high heritability (87.45%) and moderate GAM (30.12%) for the trait in cowpea. Anbuselvam *et al.* (2000) revealed that high PCV and GCV had been observed for yield per plant, number of branches per plant, plant height, number of pods per plant and 100 seed weight in cowpea.

Borah and Khan (2000) evaluated 60 cowpea genotypes. High estimates of phenotypic and genotypic coefficients of variation (PCV and GCV, respectively) were observed for number of branches and leaves, dry weight of leaves and stem, and dry matter and green fodder yield suggesting the variability potential available for these characters in fodder cowpea. Low GCV estimates were observed for days to 50% flowering, stem thickness and leaflet length, indicating low variability.

Tyagi *et al.* (2000) carried out an experiment with 24 cowpea genotypes. High estimates of GCV (42.55) were observed for plant height. And they also observed pod length in the range of 12.10 to 17.73 cm with low estimates of GCV and PCV (13.67) in cowpea. Vidya *et al.* (2002) studied fifty cultivars of yard long bean. High GCV was estimated for the yield of vegetable pods per plant, number of pods per plant and pod weight indicating the scope for the improvement of these characters through selection.

Narayanankutty *et al.* (2003) reported pod length in the range from 13.18 to 47.48 cm with low GCV (29.74) and PCV (30.17) in cowpea. They observed wide range for seeds per pod (11.65 to 18.90) with low GCV and PCV in cowpea. And they also reported the vegetable pod yield in the range from 87.13 to 789.75 g with high GCV (58.34) and PCV (58.55) in cowpea.

Vineeta Kumari *et al.* (2003) evaluated 50 cowpea genotypes and found that GCV and PCV were the highest for days to flowering and maturity, number of clusters and pods per plant, 100-seed weight and seed yield per plant. Resmi *et al.* (2004) studied 30 diverse genotypes of yard long bean and showed that the PCV and GCV were highest for pod yield per plant. Borah *et al.* (2002)

evaluated 32 cowpea genotypes and found that high GCV and PCV for plant height, number of pods per plant, seed yield per plot and 100-seed weight.

Girish, *et al.* (2006) conducted an experiment with 100 genotypes of cowpea. According to their results, plant height and seed yield showed highest phenotypic and genotypic variances, while primary and secondary branches showed lowest variances. The magnitude of PCV and GCV was high for seed yield per plant, number of pods per plant and plant height. Omoigui *et al.* (2006) revealed that the genotypic coefficient of variation (GCV) was high for days to first flower, 100-seed weight, plant height, and harvest index in cowpea.

Sheela Mary and Gopalan (2006) studied variability for both grain and fodder cowpea in F_3 and F_4 generations. The genotypic coefficients of variation were highest for the characters plant height, number of branches and leaf weight in both the generations. Souza *et al.* (2007) studied variability in cowpea populations. In that study the GCV varied from 2.35% (pod width) to 22.65% (number of pods per plant) aside from the number of pods per plant, grain yield was particularly favourable with 20.86%. The values indicated the existence of variability in cowpea genotypes for the referred traits, indicating the possibility of selection.

Soniya *et al.* (2008) studied 20 diverse genotypes of cowpea. The PCV was higher than the GCV for all the characters. Wide range of coefficient of variations were observed for plant height, number of leaves per plant followed by green pod yield, seed yield per plant, leaf area per plant, pod length and 100 seed weight at phenotypic and genotypic levels respectively, indicating high level of variability in these characters and ample scope for effective improvement. Mishra and Dash (2009) studied genetic variability in 33 genotypes of cowpea. They found high genotypic coefficient of variation (GCV) for pod yield per plant. Kumar and Devi (2009) studied 30 genotypes of yard long bean. High GCV and PCV were recorded for pod yield per plant, followed by clusters per plant, pods per plant, pods per cluster and pod weight, indicating high genetic variability.

Upadhyay and Mehta (2010) studied 32 genotypes of *Dolichos lablab*. The highest GCV was recorded for pod width followed by pod length and the lowest in number of seeds per pod. Shimelis and Shiringani (2010) assessed cowpea genotypes and found that the genotypic variance contributed >50% of the total phenotypic variance for the numbers of days to 50% flowering, seeds per pod, productive branches per plant and seed yield.

Rahim *et al.* (2010) evaluated yield and its contributing characters in 26 mungbean genotypes. The highest GCV was found for number of pods per plant followed by 100 grain weight and plant height and the lowest for pod length indicating higher degree of genetic variability for these characters. Aqsa Tabasum *et al.* (2010) studied variability in 10 mungbean genotypes. The results showed that clusters per plant were shown to have maximum genotypic coefficient of variation GCV (21.05%) followed by seed yield (17.12%) suggesting substantial amount of genetic variability. Ullah *et al.* (2011) investigated 20 genotypes of yard long bean. The GCV was high for pod yield, pod weight and pods per plant.

Manggoel *et al.* (2012) studied ten cowpea accessions. The PCV and GCV were the highest for 100 seed weight (41.46 and 38.47% respectively), followed by grain yield (38.55 and 36.76 respectively), number of peduncles per plant (36.96 and 32.86 respectively), number of flowers per plant (32.29 and 29.59 respectively), number of pods per plant (29.88 and 28.23 respectively) and days to 50% flowering (26.54 and 26.02 respectively). Low PCVs and GCVs were recorded for number of seeds per pod (24.11 and 20.66 respectively) and pod length (19.81 and 15.79 respectively).

Sivakumar *et al.* (2013) studied 22 diverse genotypes of bush cowpea. The high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for pod weight, plant height and pod length.

Subbiah *et al.* (2013) reported high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for number of pods, pod yield, pod length and crude fibre content in both F2 and F3 generations in cowpea.

Manivannan and Anandakumar (2013) assessed 42 genotypes of cluster bean. The variability range was maximum for pods per plant, followed by plant height, number of clusters per plant and seed yield per plant. Variances in terms of coefficient of variation indicated that there were little differences between phenotypic and genotypic variances for some of the characters viz., pod length, days to maturity and days to 50% flowering, indicating that these characters were less affected by environment. On the other hand, characters such as seed yield per plant, number of pods per plant and plant height were influenced by the environment.

Khan Hasan *et al.* (2013) assessed variability in cowpea. The segregating populations of C-152 x V-16 cross showed high PCV estimates for plant height, number of branches per plant, number of seeds per pod, seed yield per plant and number of pods per plant. But GCV estimate was high for the traits like number of pods per plant and seed yield per plant. Similarly, in another cross C-152 x HC-03-02, high PCV values were estimated for plant height, number of branches per plant, seeds per pod, seed yield and number of pods per plant.

Archana and Rajesh (2013) assessed variability in 30 genotypes of cowpea. High GCV was observed for leaf area index (45.17%), followed by days to 50% flowering (40.04%), plant height (34.71%), number of branches per plant (27.99%), number of pods per plant (24.84%), number of clusters per plant (24.73%) and days to maturity (18.01%).

2.2 HERITABILITY AND GENETIC ADVANCE

Heritability is the measure of transmission of characters from generation to generation. Hanson *et al.* (1956) defined heritability in broad sense, as the ratio of genotypic variance to the total phenotypic variance in the non-segregating populations. Heritability (h^2) measures the relative amount of the heritable portion of variability. It is a measure of genetic gain under selection. Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. The genetic advance is usually expressed as percentage of mean. The available literature on heritability and genetic advance in yard long bean and other crops is reviewed under here.

Sharma (1999) studied 42 diverse genotypes of cowpea. Almost all the characters showed high heritability values. Plant height showed high genetic advance coupled with high h^2 and GCV, indicating a preponderance of additive gene effects for this trait. Moderate GCV and GA estimates were observed for the other traits studied. Borah and Khan (2000) evaluated 60 cowpea genotypes. The highly heritable characters i.e., number of branches and leaves, stem and leaf dry weight, dry matter and green fodder yield, and plant height, also exhibited high genetic advance as percentage of mean, indicating additive gene action. The crude protein content, days to 50% flowering, stem thickness, and leaf length and width exhibited low genetic advance with high heritability estimates.

Tyagi *et al.* (2000) carried out study with 24 cowpea genotypes. High estimates of heritability (98.8%) and genetic advance over mean (87.14%) were observed for plant height. And they also observed pod length in the range of 12.10 to 17.73 cm in cowpea. However, the heritability (89.60%) for the trait was high but GAM (25.25) was low.

Vidya *et al.* (2002) studied fifty cultivars of yard long bean. High heritability in the broad sense, and GA estimated for the yield of vegetable pods per plant, number of pods per plant, and pod weight indicated the scope for the improvement of these characters through selection. Narayanankutty *et al.* (2003) reported pod length in the range of 13.18 to 47.48 cm with high heritability (97.20%) and GAM (60.38%) in cowpea. They also observed wide range for seeds per pod (11.65 to 18.90) with high heritability (77.50%) and low GAM (17.83%) in cowpea. And they also reported that vegetable pod yield in the range from 87.13 to 789.75 g with high heritability (99.30%) and GAM (107.81%) in cowpea.

Vineeta Kumari *et al.* (2003) evaluated 50 cowpea genotypes. High heritability and genetic gain were recorded for seed yield per plant, and number of pods and clusters per plant. Resmi *et al*. (2004) studied 30 diverse genotypes of yard long bean. High heritability coupled with high genetic advance was observed for pod yield per plant, pods per kg, inflorescence per plant, pod weight and keeping quality of pods, indicating a scope of selection for improvement of these characters.

Malarvizhi *et al.* (2005) evaluated 60 genotypes of fodder cowpea. Heritability and genetic advance were high for the characters number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem, dry matter yield and plant height indicating that these traits were controlled by additive genetic effects, providing better source population for developing high yielding fodder cowpea varieties.

Shahid Ahmed *et al.* (2005) evaluated 32 genotypes of cowpea. High heritability coupled with high genetic gain was observed for plant height (96.39 and 90.78%), number of pods per plant (67.84 and 38.39%), seed yield per plot (175.02 and 122.83%) and 100-seed weight (37.40 and 39.34%) indicating the preponderance of additive gene effects for these traits.

Girish *et al.* (2006) evaluated 100 genotypes of cowpea. The magnitude of heritability (h^2) and genetic advance (GA) was high for seed yield per plant, number of pods per plant and plant height. Days to first flower opening, days to 50% flowering and days to maturity had low genetic advance. Broad-sense heritability estimate (h2) was 98.9% for 100-seed weight, 94% for duration of reproductive phase, 84.5% for days to first flower, 83.9% for days to maturity, and 77.3% for harvest index in cowpea genotypes (Omoigui *et al.*, 2006).

Sheela Mary and Gopalan (2006) studied variability for both grain and fodder cowpea in F_3 and F_4 generations. High heritability coupled with high genetic advance as percent of mean was noticed for characters plant height, number of branches, number of leaves, leaf length, stem thickness, leaf weight, stem weight, leaf stem ratio, green fodder yield, dry matter yield and crude protein content. High heritability with moderate GA as percent of mean was exhibited for days to 50 percent flowering in F3 and F4 generations.

Eswaran *et al.* (2007) evaluated 30 genotypes of cowpea. High estimates of genetic variability coupled with high heritability and genetic advance were observed for plant height at the time of first flowering, plant height at the time of 50 percent flowering and plant height at the time of 50 percent maturity indicating their dependability for effecting selection.

Soniya *et al.* (2008) studied 20 diverse genotypes of vegetable type cowpea. In that study they, found number of clusters per plant, diameter of pod and number of seeds per pod manifested high heritability coupled with low GCV and genetic advance and indicated that simultaneous improvement in vegetable cowpea cannot be made accordingly. Only characters plant height and number of leaves per plant with moderate heritability and high genetic advance would contribute to yield improvement in cowpea.

Mishra and Dash (2009) studied genetic variability in 33 genotypes of vegetable cowpea. High estimates of heritability were observed for all the characters except nodes per branch, pod girth and seeds per pod. High estimates of heritability and genetic advance were observed for vine length, branches per plant, and inflorescences per plant, green pods per plant, pod weight, 100-seed weight and pod yield per plant. Nicole *et al.* (2009) reported that the estimated broad-sense heritability on the individual plant basis was 0.2190. However, the corresponding estimate on the plant mean basis (average of four plants) was 0.5198, which is very high for a quantitative trait. The high heritability may explain why traditional breeding for cowpea growth is so effective.

Bertini *et al.* (2009) evaluated 16 cowpea cultivars for various characters i.e., time to flowering (F), plant cycle duration (C), pod length (CVA), number of pods per plant (NVP), number of seeds per pod (NSV), weight of 100 seeds (P100S), total production (P) and production in grams per plant (P/PL). CVA, NVP, NSV, PCS, P and P/PL recorded h^2 values of more than 90%, indicating the possibility of genetic improvement through selection.

Kumar and Devi (2009) studied 30 genotypes of yard long bean. High heritability coupled with high genetic advance was observed for pod clusters per plant, pods per plant, pod yield per plant, pods per cluster and pod weight, indicating the additive gene action. Tabasum *et al.* (2010) studied variability in 10 mungbean genotypes for various plant traits i.e., primary and secondary branches, pods per cluster and pod length showed lesser variability, while clusters per plant, 100 seed weight and harvest index revealed. Moderate to high heritability estimates were found for all traits.

Upadhyay and Mehta (2010) studied 32 genotypes of *Dolichos lablab*. The highest heritability estimate was observed for marketable pod weight followed by pod width, hundred seed weight and number of pods per inflorescence. Higher heritability estimates coupled with high genetic advance as per cent of mean were observed for pod width, followed by pod weight and hundred seed weight.

Hussein Shimelis and Rhandzu Shiringani (2010) assessed cowpea genotypes. The heritability of the number of days to 50% flowering were estimated at 50%, pods per plant (23%), days to maturity (66%), productive branches per plant (53%), 100 seed weight (11%) and seed yield (55%). The presence of considerable degree of genotypic variance among tested genotypes under various environments suggested that success in cowpea breeding could possibly be achieved through direct phenotypic selection.

Rahim *et al.* (2010) evaluated 26 mungbean genotypes. A higher heritability (broad sense) estimate associated with good estimates of genetic advance expected in the next generation were observed for grain yield per plant, number of pods per plant, plant height, number of seeds per pod and 1000-grain weight suggesting these characters are governed by additive genetic effect to a great extent and improvement of these characters would be effective through phenotypic selection.

Ullah *et al.* (2011) investigated 20 genotypes of yard long bean. High to moderate heritability as well as high genetic advances were estimated for days to first flowering, days to marketable harvest, pod yield, number of pods per plant and pod weight. Lovely *et al.* (2005) studied thirteen genotypes in yard bean and reported high heritability in broad sense and genetic advance estimated for the characters viz., pod yield per plant (161% and 48%), number of pods per plant (93% and 41%) and number of clusters per plant (91% and 52%).

Manggoel *et al.* (2012) studied ten cowpea accessions. Broad sense heritability estimates were high for days to 50% flowering (79.05%), number of peduncles per plant (96.74%), number of flowers per plant (83.98%), number of pods per plant (89.23%), pod length (63.16%), number of seeds per pod (73.40%), 100 seed weight (86.84%) and grain yield (90.91%). Singh and Singh (2013) evaluated 42 divergent genotypes of French bean. High genetic advance coupled with high heritability was observed for hundred seed weight, seed yield per plant, pod yield per plant and pod yield quintals per ha, indicating there by the preponderance of additive gene action for these characters. Archana and Rajesh (2013) assessed variability in 30 genotypes of cowpea. High heritability coupled with high genetic advance was observed for plant height (99.95% and 91.62%), number of pods per plant (97.70% and 64.82%) and number of branches per plant (98.78% and 73.45%).

Costa *et al.* (2013) estimated the genetic divergence in 57 African cowpea lines for various traits i.e., number of pods per peduncle, pod length (PL), number of grains per pod (NGP), grain length (GRL), grain width, 100-grain weight (W100G) and yield. The heritability values of the traits PL, NGP, GRL, and

W100G were all higher than 70%, indicating the possibility of genetic progress with selection.

Khan *et al.* (2013) assessed variability in cowpea. The segregating populations of C-152 x V-16 cross revealed that heritability in broad sense was high for test weight, number of branches per plant and seed yield. The GAM estimates were high for all the traits studied except number of branches per plant. Similarly, in another cross C-152 x HC-03-02, GCV and heritability were high for plant height and test weight and GAM was high for all the traits studied.

Manivannan and Anandakumar (2013) assessed 42 genotypes of cluster bean. High heritability and high genetic advance as percent of mean were recorded for primary branches per plant, secondary branches per plant, pod length and days to fifty percent flowering. High heritability and moderate genetic advance as percent of mean were recorded for days to maturity and 100 seed weight. Nwofia *et al.* (2013) studied seven vegetable cowpea genotypes. High heritability in the broad sense was observed for number of seeds per pod, pod length, leaf area and plant height.

Sivakumar *et al.* (2013) studied 22 diverse genotypes of bush cowpea. In that study, yield per plant, plant height, primary branches, pod length, pod girth, pod weight and pods per plant recorded high heritability coupled with high genetic advance. Subbiah *et al.* (2013) reported high genetic advance (GA) and heritability (h2) for number of pods, pod yield, pod length and crude fibre content in both F2 and F3 generations in cowpea.

2.3 CORRELATION COEFFICIENT ANALYSIS

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield. Simple correlations are of three types viz., phenotypic, genotypic and environmental. Phenotypic correlation is the observable correlation between variables, measures the environmental deviation together with non-additive gene action. Genotypic correlation on the other hand is the inherent association between two variables. They can be estimated from replicated data only.

The knowledge of the nature of association between characters is of great asset to plant breeders to formulate evaluation or work procedures. The magnitude and direction of association is measured by correlation coefficients. Correlation studies provide information such that selections for one character result in progress for all positively correlated characters. The available literature in yard long bean and other crops on correlation coefficient analysis studies is reviewed hereunder.

Sharma and Mishra (1997) revealed that seed yield had a high positive phenotypic correlation with pods per peduncle, number of seeds per pod and harvest index in cowpea. Tyagi *et al.* (2000) carried out correlation study with twenty four genotypes in cowpea. They reported that seed yield per plant had high significant and positive correlation with days to 50 percent flowering, plant height, pod length, number of pods per plant, seed weight per pod and hundred seed weight at both phenotypic and genotypic levels.

Vidya and Oommen (2002) studied 50 cultivars of yard long bean. Pod yield per plant was positively correlated with number of pods per plant, number of pods per inflorescence, pod weight, length of harvesting period, pod girth, pod length, and number of primary branches at the genotypic level. Vineeta Kumari *et al.* (2003) evaluated 50 cowpea genotypes. Seed yield per plant was positively correlated with number of clusters and pods per plant, and 100-seed weight, but was negatively correlated with days to maturity.

Kumawat and Raje (2005) evaluated 50 cowpea genotypes. Correlation analysis showed that seed yield had significant positive correlation with branches per plant, clusters per plant, pods per plant, biological yield per plant and harvest index. Lovely and Radhadevi (2006) evaluated 50 yard long bean genotypes. The results revealed that yield per plant showed strong positive genotypic correlation with pods per cluster, pods per plant, pod weight, pod length, pod breadth and seeds per pod.

Souza *et al.* (2007) studied variability in cowpea populations. The genotypic correlations of grain yield were positive and significant and high for the number of pods per plant, and medium for number of grains per pod. The number of pods per plant is therefore a trait that can be considered in the indirect selection for higher yield in segregating cowpea populations.

Eswaran *et al.* (2007) evaluated 30 genotypes of cowpea. Seed yield per plant had high significant positive correlation with total dry matter production and harvest index both at phenotypic and genotypic levels. Mishra and Dash (2009) studied genetic variability in 33 genotypes of vegetable cowpea. Association studies among green pod yield and its contributing characters revealed that the characters branches per plant, inflorescences per plant, green pods per plant, green pod length, green pod weight, pod girth and protein content of green pod had positive and significant correlation with green pod yield.

Rahim *et al.* (2010) evaluated for yield and its contributing characters in 26 mungbean genotypes. Positive correlation was found only between days to 50% flowering and days to 80% maturity. Days to 50% flowering positively associated with plant height and number of seeds per pod and negatively correlated with 1000-grain weight. Days to 80% maturity showed strong positive correlation with pod length. Plant height had no significant correlation but it showed positive correlation with number of pods per plant, pod length and number of seeds per pod and also negative correlation with 1000-grain weight and grain yield per plant.

Aqsa Tabasum *et al.* (2010) studied variability in 10 mungbean genotypes. Plant height showed positive non-significant and significant genotypic and phenotypic correlations. Pods per cluster correlated significantly negative with seed yield. Clusters per plant, pods per plant, total plant weight and harvest index showed positive significant genotypic and phenotypic correlations with seed yield.

Upadhyay and Mehta (2010) studied 32 genotypes of *Dolichos lablab*. Correlation coefficient analysis revealed that pod length and marketable pod weight had the positive correlation with marketable green pod yield per plant. Hence, direct selection for these traits may lead to the development of high green pod yielding *Dolichos* genotypes.

Machikowal and Laosuwan (2011) evaluated 14 soybean lines for eight characters i.e., days to flowering, branches per plant, nodes per plant, pods per plant, seeds per plant, 100 seeds weight, days from flowering to maturity and yield. It was found that significantly positive phenotypic correlation was observed between seed yield and days to flowering. Further-more, genotypic correlation showed that seed yield was positively correlated with all characters except 100 seeds weight. Ullah *et al.* (2011) investigated 20 genotypes of yard long bean. Pod yield per plant showed strong positive genotypic correlation with number of pods per plant, pod weight, pod length and pod diameter.

Huque *et al.* (2012b) studied thirteen genotypes in string bean and reported significant and positive correlation both at genotypic as well phenotypic levels between number of nodes per plant and number of primary branches per plant, days to first flowering and days to 50% flowering, days to 95% pod maturity, number of pods per plant and number of cluster, and number of pods per plant and number of pods per cluster. Plant height, days to first flowering, days to 50% flowering and days to 95% pod maturity were negatively correlated with pod yield per plant both at genotypic and phenotypic levels.

Manggoel *et al.* (2012**)** studied ten cowpea accessions. Positive correlation was found between grain yield and number of peduncles per plant (r = 0.716**), flowers per plant (r = 0.776**), pods per plant (r = 0.640*) and 100seed weight (r = 0.690*). Nwofia *et al.* (2012) studied correlation analysis in cowpea genotypes. Seed yield was positively and significantly correlated to number of leaves per plant, seed weight per pod, dry matter yield per plant and number of pods per plant.

Khan *et al.* (2013) assessed variability in cowpea. Number of pods per plant and number of seeds per pod had significant positive correlation among themselves in both the crosses studied. It may be inferred that these traits have strong influence on seed yield per plant. Manivannan and Anandakumar (2013) assessed 42 genotypes of cluster bean. Number of pods per plant, clusters per plant, pods per cluster, and branches per plant had positive and significant correlation with seed yield per plant.

Singh and Singh (2013) evaluated 42 divergent genotypes of French bean. Correlation analysis indicated that pod yield per plant was significant and positively associated with days taken to first flowering and first picking, pod length and seed yield per plant.

Archana and Rajesh (2013) assessed variability and correlation in 30 genotypes of cowpea. Days to maturity had highly significant positive correlation with days to 50% flowering both genotypically and phenotypically. Protein content is significant but negatively associated with days to maturity. Number of clusters per plant showed strong positive significant correlation with protein content. Pod length exhibited significant positive correlation with protein content. Number of seeds per pod exhibited positive significant correlation with protein content and strongly correlated with pod length. Seed yield per plot exhibited strong positive significant correlation with clusters per plant and number of pods per plant. It also showed moderately positive significant correlation with protein content.

2.4 PATH COEFFICIENT ANALYSIS

Knowledge of inter-character relationships is very important in plant breeding for indirect selection for characters that are not easily measured and for those that exhibit low heritability. Correlation studies between characters have also been of great value. In the determination of the most effective breeding procedures as the number of independent characters affecting a dependent character increases, there is bound to be some amount of interdependence. Under such a complex situation, correlation alone becomes insufficient to explain relationships among the characters. Path analysis permits identification of direct and indirect causes of association and measures the relative importance of each character. The literature on the direct and indirect effects of various quantitative traits on pod yield of yard long bean and other crops is reviewed under here.

Vidya and Oommen (2002) studied 50 cultivars of yard long bean. The maximum direct effect on yield was shown by number of pods per plant followed by pod weight and number of pods per inflorescence. Number of pods per plant also exerted positive indirect effect through length of harvesting period and number of pods per inflorescence while pod weight exerted positive indirect effect via pod length and pod girth and negative indirect effect via number of pods per plant.

Kumari *et al.* (2003) evaluated 50 cowpea genotypes. Path analysis revealed that the number of clusters, pods and seeds per plant, and 100 seed weight showed the greatest positive direct effects on seed yield, whereas the number of days to maturity and flowering exhibited the greatest negative direct effects on seed yield per plant. Kumawat and Raje (2005) evaluated 50 cowpea genotypes. Path analysis indicated the high positive direct effect of clusters per plant, biological yield per plant and harvest index on seed yield per plant.

Lovely and Radhadevi (2006) evaluated 50 yard long bean genotypes. The results revealed that high positive direct effects of pods per plant on yield per plant. Eswaran *et al.* (2007) evaluated 30 genotypes of cowpea. The path coefficient analysis indicated that plant height at the time of first flowering, plant height at the time of 50 percent flowering, plant height at the time of 50 percent maturity and total dry matter production are important for effecting section.

Mishra and Dash (2009) studied genetic variability in 33 genotypes of vegetable cowpea. Path coefficient analysis showed that pods per plant had the highest positive direct effect on green pod yield followed by pod weight, seeds per pod and protein content of pod.

Rahim *et al.* (2010) evaluated for yield and its contributing characters in 26 mungbean genotypes. Days to 50% flowering showed negative direct effect on grain yield and positive indirect effect via days to 80% maturity, numbers of pods per plant, pod length and 1000-grain weight.

Tabasum *et al.* (2010) studied variability in 10 mungbean genotypes. Positive direct effects were exerted through secondary branches, pods per plant, pod length, 100 seed weight, total plant weight and harvest index while primary branches, plant height, clusters per plant and pods per cluster had negative direct effects.

Upadhyay and Mehta (2010) studied 32 genotypes of *Dolichos lablab*. Path coefficient analysis of variation for green pod yield per plant revealed that highest positive direct effect contributing to marketable green pod yield per plant was observed due to pod length (4.502) followed by length of inflorescence (1.602), whereas, marketable pod weight (3.625) and number of seeds per pod (2.833) shows highest positive indirect effect on marketable green pod yield per plant via pod length, while pod width (1.568) and hundred seed weight (1.2.8) exhibited high positive and indirect effect by pod length on marketable green pod yield per plant.

Machikowl and Laosuwan (2011) evaluated 14 soybean lines for eight characters i.e., days to flowering, branches per plant, nodes per plant, pods per plant, seeds per plant 100 seeds weight, days from flowering to maturity and yield. It was found that pods per plant gave the highest positive direct effect on seed yield, followed by branches per plant. In addition, the indirect effects of most characters were high through pods per plant.

Ullah *et al.* (2011) investigated 20 genotypes of yard long bean. The maximum direct positive effect was observed of pod weight and number of pods per plant to pod yield in cause effect analysis. Manggoel *et al.* (2012) studied ten cowpea accessions. High positive direct effects of number of peduncles per plant ($p = 0.94$), flowers per plant ($p = 1.40$) and 100-seed weight ($p = 1.45$) were found.

Nwofia *et al*. (2013) studied correlation analysis in cowpea genotypes. Seed weight per pod and number of leaves per plant had positive direct effects of 0.611 and 0.549 on seed yield. Number of pods per plant, number of leaves per plant and pod length had positive direct effects of varying magnitude to seed yield (0.367, 0.087 and 0.016, respectively). Mahmudul *et al.* (2012) studied 13 genotypes in string bean and reported that number of pods per plant, pod length, number of cluster per plant and primary branches per plant were the major direct contributors to pod yield per plant.

Singh and Singh (2013) evaluated 42 divergent genotypes of French bean. Path co-efficient analysis revealed that days taken to first flowering, days to first picking, pod length, 100- seed weight and seed yield per plant had positive direct effect on pod yield per ha. Manivannan and Anandakumar (2013) assessed 42 genotypes of cluster bean. The results showed that cluster per pod, 100-seed weight, followed by seed per pod had positive and greater direct effects on seed yield per plant and pod length, branches per plant and days to maturity had negative direct effect on seed yield per plant.

Nwofia *et al.* (2013) studied seven vegetable cowpea genotypes. Results showed that number of pods per plant showed higher positive direct effect as well as correlation on pod yield than other yield traits (0.972 and 0.936, respectively).

2.5 GENETIC DIVERGENCE

The variability among different genotypes of a species is known as genetic diversity. The multivariate analysis using Mahalanobis D^2 statistic a valuable tool to quantify the degree of divergence at genetic level (Mahalanobis, 1936).

While formulating the oriental pickling melon crop improvement program knowledge on the nature and degree of genetic divergence available in the germplasm plays a pivotal role. It is well recognized that the use of diverse parents results in superior hybrids and desirable recombinants. Thus, the genetic divergence existing in the population helps in selecting suitable parents for hybridization program. The available literature on genetic divergence in yard long bean and other crops is reviewed as follows.

Sharma and Mishra (1997) revealed that days to 50 percent flowering, plant height, pods per peduncle and harvest index contributed the most towards the genetic divergence in cowpea. Mahalanobis' D^2 statistic was used (Rewale *et al.*, 1996) to estimate genetic divergence of 12 yield related characters evaluated in 70 genotypes of *V. unguiculata* subsp. *cylendrica*. Multivariate analysis grouped the genotypes into 19 clusters, of which 11 had only one genotype each. Days to initiation of flowering, 50 percent flowering and maturity, number of inflorescences and pods per plant, pod length, hundred seed weight, seed yield per plant and harvest index made the largest contribution to the total divergence. It is proposed that high yielding genotypes with early maturity and high harvest index could be selected as parents for hybridization.

Santos *et al.* (1997) reported genetic divergence of cowpea under two different environments using Mahalanobis D^2 statistic that length of main branch, hundred seed weight and pod length were the most important characters to affect the divergence. Backiyarani *et al.* (2000) concluded that genetic divergence for physiological traits like single plant yield, harvest index and earliness in flowering together accounted for 80 percent of the total divergence in cowpea.

Kumari *et al*. (2000) reported that contribution towards genetic divergence was recorded for plant height (22.69%), number of branches (l6.82%), number of pods per cluster (l5.27%) and pod length (13.47%) in cowpea.

Borah and Khan (2002) revealed on genetic divergence in fodder cowpea, sixty fodder cowpea cultivars were grouped into 10 clusters. Dry matter yield, green fodder yield and plant height were recorded the highest contribution to total genetic divergence. These traits could be good criterion for selection of parents in hybridization programme. Narayanankutty *et al.* (2003) studied genetic variability and divergence on thirty seven genotypes of vegetable cowpea revealed significant differences for all the characters under study. The thirty-seven genotypes were grouped into eleven clusters using Mahalanobis D2 statistic. In general, the inter-cluster distances were higher than intra cluster distances. The maximum inter cluster distance was between clusters VIII and X, followed by clusters VI and X and clusters VIII and IX, respectively..

The nature of magnitude of genetic diversity was studied in a set of 45 cowpea (*Vigna unguiculata*) genotypes from indigenous and exotic sources (Nigude *et al.*, 2004). The genotypes were grouped into five clusters using Mahalanohis D^2 statistic. Cluster-I was the largest with 28 genotypes followed by cluster-II with eleven genotypes and cluster-III with four genotypes. The clusters IV and V were monogenotypic. The maximum inter-cluster distance was observed between clusters III and V followed by distance between clusters II and III. Clusters I and III exhibited the minimum inter-cluster distance. The number of branches per plant, test weight, biomass (dry weight) at harvesting and number of pods per plant had contributed considerably toward divergence.

Genetic divergence among thirty diverse genotypes of yard long bean using Mahalanobis D^2 statistic was studied and all the genotypes were grouped into four clusters. The intercluster distance was maximum between clusters I and cluster III. Heterotic combinations are expected between the selected parents of the diverse groups (Resmi *et al.*, 2005).

Kumawat and Raje (2005) showed seed yield per plant had the highest contribution towards the total genetic divergence followed by seeds per pod, days to 50 percent flowering, plant height and reproductive period in cowpea. Hettiarachchi (2006) studied genetic divergence in 81 varieties of cowpea for various characters i.e., days to flowering, days to maturity, plant height, pod length and seed yield. It was found that the pod length contributed the most while the days to maturity contributed the least to divergence among cultivars.

Sulnathi *et al.* (2007) assessed genetic divergence in 56 genotypes of cowpea using D^2 statistic for 13 yield contributing characters showed grouping of genotypes into 9 clusters. Cluster I had the maximum number of genotypes. The characters days to maturity, 100-seed weight and days to flowering were the highest contributors to D^2 values.

Valarmathi *et al.* (2007) studied genetic divergence analysis in sixty eight cowpea genotypes, which included 60 genotypes of *Vigna unguiculata* ssp. *unguiculata* and eight genotypes of *Vigna unguiculata* ssp. *sesquipedalis.* All of the accessions were grouped into twelve clusters based on Mahalonobis D^2 analysis, in which cluster I was the largest having 47 genotypes from spp. *unguiculata. V. unguiculata* spp. *unguiculata* were grouped in seven distinct clusters, whereas the genotypes of *sesquipedalis* were grouped in five other distinct clusters. Days to maturity contributed maximum to the genetic divergence followed by hundred seed weight and characters namely number of branches per plant, number of seeds per pod and total exhibited least contribution among the accessions.

Singh *et al.* (2007) assessed genetic divergence in 120 genotypes of cowpea using D^2 statistics evaluated for eight characters viz., days to flowering, number of grains per pod, number of pods per plant, pod length, harvest index, grain yield per plant and crude protein content of grains. The number of pods per plant contributed maximum towards genetic divergence followed by 100-grain weight, days to flowering and harvest index.

Suganthi and Murugan (2007) evaluated 30 genotypes of Cowpea for 10 characters to quantify the genetic diversity existing among them by using Mahalanobis D^2 statistic. These genotypes were grouped into 11 clusters. Cluster strength varied from single genotype (Cluster VI, IX and XI) to 7 genotypes (cluster III). Cluster VI had maximum seed yield per plant, number of pods per cluster, pod length, number of seeds per pod and number of pods per plant followed by cluster III. Cluster IX had maximum test weight.

Dahiya *et al.* (2007) evaluated 80 cowpea genotypes. The analysis of variance revealed significant differences for days to flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, seeds per pod, seed yield per plant, 100-seed weight, biological yield and harvest index. The 80 genotypes were grouped into 9 distinct clusters. All the clusters had more than 5 genotypes except cluster IX, which was monogenotypic.

Indradeo (2007) evaluated 44 grain cowpea for 13 characters to quantify the genetic diversity existing among them by using Mahalanobis D^2 statistic. The genotypes fell into 9 clusters. Cluster strength varied from single genotype (Cluster IV to IX) to 31 genotypes (cluster I). Cluster III had minimum days to first flower opening, days to 50 percent flowering and seed yield per plant in addition to maximum number of pod per plant and primary branches. Cluster II, V, VII had maximum yield per plant, 100-seed weight pod length and number of seeds per pod, respectively. Cluster II had minimum days to maturity, while cluster VII showed maximum days to maturity.

Genetic divergence for 13 yield characters among 33 strains of yard long bean was studied by D^2 statistic. It showed that there is a substantial genetic diversity between the strains with intra-cluster distances (D) values ranging from 10.62 to 13.69 and inter-cluster distances (D) ranging from 12.94 to 32.27. These 33 genotypes were grouped into 12 clusters. The clustering pattern revealed that genetic divergence is not necessarily associated with geographical diversity in this crop (Dash and Mishra, 2008).

Francisco *et al.* (2009) studied genetic divergence in 28 cowpea genotypes. It was observed that the D^2 distances of 89.2% of the genotypes were highest when combined with genotype CE-46 (1) the highest genetic divergence was observed between the genotypes CE-46 (1) and MNC 03-720C-11 (22) (D^2=438.585704), indicating genotype CE-46 as the most divergent of all.

Manish Sharma *et al*. (2009) studied genetic divergence in 33 genotypes of pole type French beans. The genotypes were grouped into six clusters, majority of which were accommodated in cluster I, followed by cluster VI. Maximum intra cluster distance was in cluster V followed by cluster I and the inter cluster distance was observed maximum between cluster IV and V followed by cluster I and VI. Cluster mean for different characters revealed that cluster V was the best of all from snap bean point of view and should be exploited in breeding program. Dias *et al.* (2009) assessed the genetic divergence between 28 cowpea lines. They observed that 100-grain weight (W100G) was one of the most important traits contributing to genetic divergence.

Dalsaniya *et al.* (2009) evaluated 60 Cowpea genotypes and found that inter cluster distance and mean cluster character values indicated that hybridization of cluster-X variety (JCPL-134) with cluster-IV varieties (JCPL-1, JCPL-13 and JCPL-21) and cluster-V varieties (JCPL-50 and JCPL-133) with cluster-III varieties (JCPL-26 and JCPL-131) would exhibit high heterosis and also result in transgressive segregants with higher yield.

Rahim *et al.* (2010) evaluated 26 mungbean genotypes. Twenty six genotypes were grouped into 3 clusters. Maximum number of genotypes (12) was grouped into cluster II. The maximum range of variability was observed for number of pods per plant (12.22 - 20.55) among all the characters in 3 clusters. Crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness.

Upadhyay and Mehta (2010) studied 32 genotypes of *Dolichos lablab*. It was observed that Cluster II was the biggest cluster with thirteen genotypes. Whereas, cluster I, III, IV, V comprised of 1, 4, 6 and 8 genotypes, respectively. Experimental findings revealed that the highest intra cluster distance was observed for cluster III (2.105) followed by cluster V (2.061), cluster IV (1.905) and cluster II (1.889). The highest inter cluster distance was observed between the clusters III and cluster I (5.708) followed by cluster IV and I (5.526) and cluster V and I (5.313). The minimum inter cluster distance was noted in between IV and II (2.712).

Nagalakshmi *et al.* (2010) investigated 66 genotypes of cowpea and found that cluster I had the maximum number of genotypes i.e., 22 and cluster XXII had only one genotype. Intra cluster distance analysis revealed that the minimum intra cluster distance was observed in the cluster II. The inter-cluster distance (D) was found to be the maximum between the clusters XXII and XXIII and the same was minimum between clusters II and V. The results indicated that grain yield per plant contributed maximum to the total divergence followed by 100 seed weight and days to 50% flowering. Number of branches per plant had least contribution to the total divergence followed by petiole length.

Huque *et al.* (2012a) investigated genetic divergence among 13 commercial yard long bean genotypes to select the parents for hybridization using Mahalanobis D^2 statistic. Cluster analysis was used for grouping 13 yard long bean genotypes. The genotypes fall into four clusters. Cluster III had the maximum (5) and cluster I had the minimum (1) number of genotypes. Cluster III had highest intra-cluster distance and the lowest in cluster I. The intercluster divergence ranged from 4.2 to 15.5 between clusters II and III and clusters I and II, respectively. The characteristics i.e., number of pods per plant, number of pods per cluster, days to first flowering, and vegetable pod yield per plant contributed maximum towards divergence among yard long bean genotypes.

Costa *et al.* (2013) estimated the genetic divergence in 57 African cowpea lines for various traits i.e., number of pods per peduncle, pod length (PL), number of grains per pod (NGP), grain length (GRL), grain width, 100-grain weight (W100G), and yield. The characteristics that contributed most to genetic divergence were W100G (49.7%), PL (16.7%), GRL (12.0%), and NGP (9.7%).

CHAPTER III

MATERIALS AND METHODS

A field experiment was conducted in the experimental farm of Sher-e-Bangla Agricultural University (SAU) during season '*Kharif*' 2016 to study the "Genetic diversity and character association in yield and yield contributing traits of yard long bean". The details of materials and methods used and the experimental technique adopted during the course of investigation are described below.

3.1 EXPERIMENTAL MATERIAL

A total of seven yard long bean genotypes were used in this study. These genotypes were collected from local market and shown in Table 1.

Table 1. Details of the experiential materials

Genotypes	Name of the Genotypes	Description	Sources
G1	Green Mallika	Green	Mallika Seed Co. Ltd.
G2	Toki	Deep Green	Lal Teer Seed Co. Ltd.
G3	Lal Borboti 1	Red	Banasree Agro Seed Co. Ltd.
G4	Banalota	White	Lal Teer Seed Co. Ltd.
G5	Lal Bani	Red	Lal Teer Seed Co. Ltd.
G6	Lal Borboti 2	Red	HR Hybrid Seed Co. Ltd.
G7	Kagornatoki	Deep Green	Masud Seed Co. Ltd.

3.2 THE EXPERIMENT SITE

The study was carried out in the experimental farm of SAU, Dhaka-1207 which is characterized by the sub-tropical climate and AEZ No. 28 called "Madhupur Tract".

3.3 CLIMATE AND SOIL

The geographical location of the experimental site was under the subtropical climate, characterized by three distinct seasons**,** the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris *et al.*, 1979) and also characterized by heavy precipitation during the month of May to

August and scanty precipitation during the period from October to March. The record of air, temperature, humidity and rainfall during the period of experiment were recorded from the Bangladesh Metrological Department, Agargaon, Dhaka (Appendix III, IV & V**)**. The soil was loam in texture. The experimental site was medium high land and the pH was 5.6 to 5.8 and organic carbon content was 0.82%.

3.4 DETAILS OF THE EXPERIMENT

For this study, the experiment was conducted during *Kharif*, 2016. The experiment was carried out to study the genetic variability and diversity. The experiment was laid out in a Randomized Complete Block Design (RCBD). Seed of each genotype were sown with a spacing of 50 cm x 30 cm in three replications. The plants were trained onto an inverted ‘V’ structure.

Details of Layout

1. Crop: Yard long bean
2. Number of varieties: Seven
3. Design: Randomized Complete Block Design (RCBD)
4. Replications: Three
5. Season: *Kharif*-2016
7. Total area: 15.5 m x 21.5 m = 333.25 m^2
8. Spacing: 50cm x 30cm
9. Location: The experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207.

3.5 CULTURAL PRACTICES

3.5.1 Land preparation

The experimental area was thoroughly ploughed and brought to a fine tilth. One ton of FYM and the recommended basal dose of fertilizers were incorporated in the soil before final harrowing. The entire plot was divided in to three blocks. The main and sub irrigation channels were laid out taking into account the gradient of the site.

Plate 1. Land preparation for yard long bean

3.5.2 Manures and Fertilizers

The recommended dosage of Urea, TSP, MP was applied in field at the rate of 55, 160, 160 Kg/ha respectively. Nitrogen was applied in two splits, the first dose as basal application and other split dose at 30 days after planting at flower initiation. The entire dose of phosphorus and potash were applied at the time of sowing as basal dose.

3.5.3 Seed Sowing

After the lay out, the varieties were assigned to different plots in each replication by using random numbers. The seeds of each genotype were sown by dibbling two to three seeds per hill. The gap filling was done by re-sowing within a week after germination.

3.5.4 Thinning of excess seedlings

The weak seedlings were thinned out leaving only one vigorous and healthy seedling per hill after 25 days of sowing. The remaining second half dose of nitrogen was top dressed at 30 days after sowing. All recommended cultural practices were followed to raise a good yard long bean crop.

3.5.5 Trellis

Plants were trailed on bamboo stick and tied with GI (galvanized iron) wire as reverse ‘V’ shape.

3.6 OBSERVATIONS RECORDED

Observations were recorded on five plants in each genotype in each replication for all the characters studied. The mean values of five plants were averaged and expressed as mean of the respective characters. The details of data recorded are as follows.

3.6.1 Days to first flowering

Number of days taken from the date of sowing to the day when the first flower appeared in a plot was counted.

3.6.2 Days to 50% flowering

Number of days taken from the date of sowing to the day when 50 percent of the plants in a plot flowered was counted.

3.6.3 Days to marketable harvest

Number of days taken from the date of sowing to the day when marketable pods were harvested in a plot was counted.

3.6.4 Pod length (cm)

Mean length of the ten random matured pods harvested at edible maturity stage for culinary purpose was measured and expressed in centimeters.

3.6.5 Pod diameter (cm)

The mean diameter of ten random matured pods from each of the selected tagged plants was measured in centimeters from the center of the pod with the help of Vernier calipers.

3.6.6 Number of pods per plant

Number of well filled pods on each sample plant was counted and the mean value of the random sample plants was recorded.

3.6.7 Average pod weight (g)

Average pod weight was counted from ten randomly selected pods of a genotype from each replication and the mean was computed as gram.

3.6.8 Seed number per pod

Number of seeds per pod was counted from ten randomly selected pods of a genotype from each replication and the mean was computed.

3.6.9 100 seed weight (g)

A random sample of one hundred well developed seeds were weighed and expressed in gram.

3.6.10 Pod yield per plant (g)

Weight of green, tender and marketable pods per plant from each sample plant was recorded and expressed in gram.

Plate 2. Experimental field with different genotypes at seedling stage

Plate 3. Flower of yard long bean

Plate 3. Flower of yard long bean

Plate 4. Podding stage of a yard long bean genotype

3.7 STATISTICAL ANALYSIS

The mean replicated data collected on ten traits were subjected to biometrical analysis following appropriate biometrical procedures.

3.7.1 Analysis of Variance

Analysis of Variance was carried out as per the procedure given by Panse and Sukhatme (1985). Statistical significance of variation due to genotype was tested by comparing calculated values to F-table values at one percent and five percent level of probability, respectively.

Data on the ten characters, namely days to first flowering, day to 50% flowering, days to marketable harvest, pod length (cm), pod diameter (cm), no. of pods per plant, average pod weight (g), no. of seeds per pod, 100 seed weight (g) and pod yield per plant (g) were recorded from five randomly selected plants from each plot. Mean data for each character was subjected to multivariate Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO) and Cluster Analysis (CLSA) using GENSTAT 5.13 (Mahalanobis 1936 and Digby *et al.* 1989).

3.7.2 Genotypic and phenotypic variance

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

Genotypic variance (σ^2_g) = $\frac{\text{GMS} - \text{EMS}}{\text{r}}$

Where,
GMS = Genotypic mean sum of square
EMS = Error mean sum of square
r = number of replications

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

Where,
σ^2_g = Genotypic variance
σ^2_e = Error variance

Genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma_g^2}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973) and are given below

0-10 %: Low; 11-20 %: Moderate; 21 % and above: High

Heritability

Broad sense heritability was estimated by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2{}_b\% = \frac{\sigma^2{}_g}{\sigma^2 p} \times 100$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The range of heritability in broad sense was classified as suggested by Johnson et al. (1955). Less than 30 %: Low; 30-60 %: Moderate; More than 60 %: High

Genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, GA = K. h^2. σ_p

Or Genetic advance, GA = K. $\frac{\sigma^2 g}{\sigma^2 p}.\sigma_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} \text{ X 100}$$

Genetic advance as percent mean was categorized as given below as suggested by Johnson *et al*. (1955).

0-10% - Low; 10.1-20% - Moderate; >20.1% - High

Genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Genotypic correlation, $r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} =$

Where,

$\sigma_{gxy} =$ Genotypic co-variance between the traits x and y

$\sigma^2_{gx} =$ Genotypic variance of the trait x

$\sigma^2_{gy} =$ Genotypic variance of the trait y

Phenotypic correlation (r_{pxy}) = $\frac{PCOVxy}{\sqrt{PVx.PVy}}$ = $\frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$

Where,

$\sigma_{pxy} =$ Phenotypic covariance between the trait x and y

$\sigma^2_{px} =$ Phenotypic variance of the trait x

$\sigma^2_{py} =$ Phenotypic variance of the trait y

Estimation of path co-efficient

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3….and 11 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y}$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y}$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y}$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y}$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y}$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y}$

$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.yy}$

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y}$

Where,

$r_{1.y}$ = Genotypic correlation coefficients between y and ith character (y = Fruit yield)

P_{iy} = Path coefficient due to ith character (i= 1, 2, 3,….11)

Where,

$P_{1.y}, P_{2.y}, P_{3.y.}$.……… $P_{8.y}$ = Path coefficient of the independent variables 1, 2, 3,….,8 on the dependent variable y, respectively.

$r_{1.y}, r_{2.y}, r_{3.y}$, …., $r_{8.y}$ = Correlation coefficient of 1, 2, 3,…., 8 with y, respectively.

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

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots + r_{8.y}P_{8.y})$

Where,

$P^2_{RY} = R^2$

and hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the ith character on yield y.

$r_{1.y}$ = Correlation of the ith character with yield y.

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 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), principal coordinate analysis (PCO), Cluster analysis and canonical vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

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 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.

Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

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.

Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster

n = Number of all possible combinations between the populations in cluster

Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average inter-cluster distance= $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible

combinations of the populations in cluster i and j

n_i= Number of populations in cluster i

n_j= Number of populations in cluster j

Cluster diagram

Using the values of intra and inter-cluster distances (D = $\sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chaudhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

Plates 5. Yard long bean plants with pods

Plate 6. Different genotypes of yard long bean plants with pods

Plate 7. Pods of different genotypes

Plate 8. Experimental plot

CHAPTER IV

RESULTS AND DISCUSSIONS

The results of the study entitled "Genetic diversity and character association in yield and yield contributing traits of yard long bean" is presented as follows:

4.1 ANALYSIS OF VARIANCE

The estimated yield and yield contributing traits subjected to analysis of variance. The mean square values are given in Table 2. The mean sum of square due to genotypes revealed significant difference for different traits viz. days to 1st flowering, days to 50% flowering, days to marketable harvest, pod length (cm), pod diameter (cm), no. of pod per plant, average pod weight (g), no. of seed per pod, 100-seed weight (g) and pod yield per plant (g), whereas, the mean sum of square due to replication for number of pods per plant was also significant. Thus, considerable amount of genetic variability was present in the experimental material which can be exploited for improvement of pod yield and yield related attributes in yard long bean. Similar results were reported by Manju (2006), Sivakumar *et al.*, (2014) and Litty and Celine (2015). The co-efficient of variation (CV) were below 10% (Table 3) for all the characters except pod diameter revealed that confirming the reliability of the experiment and also suggesting less G x E interactions.

Table 2. Analysis of variance (ANOVA) for ten in traits in yard long bean

Source	Df	Mean sum of square (MSS)									
		DFF	D50%F	DMH	PL	PD	NPP	APW	NSP	HSW	PYP
Replication	(r-1) 2	0.19	1.86	2.48	3.57	0.01	0.59	0.13	0.19	0.06	208.55
Genotype	(g-1) 6	5.05**	6.97**	8.49**	125.32**	0.03**	12.55**	4.63**	2.62*	6.41**	2830.36**
Error	(r-1)(g-1) 12	0.52	0.63	0.75	25.10	0.00	0.14	0.74	0.82	0.20	100.97

*= Significant at the 0.05 level, ** = Significant at the 0.01 level.

DFF: days to 1st flowering, D50%F: days to 50% flowering, DMH: days to marketable harvest, PL: pod length (cm), PD: pod diameter (cm), NPP: no. of pod per plant, APW: average pod weight (g), NSP: no. of seed per pod, HSW: 100 seed weight (gm) and PYP: pod yield per plant (g).

4.2 MEAN PERFORMANCE

4.2.1 Days to 1st flowering

Days to first flowering varied from 35.00 to 38.67 days with the average days being 36.62 days (Table 3). The earliest flowering was observed in the variety Toki (35.00 days) which was statistically similar with Kagornatoki (35.67) and Lal Bani (36.00) While, the variety Lal Borboti-2 (38.67 days) took the maximum days to first flowering which was similar in statistically with Banalota (38.00).

4.2.2 Days to 50% flowering

The data pertaining to days to 50 percent flowering depicted in Table 3 &4. The days taken to 50 percent flowering in different genotypes varied from 41.00 to 45.33 days with an overall mean of 42.57. Maximum days to 50 percent flowering is exhibited by genotype Lal Borboti (45.33) which was statistically similar with Banalota (44.00) whereas, earliest flowering is exhibited by the cultivar Lal Bani (41.00) and it was statistically similar to Toki (41.67), Lal Borboti-1 (42.00) and Green Mallika (42.00) (Table 4).

Table 3. Range, mean, CV (%) of 10 traits in yard long bean

Parameters	Range		Mean	CV (%)
	Min.	Max.		
Days to 1st flowering	35.00	38.67	36.62	1.98
Days to 50% flowering	41.00	45.33	42.57	1.87
Days to marketable harvest	60.67	65.33	62.38	1.39
Pod length (cm)	46.97	65.73	54.21	9.24
Pod diameter (cm)	0.41	0.73	0.57	11.79
No. of pod per plant	5.39	10.99	7.26	5.10
Average Pod weight (g)	13.18	16.58	14.60	5.88
No. of seed per pod	19.33	21.70	20.16	4.50
100 seed weight (gm)	9.44	13.75	12.11	3.69
Pod yield per plant (g)	79.07	166.67	108.24	9.28

Min:minimum; Max:maximum; CV (%):coefficient of variation

Table 4. Mean performance of ten characters of 10 yard long bean

Genotype	DFF	D50% F	DMH	PL	PD	NPP	APW	NSP	HSW	PYP
G1	36.67b	42.00b	61.67b	53.21bc	0.4133c	10.99a	14.18bc	21.70a	11.86c	166.7a
G2	35.00c	41.67b	60.67b	46.97c	0.5533b	8.647b	13.21c	21.23ab	9.440d	121.4b
G3	36.33bc	42.00b	62.00b	49.23bc	0.5333bc	6.147d	13.18c	19.83bc	11.41c	94.00c
G4	38.00a	44.00a	64.00a	49.73bc	0.7267a	6.107d	16.58a	19.43c	13.54a	89.93c
G5	36.00bc	41.00b	61.00b	57.87ab	0.6533ab	7.967c	15.71ab	20.07abc	12.04bc	121.1b
G6	38.67a	45.33a	65.33a	65.73a	0.5433bc	5.613de	14.62bc	19.53bc	12.72b	85.47c
G7	35.67bc	42.00b	62.00b	56.70abc	0.5867b	5.39e	14.69bc	19.33c	13.75a	79.07c

Means with the same letter are not significantly different; DFF: days to 1st flowering, D50%F: days to 50% flowering, DMH: days to marketable harvest, PL: pod length (cm), PD: pod diameter (cm), NPP: no. of pod per plant, APW: average pod weight (g), NSP: no. of seed per pod, HSW: 100 seed weight (gm) and PYP: pod yield per plant (g).

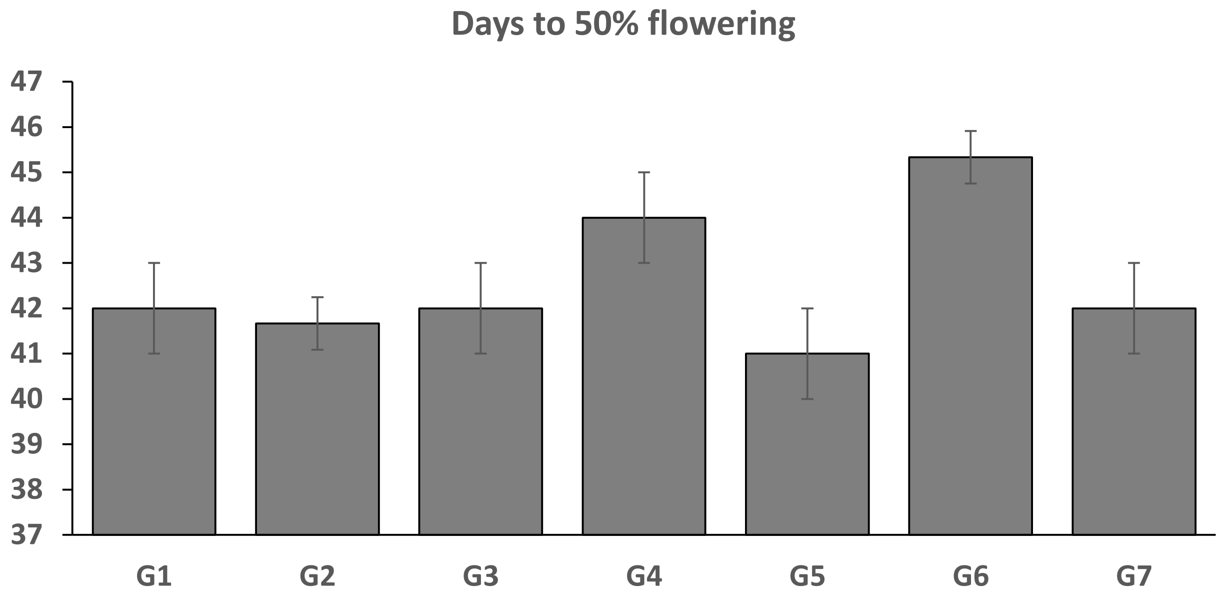

Figure 1. Variation in mean performance of yard long bean genotypes on days to 50% flowering

4.2.3 Days to marketable harvest

Days to marketable harvest ranged from 60.67 to 65.33 days and grand mean was calculated 62.38 days (Table 3). The Genotype Toki was earliest for days to first picking (60.67 days) insignificantly followed by Lal Bani (61.00 days). While, Lal Borboti-2 was the latest for the same (65.33 days) which was insignificantly followed by Banalota (64.00 days).

4.2.4 Pod length (cm)

Significant difference was observed for the studied verities for pod length (Table 2). The pod length of different genotypes recorded in the range of 46.97 cm to 65.73 cm with average mean of 54.21. The maximum length of pod recorded in the variety Lal Borboti-2 (65.73 cm) which was statistically similar with Lal Bani (57.87 cm) and Kagornatoki (56.70 cm). On the other hand, genotype Toki recorded minimum pod length ((46.97 cm) which was similar in statistically with Lal Borboti-1 (49.23 cm) and Banalota (49.73 cm).

4.2.5 Pod diameter (cm)

Pod diameter ranged from 0.41 to 0.73 cm and the average value was 0.57 cm (Table 3). Pod diameter was observed maximum in genotype Banalota (0.73 cm) and it was statistically similar with Lal Bani (0.65 cm). The minimum pod diameter was observed in in genotype Green Mallika (0.41 cm) which was similar in statistically with Lal Borboti-1 (0.533 cm).

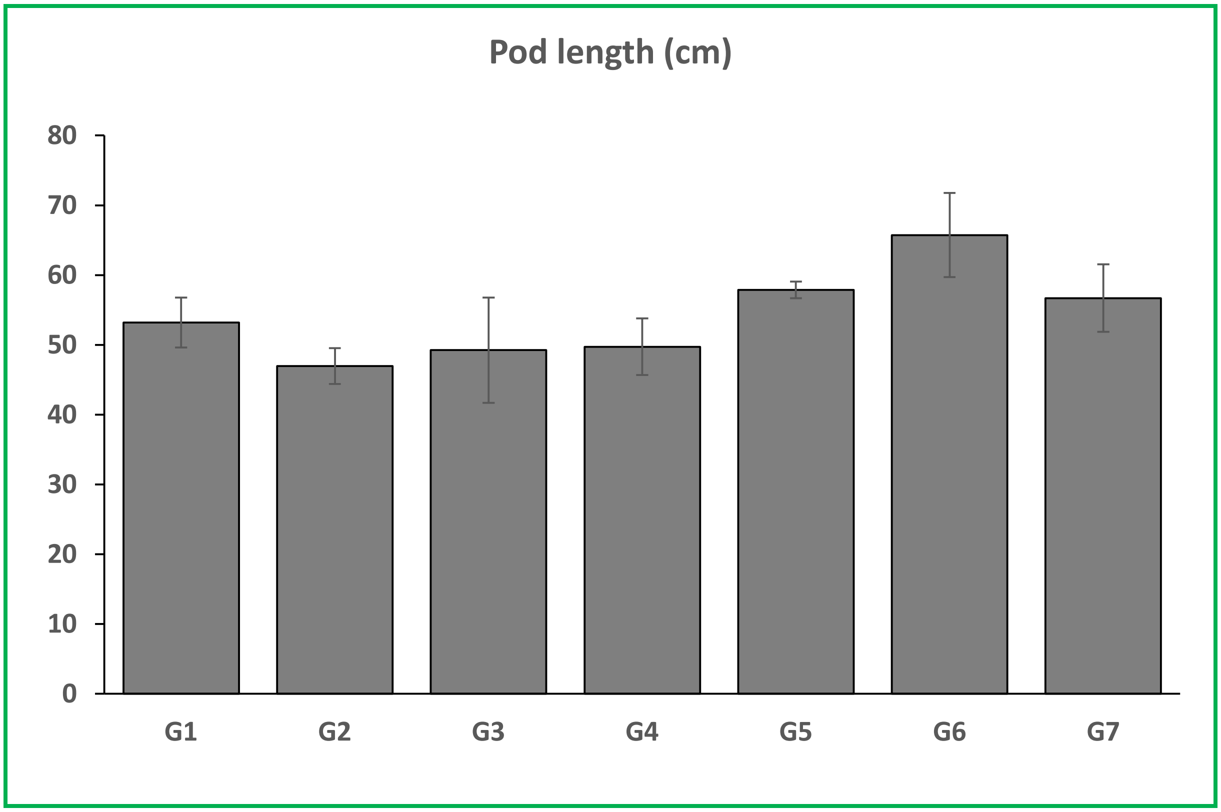

Figure 2. Variation in mean performance of yard long bean genotypes on pod length

4.2.6 No. of pod per plant

Number of pods per plant was exhibited significant difference among the studied verities (Table 2). It was varied from 5.39 to 10.99 with an overall mean of 7.26. Highest number of pods per plant recorded in Green Mallika (10.99) which was significantly followed by Toki (8.647) and Lal Bani (7.967). The lowest number of pods per plant was exhibited by Kagornatoki (5.39) and it was statistically similar with Lal Borboti-2 (5.613) (Table 4).

4.2.7 Average pod weight (g)

The weight of pod range from 13.18 to 16.58 g, while, the grand average of pod weight was recorded 14.60 g. The maximum pod weight was observed in genotype Banalota (16.58 g) which was similar in statistically with Lal Bani (15.71 g) (Table 4). The minimum pod weight was recorded in genotype Lal Borboti-1 (13.18 g) and it statistically similar with Toki (13.21 g).

4.2.8 No. of seed per pod

The average number of seeds per pod was recorded 20.16 and it ranged from 19.33 to 21.70 seeds per pod (Table 3). The Maximum number of seeds per pod was observed in genotype Green Mallika (21.70) and it was similar in statistically with Toki (21.23) and LalBani (20.07). While it was minimum in genotype Kagornatoki (19.33) which was similar in statistically with Banalota (19.43) and Lal Borboti-2 (19.53).

4.2.9 100 seed weight (gm)

100 seed weight ranged from 9.44 g to 13.75 g, while, the average weight of 100 seeds were recorded 12.11 g (Table 3). The maximum 100 seed weight was observed in genotype Kagornatoki (13.75 g) and it was statistically similar with Banalota (13.54 g). The minimum weight of 100 seed was in the genotype Toki (9.44 g).

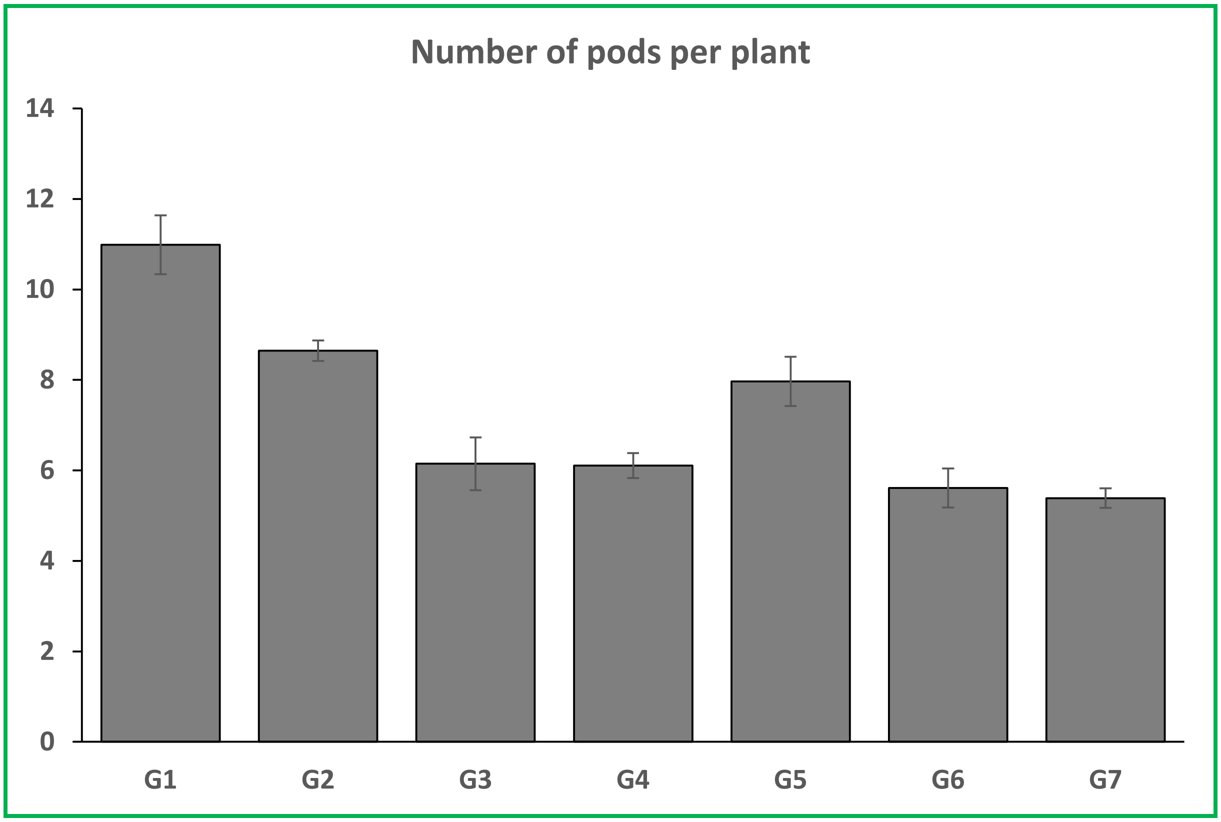

Figure 3. Variation in mean performance of yard long bean genotypes on number of pods per plant

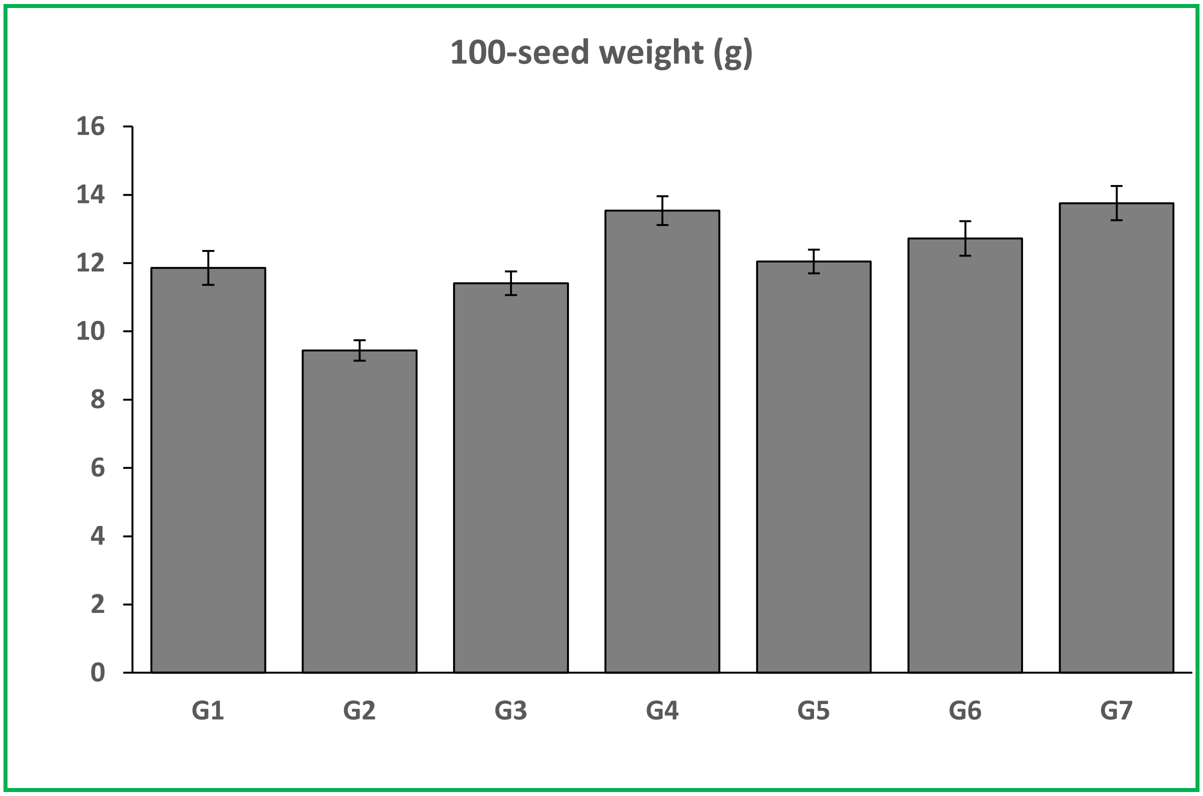

Figure 4. Variation in mean performance of yard long bean genotypes of hundred seed weight

4.2.10 Pod yield per plant (g)

Yield is the vital character considered for selection. Pod yield per plant was exhibited significantly difference among the tested genotypes according to analysis of variance (Table 2). Pod yield per plant varied from 79.07 g to 166.7 g with an overall mean of 108.24 (Table 3). The maximum green pod yield recorded in genotype Green Mallika (166.7 g) significantly followed by Lal Bani (121.1 g) and Toki (121.4 g). While minimum pod yield per plant recorded in Kagornatoki (79.07 g) which was statistically similar with Lal Borboti-2 (79.07 g).

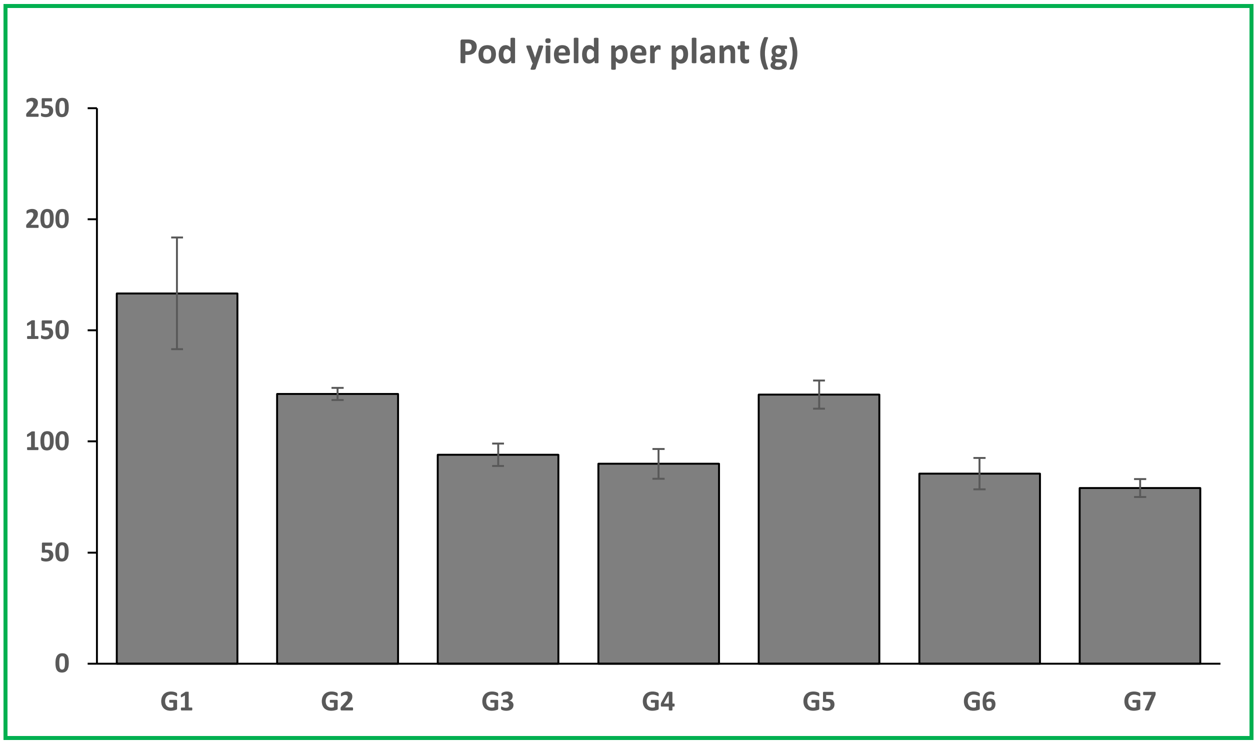

Figure 5. Variation in mean performance of yard long bean genotypes on pod yield per plant

4.3 VARIABILITY PARAMETERS

Estimated variability components viz. phenotypic and genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent of means (GA%) for 10 characters are presented in Table 5, 6 & 7.

4.3.1 Phenotypic and Genotypic variance

Estimation of phenotypic and genotypic variance in a population is decisive factor for scope and efficiency of selection of individuals for future breeding program in crop species. The seven genotypes of yard long bean in present investigation were grown to estimate the variance parameters for ten characters comprising yield and yield attributing traits. The highest phenotypic variances were calculated for pod yield per plant (1010.77) followed by pod length (58.51) and while the lowest value was recorded for pod diameter (0.01) followed by number of seeds per pod (1.42), days to first flowering (2.03) and average pod weight (2.03) (Table 5). The genotypic variance ranged from 0.01 to 909.80. The highest genotypic variance was observed in trait pod yield per plant (909.80) followed by pod length (33.41) while the minimum genotypic variance was performed by the trait pod diameter (0.01) followed by number of seeds per pod (0.60). This study result showed that the traits exhibited phenotypic variances higher than their respective genotypic variances thus revealing the great significant influence of environmental factors in the expressions of the traits in yard long bean genotypes and the apparent variation is not only due to the genotypes but also due to the influence of environment. Low difference between the traits for σ^2p and σ^2g indicated that low environmental influence on these characters. Low difference of phenotypic and genotypic variance were observed in then traits days to 50% flowering (2.75 and 2.11), pod diameter (0.01 and 0.01), number of pods per plant (4.28 and 4.14) and 100 seed weight (2.27 and 2.07) indicated low environmental influences on the expression on these traits. Large difference between σ^2p and σ^2g indicating large environmental influences on expression of any character. High phenotypic and genotypic variance was found the traits pod length (58.51 and 33.41) and pod yield per plant (1010.77 and 909.80) suggested that large environmental influences on the expression of the genes controlling of these trait. According to Manivannan and Anandakumar (2013) research characters such as seed yield per plant, number of pods per plant and plant height were influenced by the environment strongly.

Table 5. Estimation of genotypic and phenotypic variance for ten characters in yard long bean

Parameters	**σ^2p**	**σ^2g**	**σ^2 e**
Days to 1st flowering	2.03	1.51	0.52
Days to 50% flowering	2.75	2.11	0.63
Days to marketable harvest	3.33	2.58	0.75
Pod length (cm)	58.51	33.41	25.10
Pod diameter (cm)	0.01	0.01	0.00
No. of pod per plant	4.28	4.14	0.14
Average Pod weight (g)	2.03	1.30	0.74
No. of seed per pod	1.42	0.60	0.82
100 seed weight (gm)	2.27	2.07	0.20
Pod yield per plant (g)	1010.77	909.80	100.97

σ^2p:Phenotypic variance; σ^2g: Genotypic variance; σ^2e:Environmental variance

4.3.2 Phenotypic and genotypic coefficient of variation

An estimate of the magnitude of phenotypic and genotypic coefficient of variation present in a population is of great importance as it provides the basis for effective selection. The GCV provides a valid basis for comparing and assessing the range of genetic variability for quantitative characters and PCV measures the extended of total variation. The phenotypic coefficient of variation (PCV) ranged between 2.93% (days to marketable harvest) to 29.37% (pod yield per plant) while genotypic coefficient of variation (GCV) ranged between 2.57% (days to marketable harvest) to 28.00% (number of pods per plant) (Table 6). High proportion of GCV to PCV is desirable in selection process because it depicts that the traits are much under the genetic control rather than the environment (Kaushik *et al.*, 2007). High difference between PCV and GCV was observed in pod length (14.11% and 10.66%) and pod diameter (19.75% and 15.85%) which suggested that environment has a significant role on the expression of these traits. The magnitudinal differences were medium to low in GCV and PCV for average pod weight (9.77% and 7.80%), number of seeds per pod (5.91% and 3.84%), 100 seeds weight (12.44% and 11.88%) and pod yield per plant (29.37% and 27.87%) **(**Table 6) suggesting the little role of environment in the expression of these traits. The closer magnitude of genotypic and phenotypic coefficients of variation for days to first flowering (3.89% and 3.35%), days to 50% flowering (3.89% and 3.41%), days to marketable harvest (2.93% and 2.57%) and number of pods per plant (28.46% and 28.00%) indicated that a greater magnitude was played by genotype rather than environment. Improvement of these characters through selection is desirable. These results were in agreement with earlier reports by Panicker (2000), Selvam *et al.* (2000), Jyothi (2001), Kutty *et al.* (2003), Madhukumar (2006), Sivakumar *et al.* (2014) and Litty and Celine (2015).According to Sivasubramaniah and Meron (1973) PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. Based on this delineation PCV and GCV recorded in this study, days to first flowering (3.89% and 3.35%), days to 50% flowering (3.89% and 3.41%), days to marketable harvest (2.93% and 2.57%), average pod weight (9.77% and 7.80%) and number of seeds per pod (5.91% and 3.84%) had low values (<10%) for both phenotypic and genotypic coefficient of variations. The low PCV and GCV value of traits suggests the higher influence of environment on these traits thus; selection on the phenotypic basis would not be effective for the genetic improvement. It is indicating low variability which limits the scope for improvement of these characters through selection. Similar results were reported by Lovely (2005), Manju (2006), Sivakumar *et al.*, (2014) and Litty and Celine (2015).

Moderate GCV and PCV were found in pod length (14.11% and 10.66%), pod diameter (19.75% and 15.85%) and 100 seed weight (12.44% and 11.88%), respectively (Table 6). Medium PCV and GCV value suggests that these characters are controlled more of by the genetic factors. Hence, these characters amenable to selection for further improvement. Among all characters exhibiting high degree of genotypic and phenotypic coefficients of variation were in number of pods per plant (28.46% and 28.00%) and pod yield per plant (29.37% and 27.87%), respectively. The results of this study suggest that traits with high PCV and GCV are amenable for selection. The high PCV and GCV value with low magnitude of differences between the two genetic parameters indicates that the less environmental influence on the phenotypic expression. The study thus revealed that the character with high PCV and GCV contributes to maximum variability. Hence, selection of desired character uses phenotypic value may be effective in improving the character.

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Table 6. Phenotypic and genotypic coefficient of variance for the ten characters in yard long bean

Parameters	PCV (%)	GCV (%)	ECV (%)
Days to 1st flowering	3.89	3.35	1.98
Days to 50% flowering	3.89	3.41	1.87
Days to marketable harvest	2.93	2.57	1.39
Pod length (cm)	14.11	10.66	9.24
Pod diameter (cm)	19.75	15.85	11.79
No. of pods per plant	28.46	28.00	5.10
Average Pod weight (g)	9.77	7.80	5.88
No. of seed per pod	5.91	3.84	4.50
100 seed weight (gm)	12.44	11.88	3.69
Pod yield per plant (g)	29.37	27.87	9.28

PCV:Phenotypic coefficient of variation; GCV:Genotypic coefficient of variation; ECV:Environmental coefficient of variation

4.3.3 Heritability and genetic advance

Estimation of heritability serves as a useful guide to breeder for determination of variation that is due to genotypic broad sense heritability or narrow sense heritability effects. Traits with high broad sense heritability estimates suggest that they have high genetic potential; the effect of the environment in determining them is low. According to Robinson *et al.* (1955) heritability is categorized as low (0-30%), moderate (31-60%) and high > 60%. High heritability was observed in the traits days to first flowering (74.22%), days to 50% flowering (76.88%), days to marketable harvest (77.38%), pod diameter (64.39%), number of pods per plant (96.78%), average pod weight (63.76%), 100 seed weight (91.21%) and pod yield per plant (90.01%) (Table 7) indicated to be effective in the selection of superior genotypes on the basis of phenotypic performance. Moderate heritability was performed by number of seeds per pod suggests improvement through selection.

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented (Table 7). In this study, genetic advance ranged between 4.67% for days to marketable harvest to 56.74% for number of pods per plant. Genetic advance as percent mean was categorized as high (≥20%), moderate (10-20%) and low (0-10%) (Johnson *et al.*, 1955). As per this suggestion, the highest (≥20%) genetic advance was observed for pod diameter (26.20%), number of pods per plant (56.74%), 100 seeds weight (23.37%) and pod yield per plant (56.46%). Moderate genetic advance (10-20%) was observed for pod length (16.60%) and average pod weight (12.84%). Low genetic advance (<10%) was observed for days to first flowering (5.95%), days to 50% flowering (6.16%), days to marketable harvest (4.67%) and number of seeds per pod (5.14%).

The knowledge of the heritability along with genetic advance aids in drawing valuable conclusions for selection of breeding methods to be employed for further improvement of the traits. Higher estimates of broad sense heritability (more than 60%) coupled with the higher genetic advance (more than 20%) for number of pods per plant (96.78% and 56.74%), pod yield per plant (90.01% and 54.46%), pod diameter (64.39% and 26.20%) and 100 seed weight (91.21% and 23.37%) is indicative of additive gene action and selection based on these parameters would be more reliable. Previous workers (Sobha, 1994; Vidya *et al.*, 2002) also supported our findings for number of pods per plant and pod yield per plant.

High h^2_b along with moderate GA for the characters average pod weight (63.76% and 12.84%) indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. High heritability accompanied (more than 60%) with low genetic advance (less than 10%) for days to first flowering (74.22% and 5.95%), days to 50% flowering (76.88% and 6.16%) and days to marketable harvest (77.38% and 4.67%) indicated advancement of non-additive gene action and the high heritability is being exhibited due to favourable influence of the environment rather than genotypes. This result corroborates earlier observations of Vidya *et al.* (2002).

Moderate h^2_b with moderate GA for the trait pod length (57.10% and 16.60%) revealed the possibility of predominance of both additive and non additive gene action in the inheritance of this trait. Moderate heritability and low genetic advance for number of seeds per pod (42.20% and 5.14%) also has been reported by Vidya *et al.* (2002) and Nath *et al.* (2009).

Johnson *et al.* (1955) suggested that high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes than heritability values alone. So, it was observed that number of pods per plant and pod yield per plant exhibited high GCA, high heritability and high genetic advance in this study.

Table 7: Heritability and genetic advance for the ten characters in yard long bean

Parameters	**h^2_b**	**GA (5%)**	**GA (% mean)**
Days to 1st flowering	74.22	2.18	5.95
Days to 50% flowering	76.88	2.62	6.16
Days to marketable harvest	77.38	2.91	4.67
Pod length (cm)	57.10	9.00	16.60
Pod diameter (cm)	64.39	0.15	26.20
No. of pod per plant	96.78	4.12	56.74
Average Pod weight (g)	63.76	1.87	12.84
No. of seed per pod	42.20	1.04	5.14
100 seed weight (gm)	91.21	2.83	23.37
Pod yield per plant (g)	90.01	58.95	54.46

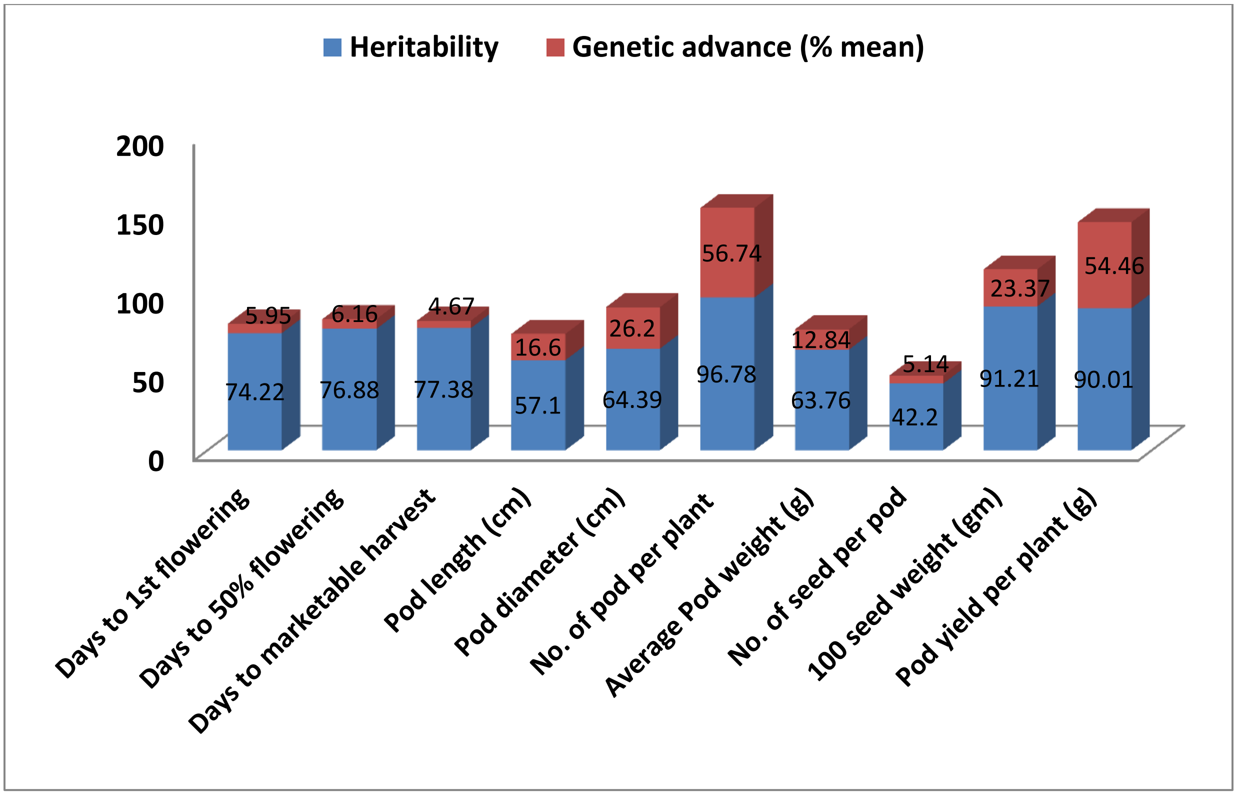

Figure 6. Comparison of heritability and genetic advance percent of mean

4.4 CHARACTER ASSOCIATION

Mutual association of traits is often expressed by phenotypic and genotypic correlations (Akinyele and Osekita, 2006). Phenotypic correlation is directly proportional to genotypic and environmental correlations. On the other hand, a positive genetic correlation between two desirable traits makes selection easy for improving both traits simultaneously while the reverse is the case for negative correlation. In the present study, genotypic correlation coefficients were higher than corresponding phenotypic correlation coefficients, indicating greater contribution of genotypic factor in the growth and development of these traits association (Table 8).

4.4.1 Association of yield with other traits

Significantly ($P<0.05$) positive genotypic and phenotypic relationships were found for number pods per plant (0.974 and 0.970) and number of seeds per pod (0.932 and 0.767) with pod yield per plant. Significant and positive genotypic correlation coefficients are an indication that selection of yard long bean genotypes for future breeding programme should be fundamentally based on the superiority of the genotypes alongside with their phenotypic expression. This implies that these two traits should be given high priority during selection. On the other hand, significantly ($P< 0.01$) negative correlations were exhibited for days to maturity (-0.537 and -0.503), days to 50% flowering (-0.483 and -0.429) and days to first flowering (-0.293 and -0.256) with pod yield per plant. It could be implied that yard long bean genotypes which flowered early would produce more pod yield. This agrees with the previous assertion by Umar *et al*. (2010) and Adeigbe *et al.* (2011).

Table 8. Genotypic (G) and phenotypic (P) correlation with yield

Traits		D50%F	DMH	PL	PD	NPP	APW	NSP	HSW	PYP
DFF	G	0.954**	0.992**	0.638**	0.242	-0.365	0.572**	-0.455*	0.583**	-0.293
	P	0.833**	0.869**	0.356	0.051	-0.291	0.351	-0.377	0.489*	-0.256
D50%F	G		0.978**	0.562**	0.229	-0.506*	0.316	-0.493*	0.449*	-0.483*
	P		0.976**	0.369	0.039	-0.439*	0.275	-0.403	0.423	-0.429
DMH	G			0.657**	0.298	-0.590**	0.450*	-0.635**	0.602**	-0.537*
	P			0.555**	0.082	-0.516*	0.312	-0.514*	0.555**	-0.503*
PL	G				-0.061	-0.330	0.266	-0.477*	0.524*	-0.307
	P				-0.043	-0.273	0.283	-0.303	0.441*	-0.154
PD	G					-0.604**	0.829**	-0.885**	0.465*	-0.645**
	P					-0.489*	0.623**	-0.434*	0.283	-0.480*
NPP	G						-0.259	0.976**	-0.552**	0.974**
	P						-0.204	0.767**	-0.512*	0.970**
APW	G							-0.695**	0.800**	-0.268
	P							-0.249	0.577**	-0.119
NSP	G								-0.857**	0.932**
	P								-0.552**	0.767**
HSW	G									-0.500*
	P									-0.439*

**, Significant at 1% level; * ,Significant at 5% level; DFF: days to 1st flowering, D50%F: days to 50% flowering, DMH: days to marketable harvest, PL: Pod length (cm), PD: Pod diameter (cm), NPP: no. of pod per plant, APW: average Pod weight (g), NSP: no. of seed per pod, HSW: 100 seed weight (gm) and PYP: pod yield per plant (g).

4.4.2 Correlations with yield components

Days to first flowering was significant and positive correlation with days to 50% flowering (0.954 and 0.833), days to marketable harvest (0.992 and 0.869), plant height (0.638 and 0.356), average pod weight (0.572 and 0.351) and hundred seed weight (0.583 and 0.489) at both genotypic and phenotypic levels. It was negatively correlated at genotypic and phenotypic levels with number of seeds per pod (-0.455 and -0.377) and number of pods per plant (-0.365 and -0.291).

Genotypic and phenotypic significant correlation coefficient was observed of days to 50% flowering with days to marketable harvest (0.978 and 0.976), plant height (0.562 and 0.369) and hundred seed weight (0.449 and 0.423). It was genotypic and phenotypic negative correlation with number of pods per plant (-0.506 and -0.439) and number of seeds per pod (-0.493 and -0.403).

Days to marketable harvest exhibited significant positively correlated with days to first flowering (0.992 and 0.869), days to 50% flowering (0.978 and 0.976), pod length (0.657 and 0.555), pod weight (0.450 and 0.312) and hundred seed weight (0.602 and 0.555) at both genotypic and phenotypic level. It was positively correlated with pod diameter (0.298 and 0.082) at both levels. Days to marketable harvest negatively significant correlated with number of pods per plant (-0.590 and -0.510) and number of seeds per pod (-0.635 and -0.514) at both levels.

Pod length was positively significant correlated with days to first flowering (0.638 and 0.356), days to 50% flowering (0.562 and 0.369), days to marketable harvest (0.657 and 0.555), hundred seed weight (0.524 and 0.441) at both levels. It was positively correlated with pod weight (0.266 and 0.283) at both levels. Pod length was exhibited negatively correlated with number of seed per pod (-0.477 and -0.303), number of pod per plant (-0.330 and -0.273) and pod diameter (-0.061 and -0.043).

Pod diameter was positively and significantly correlated with pod weight (0.829 and 0.623) and hundred grain weight (0.465 and 0.283); and positive insignificant correlation with days to first flowering (0.242 and 0.051) and days to marketable harvest (0.298 and 0.082). It was significant negatively correlated with number of pods per plant (-0.604 and -0.489) and number of seeds per pod (-0.885 and -0.434).

Number of pods per plant was correlated as significantly and positively with number of seeds per pod (0.976 and 0.767) at both levels. Number of pods per plant had genotypic and phenotypic significant negative correlation days to 50% flowering (-0.506 and -0.439), days to marketable harvest (-0.590 and -0.516), pod diameter (-0.604 and -0.489) and hundred seed weight (-0.552 and -0.512).

Pod weight had both genotypic and phenotypic positively significant correlation with pod diameter (0.829 and 0.623) and hundred seed weight (0.800 and 0.577). It was negative significant correlation with number of seeds per pod (-0.695 and -0.249) and insignificant negative correlation with number of pods per plant (-0.259 and -0.204).

Number of seeds per pod was positively significant correlated at both levels with number of pods per plant (0.976 and 0.767) and it had significant negative correlated with days to marketable harvest (-0.635 and -0.514), pod diameter (-0.885 and -0.434), pod weight (-0.695 and -0.249) and hundred seed weight (-0.857 and -0.552).

Hundred seed weight had positive significant correlated with days to first flowering (0.583 and 0.489), days to marketable harvest (0.602 and 0.555), pod length (0.524 and 0.441) and pod weight (0.800 and 0.577) at both genotypic and phenotypic levels. It had negative significant associated with number of pods per plant (-0.552 and -0.512) and number of seeds per pod (-0.857 and -0.552).

4.5 PATH COEFFICIENT ANALYSIS

In the present study, the correlations were partitioned into direct and indirect effects to identify relative importance of yield component towards pod yield of yard long bean. Pod yield yard long bean is important as this is utilized as vegetable throughout the world. Hence, the direct effect and positive association with pod yield per plant was considered essential. Among the nine yield component traits, days to first flowering (0.502), days to marketable harvest (1.269), number of pod per plant (0.600), pod weight (0.185) and number of seeds per pod (0.143) (Table 9) which was consistant with the findings of previous reports (Lal *et al*., 2007; Nath *et al*., 2009; Udensi *et al.*, 2012). The direct selection for these characters could be beneficial for yield improvement of yard long bean. Number of pods per plant and number of seeds per pod also showed positive correlation with pod yield per plant. Though Days to first flowering, days to 50% flowering and days to marketable harvest had had significant negative correlation with pod yield per plant but their direct and indirect effects were high positive. In such case, direct and indirect selection based on these characters would be very effective.

Table 9. Direct (bold) and indirect effects of different traits at genotypic level on yield

	Effect via									r_g(yield)
	DFF	D50%F	DMH	PL	PD	NPP	APW	NSP	HSW	
DFF	**0.502**	-1.471	1.259	-0.170	-0.086	-0.219	0.106	-0.065	-0.149	-0.293
D50%F	0.479	**-1.542**	1.241	-0.149	-0.081	-0.304	0.058	-0.070	-0.114	-0.483*
DMH	0.498	-1.508	**1.269**	-0.175	-0.105	-0.354	0.083	-0.091	-0.154	-0.537*
PL	0.320	-0.867	0.834	**-0.266**	0.022	-0.198	0.049	-0.068	-0.134	-0.307
PD	0.121	-0.353	0.378	0.016	**-0.354**	-0.362	0.153	-0.127	-0.119	-0.645**
NPP	-0.183	0.780	-0.749	0.088	0.214	**0.600**	-0.048	0.162	0.141	0.974**
APW	0.287	-0.487	0.571	-0.071	-0.293	-0.155	**0.185**	-0.099	-0.204	-0.268
NSP	-0.228	0.760	-0.806	0.127	0.313	0.682	-0.129	**0.143**	0.219	0.932**
HSW	0.293	-0.692	0.764	-0.139	-0.165	-0.331	0.148	-0.123	**-0.255**	-0.500*

Residual effect (R), **0.421 ;** **, Significant at 1% level; * ,Significant at 5% level;

DFF: days to 1st flowering, D50%F: days to 50% flowering, DMH: days to marketable harvest, PL: Pod length (cm), PD: pod diameter (cm), NPP: no. of pod per plant, APW: average Pod weight (g), NSP: no. of seed per pod, HSW: 100 seed weight (gm) and PYP: pod yield per plant (g).

4.6 Genetic divergence studies

Divergence analysis is performed to identify the most diverse genotypes for a rational choice of potential parents for breeding program. It was observed that the ten genotypes of yard long bean were distributed at random among the clusters based on their genetic distance. Sivakumar *et al.* (2014) also reported genetic divergence in yard long bean. In general, the pattern of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic materials among the farmers and breeders of different regions. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection are responsible for genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster was also recorded earlier in yard long bean (Hazra *et al.*, 1992).

Distribution of genotypes

The seven genotypes were grouped into three clusters (Table 10). Cluster III is the largest comprised with four genotypes followed by cluster II and I with two and solitary genotypes, respectively. Cluster III included the highest 57.14% genotypes followed by cluster II and I with 28.57% and 14.29%, respectively. A dendrogram using average linkage was presented in Figure 7 showing different cluster members.

Table 10. Distribution of different genotypes of yard long bean in different clusters

Cluster no.	Genotypic Code	Name of Genotypes	No. of population	Percent
I	G1	Green Mallika	1	14.29
II	G2, G5	Toki, Lal Bani	2	28.57
III	G3, G4, G6, G7	Lal Borboti 1, Banalota, Lal Borboti 2, Kagornatoki	4	57.14
Total			7	100.00

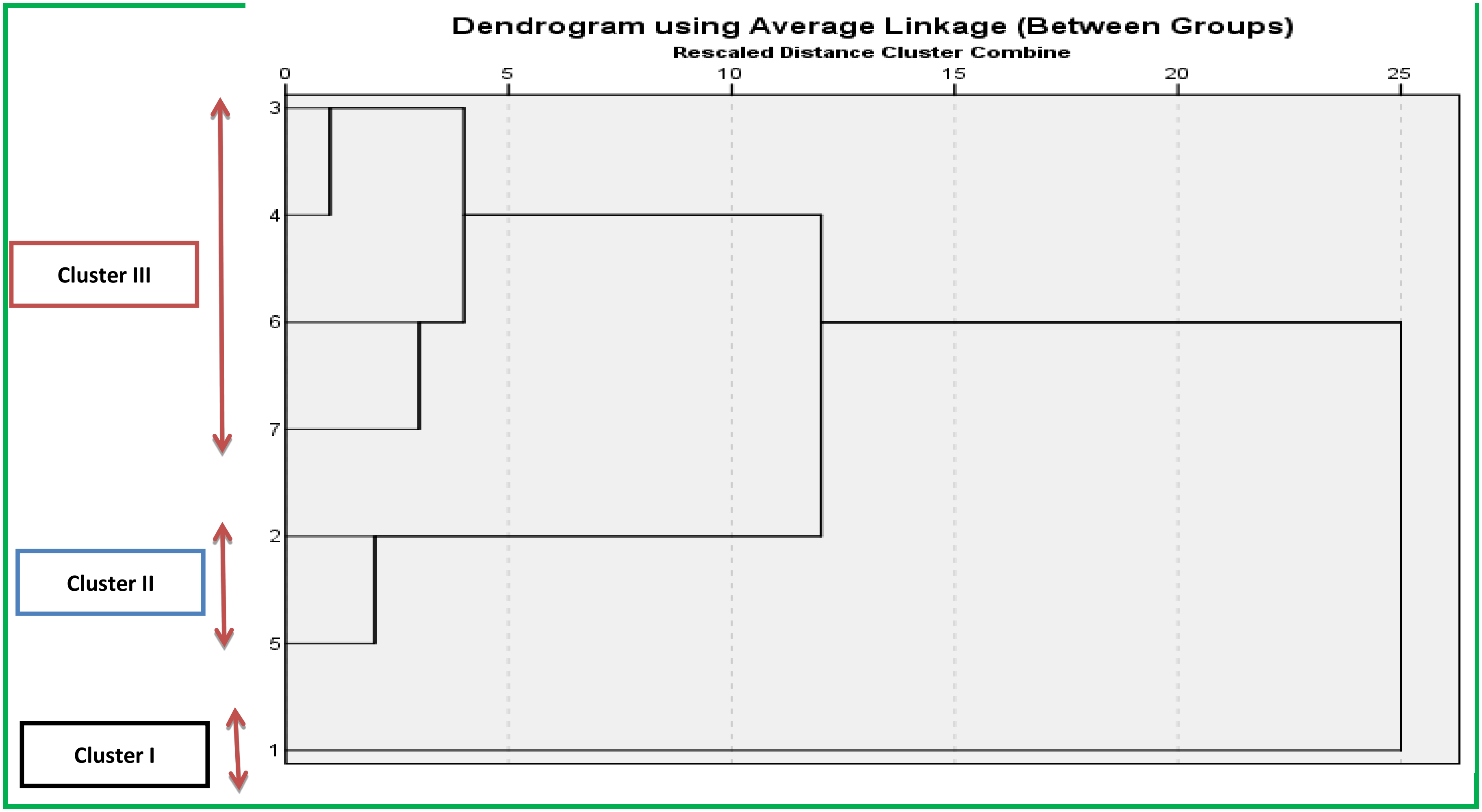

Figure 7. Dendrogram showing different genotypes in different clusters

Cluster mean

The cluster means reveal the best cluster for various characters. Depending upon the aim of breeding, potential lines can be selected from different clusters as parents in a hybridization program. The cluster means are shown in Table 11. Cluster III showed the highest cluster mean for the characters viz., days to first flowering, days to 50% flowering, days to marketable harvest, pod length, pod diameter, pod weight and 100 seed weight. Cluster III also showed the lowest cluster mean for number of pods per plant, number of seeds per pod and pod yield per plant.

The highest cluster mean for number of pods per plant, number of seeds per pod and pod yield per plant were noticed in cluster I. It also had lowest cluster mean for pod diameter and pod weight. Cluster II had recorded intermediate cluster means but some of lowest mean such as days to first flowering, days to 50% flowering, days to marketable harvest, pod length and 100 seed weight. For crop improvement programs, intercrossing of genotypes from those clusters with outstanding mean performance would be effective.

Table 11. Cluster mean for yield and yield related characters in yard long bean varieties

Characters	I	II	III
Days to 1st flowering	36.67	35.50	37.17
Days to 50% flowering	42.00	41.33	43.33
Days to marketable harvest	61.67	60.83	63.33
Pod length (cm)	53.21	52.42	55.35
Pod diameter (cm)	0.41	0.60	0.60
No. of pod per plant	10.99	8.31	5.81
Average Pod weight (g)	14.18	14.46	14.77
No. of seed per pod	21.70	20.65	19.53
100 seed weight (gm)	11.86	10.74	12.86
Pod yield per plant (g)	166.67	121.27	87.12

Cluster distance

Maximum divergence would be shown by clusters which possess maximum intercluster distance between them. The averages inter and intracluster distances are presented in Table 12& 13. The inter cluster distance was maximum between cluster I and cluster III (79.856) indicating that genotypes belonging in this cluster are diverse (Table 12& 13). The least intercluster distance was recorded between cluster II and cluster III (34.64). The intracluster distance was high for cluster III (2.65). The intracluster distances was least and zero for cluster I and cluster II as they are the solitary ones and two genotypes, respectively indicating close relationship among the genotypes included in these clusters. The intra-cluster distance was computed by using the values of inter-accession distance from distance matrix according to Singh and Chaudhary (1985). Higher inter- and intra-cluster distances indicate higher genetic variability among genotypes between and within clusters, respectively. The minimum inter- and intra-cluster distance indicates closeness among the genotypes of two clusters and within the clusters also. These relationships were also reflected in the scattered diagram (Figure 8).

Hence, intermating between the genotypes included in these clusters was expected to give transgressive segregates in the advanced generation. Kalloo *et al.* (1980) suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants.

Genotypes belonging to these clusters could be regarded as useful sources of gene for improving pod yield of yard long bean. On the other hand, genotypes belonging to Cluster II had taken the earliest days to reaching first flowering and 50% flowering which could be helpful for breeding an early plant type. Hybridization between genotypes belonging to cluster I and Cluster III and cluster II and III could combine higher pod productivity with early maturity that can be fitted well in multiple cropping systems.

Table 12. Intra (Bold) and inter cluster distances (D^2) for yard long bean genotypes

Cluster	I	II	III
I	**0.00**	45.644	79.856
II		**0.00**	34.640
III			**2.65**

Table 13. The nearest and farthest clusters from each cluster between D^2 values in yard long bean

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**II (**45.644)	**III (**79.856)
2	**II**	**III (**34.640)	**I (**45.644)
3	**III**	**II (**34.640)	**I (**79.856)

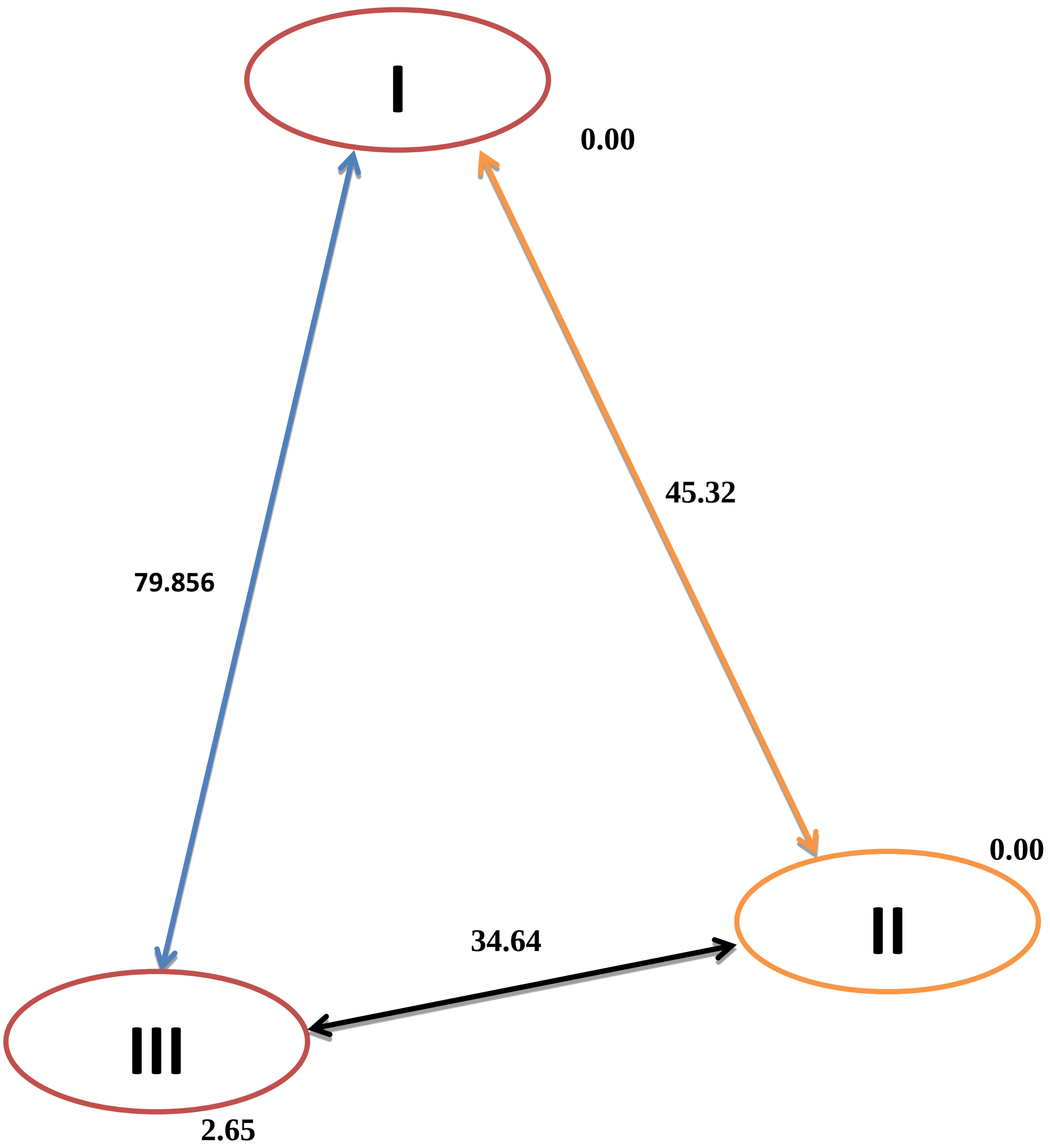

Figure 8. Cluster diagram showing average intra and inter cluster distance

Principle component analysis

The PCA yielded Eigen values of each principal component axes of ordination of genotypes with the first axes totally accounting for the variation among the genotypes (Table 14). The result revealed that the first axis largely accounted for the variation among the yard long bean genotypes (53.28%) followed by second axis (19.77%). The first four axes accounted for 92.10% of the total variation among eight characters describing seven yard long bean accessions, while the first two accounted 73.05%. A research was done by Tanaka and Niikuara (2003). They analyzed the cabbage characters using the PCA for characters associated with head form and weight. The characters were analyzed for correlations with Eigen value. Their results for head weight are in agreement with the results from our study.

On the basis of principal scores I and II from the principal component analysis, a two dimensional scatter diagram using component score I as X-axis, component score 2 as Y-axis was constructed (Figure 9). The distribution of genotypes in scattered diagram revealed that considerable diversity exists among the genotypes.

Table 14. Eigen values and yield percent contribution of different traits of yard long bean genotype

Principal component axes	Initial Eigen values		
	Total Eigen values	% of Variance	Cumulative %
I	5.861	53.28	53.28
II	2.175	19.77	73.05
III	1.281	11.64	84.70
IV	0.815	7.40	92.10
V	0.657	5.97	98.07
VI	0.212	1.90	99.97
VII	0.012	0.03	100.00

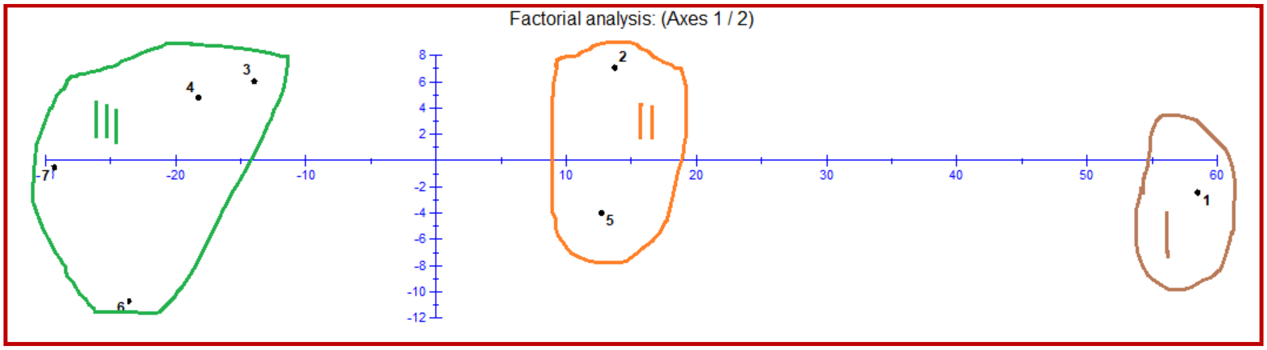

Figure 9. Distribution of genotypes in scattered diagram

Distance matrix

The lowest distance was 0.2213 which was observed between Lal Borboti 2 and Kagornatoki followed by the distance 0.267 was observed between the Banolota and Kagornatoki (Table 15 and Figure 10). The highest genotypic distance was observed between Green Mallika and Kagornatoki (0.9967) followed by Green Mallika and Banalota (0.8638) and Green Mallika and Lal Borboti 1 (0.7848). If we want to go for a further research programme, hybridization between Green Mallika and Kagornatoki will give better segreated material as they have the highest distance matrix. By further selection of those segregated generation, better qualitative or quantitative line might be explored than the previous types.

Table 15: distance matrix between pairs of genotypes

Sl.		1	2	3	4	5	6
		Green Mallika	Toki	Lal Borboti 1	Banalota	LalBani	Lal Borboti 2
2	Toki	0.4698					
3	Lal Borboti 1	0.7848	0.4386				
4	Banalota	0.8638	0.6091	0.3062			
5	Lal Bani	0.4818	0.3617	0.4193	0.4365		
6	Lal Borboti 2	0.9331	0.6959	0.3568	0.3398	0.5097	
7	Kagornatoki	0.9967	0.7231	0.3218	0.2670	0.5625	0.2213

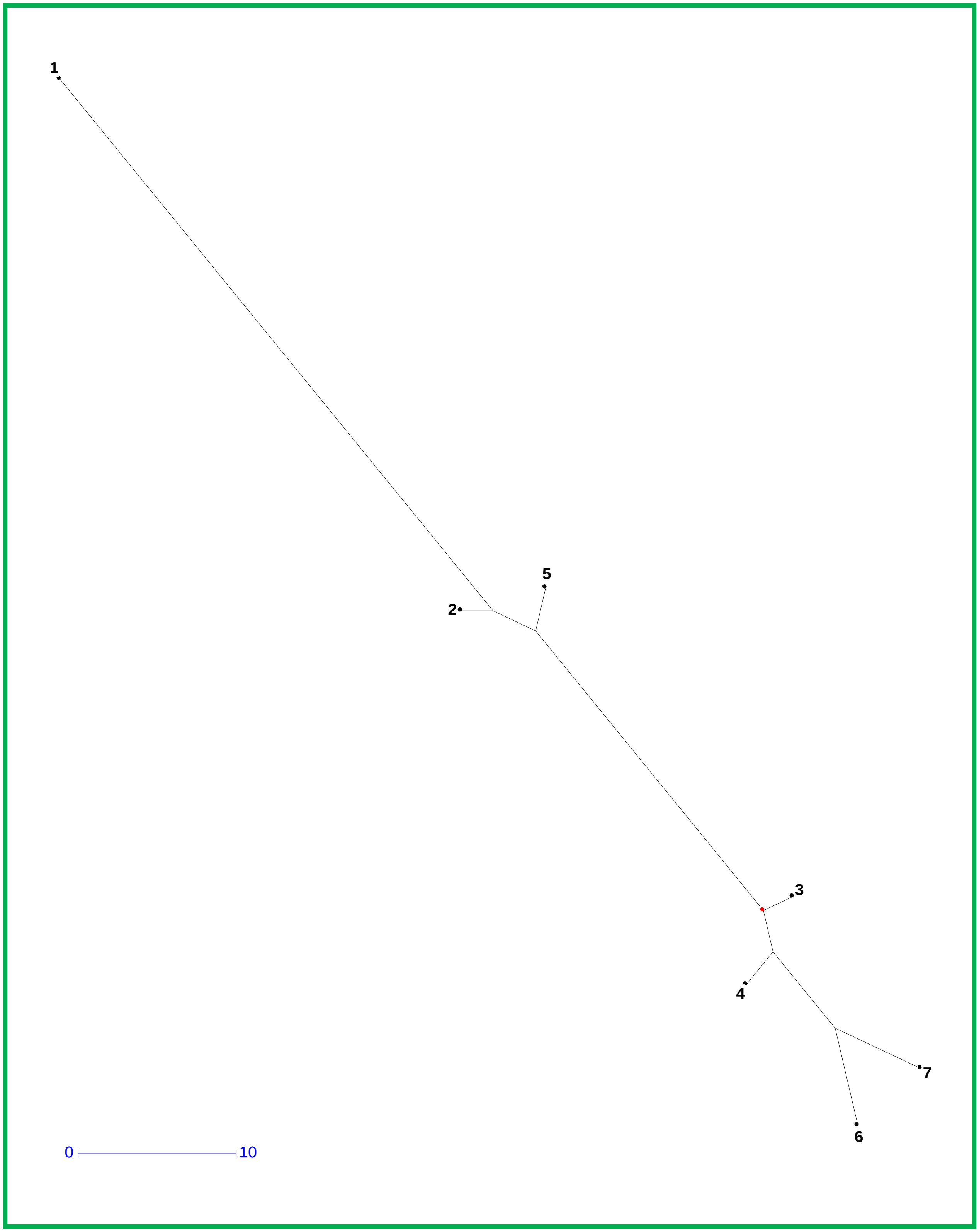

Figure 10. Tree neighboring joining

Selection of genotypes

The selection for desirable types should not only be based on yield, the other yield components should also be considered. Direct selection for yield is often misleading in yard long bean because vegetable pod yield is under polygenic control. Thus, knowledge on degree of interrelationship that exists among different component characters and with vegetable pod yield is important for devising an efficient selection criterion for fruit yield and a basis for planning and efficient breeding program. Considering diversity, variability and all agronomic traits the genotypes Toki and Lal Bani could be selected for earliness. Green Mallika could be selected for high pod per plant and high pod yield per plant (Table 16).

Table 16. Finally selected genotypes for important traits

Sl. No.	Selection traits	Genotypes	Cluster No.
1	Days to maturity (earliness)	Toki, Lalbani	II
2	Number of pods per plant	Green Mallika	I
3	Pod yield per plant	Green Mallika	I

CHAPTER V
SUMMARY AND CONCLUSION

Significant differences were observed among the genotypes for all the traits including days to first flowering, days to 50% flowering, days to marketable harvest, pod length (cm), pod diameter (cm), number of pods per plant, pod weight (g), number of seeds per pod, hundred seed weight (g) and pod yield per plant (g). Lowest days to first flowering were recorded in Toki (35.00) and highest in Banalota (38.00). The minimum days to 50% flowering was observed in Lal Bani with 41.00 DAS while in Banalota is maximum with 44.00 DAS. The range of days to marketable harvest were recorded from 60.67 (Toki) to 65.33 days (Lal Borboti-2). The longest pod was produced by the genotype Lal Borboti-2 (65.73 cm) and shortest in the genotype Toki (46.97 cm).

The genotype Green Mallika (10.99) represented the maximum number of pods per plant and the minimum was observed by the genotype Kagornatoki (5.39). The highest pod weight was found in genotype Banalota (16.58g) and the lowest was observed in the genotype Lal Borboti-1 (13.18 g). The genotype Green Mallika (21.70) represented the highest no. of seeds per pod and the lowest was observed by the genotype Kagornatoki (19.33). The maximum 100-seed weight was produced by the genotype Banalota (13.54 g) and minimum in the genotype Toki (9.44 g). Genotype Green Mallika (166.7 g) produced the highest pod yield per plant and genotype Kagornatoki (79.07 g) produced the lowest yield per plant.

Phenotypic variance was higher than the genotypic variances for all the traits. Phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. High PCV and GCV were found for no. of pods per plant (28.46 and 28.00) and pod yield per plant (29.37% and 27.87%). High heritability was recorded by number of pods per plant

(96.78%), 100 seeds weight (91.21%), pod yield per plant (90.01%), days to first flowering (74.22%) and days to 50% flowering (76.88%). Genetic advance in percent of mean was high for pod diameter (26.20%), number of pod per plant (56.74%), 100 seed weight (23.37%) and pod yield per plant (54.46) and lowest for length of pod (9.10). High heritability couple with high genetic advance as percent of mean was noticed for the traits, pod diameter, number of pods per plant, 100-seed weight and pod yield per plant provided opportunity for selection of high yielding genotypes.

Genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients in most of the associations which might be due to masking or modifying effect. Very close genotypic and phenotypic correlations were observed the traits, days to 50% flowering with days to maturity; days to maturity with pod length, days to maturity with hundred seed weight, number of pods per plant with pod yield per plant, which might be due to reduction in error (environmental) variance, thus selection for higher yield on the basis of above traits would be reliable.

Pod yield per plant positively and significantly correlate with number of pods per plant (0.974 and 0.970) and number of seeds per pod (0.932 and 0.767) at both genotypic and phenotypic levels. Pod yield was exhibited negative significant correlated with days to maturity (-0.537 and -0.503) which indicated that yield would be increased with the decreased of days to maturity. Days to maturity was correlated positively and significantly in genotypic and phenotypic levels with days to first flowering (0.992 and 0.869), days to 50% flowering (0.978 and 0.976), pod length (0.657 and 0.555) and hundred seed weight (0.602 and 0.555). Highly significant positive correlations were recorded for number of pods per plant with number of seeds per pod (0.976 and 0.767). Highly significant positive correlation of pod weight with pod diameter (0.829 and 0.623) and hundred seed weight (0.800 and 0.577) at both genotypic and phenotypic levels.

Path analysis revealed days to first flowering (0.502), days to maturity (1.269), number of pods per plant (0.600), pod weight (0.185) and number of seeds per pod (0.143) had direct positive effect on pod yield per plant, indicating these are the main contributors to pod yield per plant. The highest positive indirect effects on pod yield per plant were obtained by days to first lowering (1.259) and days to 50% flowering (1.241) via days to maturity. Days to first flowering, days to 50% flowering, days to maturity, pod length, pod diameter and 100 seeds weight had positive indirect effect on pod yield per plant through pod weight.

Genetic diversity among seven genotypes was performed through principal component analysis (PCA), cluster analysis using GENSTAT, JASP and Darwin software. The first three components with Eigen value were greater than unity contributed a total of 84.70% variation towards the divergence. As per PCA, D^2 and cluster analysis, the genotypes were grouped into three different clusters. Cluster III and II composed of four and two varieties, respectively. Cluster I was performed as solitary cluster. The highest inter-cluster distance was observed between clusters I and III (79.856) indicating diverse genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III (34.640) .

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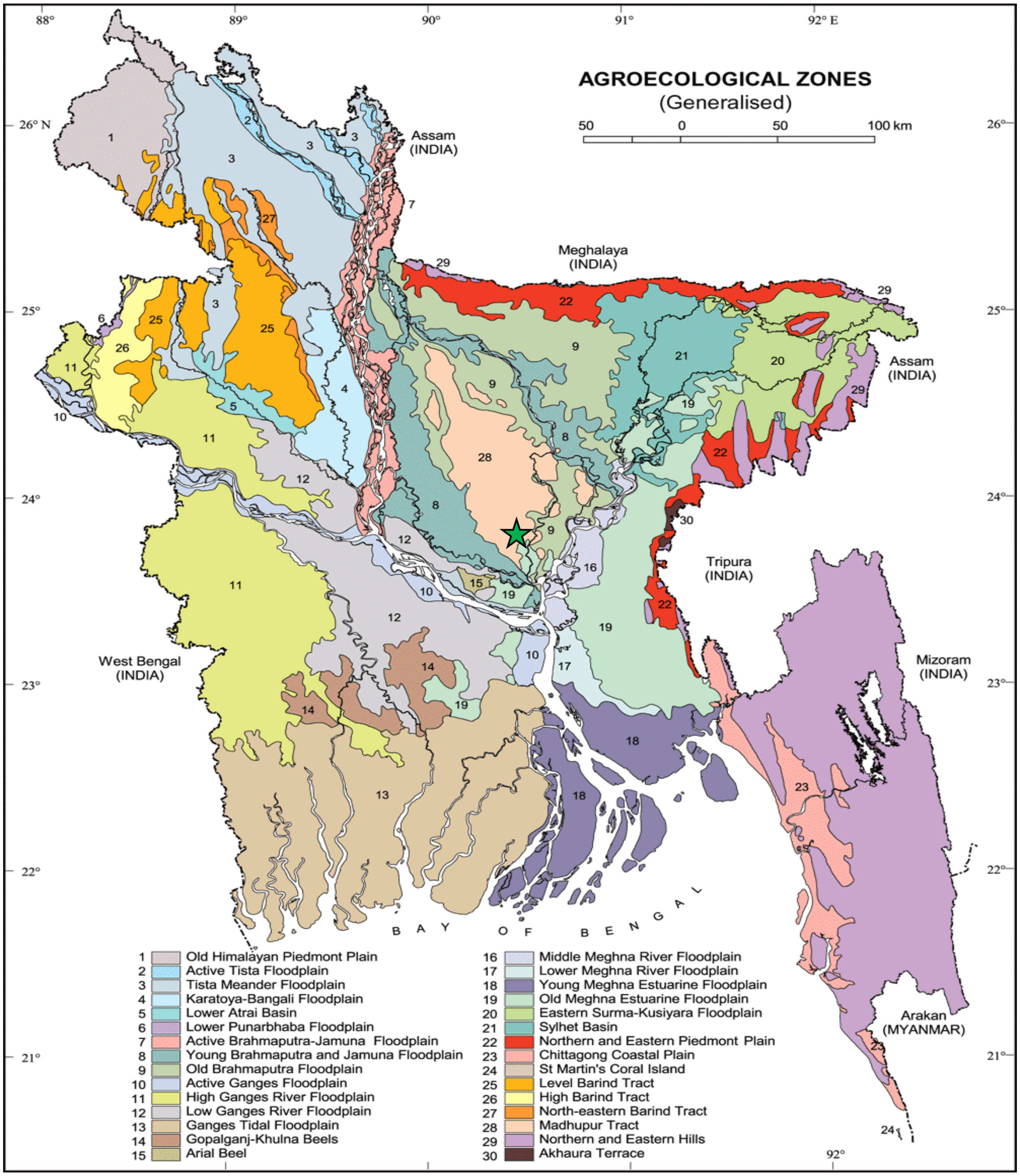
APPENDICES

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. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
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 (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2016 to February, 2017.

Month	Air temperature (ºc)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
June, 2016	31.2	27.7	79	315	4.8
July, 2016	31	26.3	79	329	4.5
August, 2016	29.3	26	73	248	5.1
September, 2016	28.1	22.1	71	134	5.7

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka – 1212