PHENOTYPIC EVALUATION OF GENOTYPES BASED ON AGRO-MORPHOLOGICAL AND NUTRITIONAL TRAITS OF KIDNEY BEAN (*Phaseolus vulgaris* L.)

REEMANA FATEMA

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY

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REEMANA FATEMA

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Approved by:

(Dr. Jamilur Rahman)	**(Dr. Md. Shahidur Rashid Bhuiyan)**
Supervisor	**Co-supervisor**

(Dr. Jamilur Rahman)
Chairman
Examination Committee

Dr. Jamilur Rahman
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mobile: +8801552323928

This is to certify that thesis entitled, "Phenotypic evaluation of genotypes based on agro-morphological and nutritional traits of kidney bean (Phaseolus vulgaris 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* ***DEPARTMENT OF GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by REEMANA FATEMA Registration No. 11-04277 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2016
Place: Dhaka, Bangladesh

(***Dr. Jamilur Rahman***)
Supervisor


Humbly Dedicated
to my Parents,
Brother and Family

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SOME COMMONLY USED ABBREVIATIONS

Full Word	Abbreviation
Agro- Ecological Zone	AEZ
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Centimeter	cm
Co- efficient of Variation	CV
Days after Sowing	DAS
Degree Celcius	℃
Degrees of Freedom	d.f
Etcetra	etc
Food and Agriculture Organization	FAO
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$б_g^2$
Gram	g
Hectare	ha
Heritability in broad sense	h_b^2
Journal	*J.*
Kilogram	kg
Meter	m
Mean Sum of Square	MSS
Millimeter	mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic Variance	$б_p^2$
Randomized Complete Block Design	RCBD
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	T.S.P

PHENOTYPIC EVALUATION OF GENOTYPES BASED ON AGRO-MORPHOLOGICAL AND NUTRITIONAL TRAITS OF KIDNEY BEAN (*Phaseolus vulgaris* L.)

REEMANA FATEMA

ABSTRACT

In prospect of Bangladesh low yield and disease susceptibility are considered the main impediments for the negligence in breeding efforts for improving Kidney bean. The present investigation was undertaken to determine the extent of genetic variability, association and direct-indirect effects of component traits on seed yield, diversity among genotypes and analysis of nutrient components of Kidney bean. The research was based on the evaluation of 18 genotypes collected from Sylhet, Bandarban regions and Bangladesh Agricultural Research Institute, considering 17 quantitative characters during Rabi season of 2016-2017 in research farm of Sher-e-Bangla Agricultural University. The analysis of variance showed significant variation in all the traits studied here except pod diameter, dry weight of pod and number of seeds/pod. The phenotypic variances were greater than genotypic variances with little differences in all traits except 1000-seed weight, seed yield/plant and seed yield/hectare. High heritability coupled with high genetic gain was observed in leaf area, 1000-seed weight and seed yield/plant which indicates the effect of additive genes. The correlation studies unraveled seed yield/hectare had highly significant positive relation with number of pods/plant, number of seeds/pod and seed yield/plant, where seed yield/plant followed by number of seeds/pod showed the highest positive direct effect on the seed yield/hectare. Selection of these traits might cause the probability of simultaneous improvement of Kidney bean. The genotypes were grouped in four clusters by diversity (D^2) analysis where cluster I comprised 7 genotypes and cluster III 1 genotype. Furthermore, highest inter and intra cluster distance was found between Cluster I and Cluster III (23.742) and cluster IV (0.900) respectively. Principle component analysis revealed first three component contributed 74.8% towards genetic diversity in Kidney bean. Significant variation was present in nutrient components viz. carbohydrate, protein, fat, fiber, ash and moisture content. Local varieties of Sylhet proved to have more carbohydrate (60.24-64.03%), fiber (2.08-2.46%) and ash (2.31-2.95%), whereas local varieties of Bandarban seemed to possess more protein content (23.05-23.11%) than released varieties from BARI. Therefore, hybridization program can be performed between the local varieties of Sylhet and Bandarban to evlove super quality Kidney bean varietis. It might be concluded that G1 (BARI Jharseem -1), G3, G4, G5, G6, G9 (BARI Jharseem-2), G10 (advanced line) and G12 (advanced line) had potential for improvement based on the genetic merit of yield and contributing factors.

Chapter I

Introduction

CHAPTER I
INTRODUCTION

Kidney bean *(Phaseolus vulgaris* L.) is widely cultivated in the world due to its high market value and good nutritional composition; high protein content in dry seed, and good source of fiber in fresh pod. It is the one of the most important source of protein and calories. It is consumed either as dry bean (pulse) or fresh pod. This edible pulse has various names such as French bean, Bush bean, Haricot bean, Navy bean, Snap bean, Pinto bean, Green bean, Raj bean, Common bean, Basic bean, Pole bean, Wax bean, String bean and Bonchi.

Knowledge of bean genetics would suggest that Kidney beans were derived from dry beans because more genetic changes were believed to require for evolution of Kidney beans from the wild bean compared to dry beans. However, Singh *et al.* (1991) suggested that native American groups might have originally gathered wild beans for their young green pods. Young pods would have required less cooking time than seeds. Kidney bean has evolved from wild growing vine distributed in the high lands of Middle-America and Andes (www.plantsciences.ucdavis.edu). These two domestications, led to two groups of cultivars with contrasting agronomic characteristics. During this evolution, some marked changes has affected this plant from climbing to dwarf plants, which has taken place both in the middle American and Andean domestication centers (Schoonhoven and Voysest, 1991). Red kidney beans are thought to have originated in Peru. Spaniards and Portuguese took Kidney bean to Europe, Africa and other parts of the Old World (Duke, 1981).

Since the plants produce a variety of large red kidney shaped beans, it is called Kidney bean. In Bangladesh it is known as 'Forashi Sheem'. It is self-pollinated annual diploid species (2n= 2x= 22) which belongs to family- Fabaceae, subfamily- Papilionoideae, tribe- Phaseoleae, subtribe- Phaseolinae (www.plantsciences.ucdavis.edu). Kidney beans are consumed in larger quantities in developed countries, where there is greater flexibility in foods available, compared to developing countries. On a daily utilisation basis, developed countries consumed 3.1 g/day compared to 1.1 g/day in developing countries (Rubatzky and Yamaguchi, 1997). The five top producer countries of dry

beans in 2014 were, in annual average, India (300000 tonnes), Brazil (136059 tonnes), Myanmar (109600 tonnes), the People's Republic of China (48406 tonnes) and the United States (46000 tonnes). Myanmar, China and the United States are the main exporters, with India and the European Union being the largest importers (FAOSTAT, 2017).

There is no official record kept of the production of Kidney bean. Being a short duration crop Kidney bean can be grown under different cropping patterns of hills and plains of Bangladesh. It is not new crop in our country as it is grown in the areas of Jessore, Rangpur, Comilla, Cox's Bazar, Chittagong Hill Tracts and Sylhet in Bangladesh. Recently, Hortex Foundation and BRAC are trying to extent the production area because Kidney bean is now an exportable vegetable among other. Recently cultivation of Kidney bean is gaining popularity in Bangladesh mainly because of its demand as a commodity for export. In 2014, total production was recorded as 110116 tonnes in Bangladesh, where yield was recorded 6.043 tonnes/ hectare and the seed production was 729 tonnes. (FAOSTAT, 2017).

Its dry seed contains 21.1% protein, 69.9% carbohydrates, 1.7% fat, 381 mg calcium, 425 mg phosphorous and 12.4 mg iron per 100 g of edible part (Ali and Kushwaha, 1987). The seed contain cholesterol-lowering fiber. Thus, it helps preventing heart disease, reduces the risks of cancer, prevents blood sugar levels from rising too rapidly after a meal, which is good choice for individuals with diabetes, insulin resistance or hypoglycemia. It has both carminative and reparative properties against constipation and diarrhoea, respectively. In addition, trypsin inhibitor of Kidney bean possesses pesticidal properties which can be extracted and used as biopesticide. Kidney bean contains high amount of PHA (Phytohemagglutinin). The content of total protein in Kidney bean seeds is reported to be between 17–23%, of which 2.4–5% is PHA. PHA exhibits many interesting biological properties, such as specificity for human blood types, agglutination of malignant cells, mitogenic effect, karyotype analysis, inhibit HIV-1 reverse transcriptase, inhibit growth of lymphoid tumor.

Over a period of at least 7000 to 8000 years, the Kidney bean has evolved from a wild growing vine to a major leguminous crop grown worldwide. Domestication is essentially a selection process the progress from which is a function of genetic

variability present in world population for different traits, heritability of these traits and the extent of selection pressure applied by earlier farmers. However, the selection pressure under domestication and sampling effects lead to a reduction in genetic variation among the cultivars. The narrow genetic base of Kidney bean cultivars provides the task to the breeders to broaden the genetic diversity through collection of exotic cultivars, local cultivars, landraces, and wild common beans or create it through induced mutation or genetic hybridization.

Yield is a complex quantitative character is greatly dependent on several related characters. For the improvement of yield and other desirable characters, a knowledge of the magnitude of variation in the available genotypes, the relation of characters with yield, extent of environmental influences on these traits and the heritability of the characters is essential (Saifullah and Rabbani, 2009).

Correlation coefficient, in general, shows association among characters (Toker and Cagirgan, 2004). However, correlation studies do not provide the exact picture of relative importance of direct and indirect effects of each of the component characters. Path analysis has been used by the breeders (Ali *et al*., 2009) to identify the traits that are useful selection criteria to improve crop yield. As crop yield is used to determine the amount of direct and indirect effects of causal components on the effect component (Dewey and Lu, 1959).

Genetic diversity has the evolutionary significance in the survival and adaptations of species in different agro-climatic conditions. It is one of the prerequisites for the crop improvement program. If there is not enough genetic diversity among genotypes it is impossible to increase the yield and other desirable characters among the genotypes. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding program

Till date very few studies have been carried out on Kidney been improvement in Bangladesh regarding its characterization, estimation of genetic diversity, study of correlation of yield and its contributing characters in Kidney beans. Hence, genetic improvement of this crop is necessary to increase yield of fresh edible bean and seed

product ion. Therefore, the present research work was taken on 18 genotypes to meet the following objectives:

1. To collect and characterize the different genotypes of Kidney bean.
2. To study the genetic diversity among the different genotypes of Kidney bean.
3. To determine correlation and path analysis of yield and yield contributing traits.
4. To compare the nutrient components of the dry seeds among the different Kidney bean genotypes.
5. To select and isolate desired genotypes for use in future breeding programs

Chapter II

Review of Literature

CHAPTER II
REVIEW OF LITERATURE

Success of yield improvement largely depends upon the magnitude and nature of genetic variability present in yield contributing traits. If the variability in among germplasm the population is largely of genetic nature with least environmental influence, the probability of isolating genetically superior genotypes is high. The genes required for crop improvement are present in different lines, strains, varieties or population of the crop species and their relatives and wild relatives. Improvement is possible on the basis of heritable variation. For the improvement of Kidney bean variability in yield contributing traits is necessary. Therefore, detailed information about genetic architecture of pod yield and its attributes should be the main concern.

Studies on genetic variability with the help of suitable biometrical tools such as coefficient of variability, heritability, genetic advance and genetic diversity become indispensable in breeding programs for tangible results of desired values. To obtain a better insight of ancillary characters under selection, correlation and path coefficient analysis are the tools, which are being effectively used for determining the rate of various yield components in different crops, leading to the selection of superior genotypes.

Keeping in view the objectives of the present investigation, the review of literature concerned to the studies on "Phenotypic evaluation of genotypes based on agro-morphological and nutritional traits of kidney bean *(Phaseolus vulgaris* L.)**"** was conducted for this thesis outlined under the following major heads.

2.1 Genetic and phenotypic coefficient of variation.
2.2 Heritability and genetic advance.
2.3 Correlation coefficient analysis.
2.4 Path coefficient analysis.
2.5 Genetic diversity analysis
2.6 Nutrient component analysis

2.1 GENETIC AND PHENOTYPIC COEFFICIENT OF VARIATION

The variability available in the population can be partitioned in to heritable and non-heritable components viz., phenotypic and genotypic coefficients of variation, heritability and genetic advance on which selection can be effectively carried out. The value observed when a quantitative character is measured on an individual, is the phenotypic value. The phenotypic value is divided into genotypic and environmental components. An important objective is to assess the relative importance of the genotype versus environment. High heritability alone is not enough to make efficient selection in segregating generations, unless information is accompanied for substantial amount of genetic advance (Johanson *et al*., 1955).

The importance of maintaining genetic diversity in a population is essential to its future viability, especially in a changing world. Genetic diversity offers a number of benefits to individual populations, including an increased ability to adapt to future environmental conditions such as those brought on by climate change. In addition to environmental adaptation, it also allows individual populations to exploit niches in their given habitat, compete with species who share the same resources, while also offering protection from parasites and disease (Castric *et al*. 2001).

In the latest part of the 19th century, Galton (1889) indicated that only a part of continuous variation was due to heredity. Johanssen's (1909) study in a self-pollinated crop, French bean, highlighted the contribution of genetic and environmental components to the total variance and revealed that the genetic component was relatively constant over generations which were subsequently confirmed by East (1916). Fisher (1918) was the first person to separate genetic variance into subcomponents: additive effect of genes, dominance deviation from the additive scheme and deviation from the additive scheme attributed to inter-allelic interactions. Coimbra *et al.* (1998) evaluated twenty-five bean genotypes of French bean for the influence of 7 characters of agronomic importance on seed production per unit area. Wide genetic variability was observed for all the characters, especially number of pods per plant, number of seeds per pod.

The highest estimates of phenotypic and genotypic coefficients of variability were recorded for green pod yield per plot and hectare followed by green pod yield per plant

and number of pods per plant, whereas moderate coefficients of phenotypic and genotypic variability were recorded for pod length and average pod weight in French bean. (Rai *et al*. 2004). Burton (1952) suggested, that genotypic coefficient of variation together with heritability estimates would give the best scope for getting desirable characters through selection of parents for hybridization. Falconer (1981) emphasizes that when the genotypes are evaluated in more than one season with the objective of quantifying the diversity found in the interaction, evaluation of genetic diversity in more than one environment could bring forth more clarifying results on the behavior of genotypes with a subsequent influence on the performance of these in future breeding programs (Teixeira *et al*., 2004). According to Gnanesh (2005) and Rai *et al*. (2010), low variability was observed for pod width followed by number of pods per inflorescence, number of primary branches per plant and number of seeds per pod of Kidney bean.

Burton (1953) suggested that GCV (Genotypic Covariance) together with heritability estimates would give the best result of the amount of genetic advance to be expected from selection. Shah *et al.* (1999) evaluated thirty exotics, as well as, indigenous accessions of French bean (*P. vulgaris*) to know genetic variability. All the eight agro-economic traits exhibited a wide range of phenotypic variation. Dahiya *et al*. (2000) derived genotypic and phenotypic coefficients of variation from data on 16 quantitative traits in 48 genotypes of Kidney bean grown. Significant differences were observed for all the traits under study. The highest GCV and PCV were observed for days to first flowering, days to 50% flowering, days to pod initiation, plant height, and primary branches per plant and pod clusters per plant.

Raffi and Nath (2004) conducted an experiment to study the performance, as well as the genetic variability of yield and yield contributing characters viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, pod length, number of seeds per plant and 20-seed weight of 31 bean genotypes, Significant variations were observed among the genotypes for all the characters studied. The highest genotypic and phenotypic variations were observed for days to maturity and pod length, respectively. Singh *et al*. (2007) studied on forty-five varieties of French bean (*Phaseolus vulgaris*) originating from different eco-geographical regions of the country were grown to study the pattern of genetic variability. They were a wide range of variability for all the traits

in the genotypes. Singh *et al.* (2007) studied on Sixty-six genotypes of French bean for variability, highly significant differences were observed in the genotypes for all the characters under study. Both genotypic and phenotypic coefficient of variations was generally high for number of branches/plant and moderate for plant height, number of seeds/pod number of pods/plant, pod length and average seed yield/plot. The characters like days to 50% flowering and pod diameter showed low genotypic and phenotypic coefficient of variations.

Rai *et al.* (2010) reported wide range of phenotypic variation values observed in 66 pole type French bean genotypes. Number of pods per plant, 100seed weight, green pods yield per plant showed high heritability along with high genetic advance. Association studies revealed that pod yield per plant exhibited significant positive correlation with number of pods/plant, % fruit set per cluster and 100 seed weight at both genotypic and phenotypic level. Mishra *et al*. (2008) conducted an experiment using thirty-three genotypes (including check variety "Lakshmi") of pole type French bean (*Phaseolus vulgaris* L.) to find out the genetic variability. A wide range of variability was observed for all the traits. However, maximum variability was observed for number of pods per plant. Ahmed (2011) used ten Kidney bean genotypes to study their performance, genetic variability for yield and yield contributing characters viz., days to 50% flowering, plant height (cm), number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and seed yield (q/ha). Significant variations were observed for all the characters in all the genotypes used in the experiment. Highest genotypic and phenotypic variations were observed for plant height followed by No. of pods/plant and pod length.

Pandey *et al.* (2011) studied variability among 18 exotic and indigenous French bean (*Phaseolus vulgaris* L.) genotypes collected from different sources. The results of the study showed that the variability was higher in adaptation, vegetative growth, floral and pod characteristics. Angadi *et al.* (2011) assessed twelve genotypes of French bean for variability. Highly significant differences were observed in the genotypes for all the characters. Both genotypic and phenotypic coefficient of variations was generally high for number of pods per plant, tenderness of pod, weight of ten pods, pod yield per plant, total yield per hectare and shelf life of pods and moderate for plant height, number of branches, days to 50% flowering, pod length and pod width. Whereas, stem thickness,

chlorophyll content, ovule number per pod, number of seeds per pod exhibited low genotypic and phenotypic coefficient of variation.

Makhdoomi and Dar (2011) carried out an experiment to elucidate the various parameters of genetic variability. Thirty-five genotypes of common bean were evaluated in field trials with three replications. The analysis of variability parameters revealed presence of substantial variability for all traits in all the genotypes used in the experiment. Highest genotypic and phenotypic variations were observed for days to maturity and pod length respectively. Kamaluddin (2011) used ten common bean genotypes to study their performance and genetic variability for yield and yield contributing characters viz., days to 50% flowering, plant height (cm), number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and seed yield (q/ha). Significant variations were observed for all the characters in all the genotypes used in the experiment. Highest genotypic and phenotypic variations were observed for plant height followed by number of pods/plant and pod length.

Sabokdast and Khyalparast (2008) conducted an investigation in order to determine the relationship between grain yield and yield components, using 30 common bean cultivars in a randomized complete block design with four replications in the field. The result showed that there were significant differences among varieties in terms of trait under study, indicating the existence of genetic variation among cultivars.

Patil *et al*. (1993) reported that a wide range of variation was noticed for the characters, days to flower, plant height, number of pods per plant, 100 seed weight and yield per plant, whereas, PCV and GCV were high for 100 seed weight and plant height.
Kapila and Pawar (1997) reported high magnitude of genetic variability in the French bean germplasm. Yield per plant, pods per plant, 100 seed weight, plant height and seeds per pod showed high phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) indicating larger variability for these traits.

Deepak Shah *et al.* (1999) found significant differences for all the quantitative traits. Phenotypic (PCV) and genotypic coefficient of variation (GCV) were high for average weight of pods, pod yield per plant, plant height and pod length and low for number of primary branches and number of pods per plant in Kidney bean.

2.2 HERITABILITY AND GENETIC ADVANCE

The heritability is important in determining whether the phenotypic difference observed among the individuals are due to genetically changes or the results of environmental factors because only the genetic component of variation is transmitted to the next generation. The estimated of heritability help the plant breeder in selection program and explore the possibility and extent to which improvement can be brought about through selection for the concerned trait.

Improvement in the performance of selected over the base population can be termed as genetic advance. The ultimate goal of the plant breeder is to have higher genetic advance for the material selected, since it is an indicator for the genetic improvement made in a population under selection. The genetic gain that can be expected for a particular character through selection is the product of heritability, phenotypic standard deviation and selection differential (Burton and Devane, 1953). Johannsen (1909) stressed that for estimating the actual effects of selection, heritability alone could not be the sole guideline for improvement since high heritability does not mean high expected genetic advance. High heritability estimates were observed for pod yield/plant and pods/plant for both the years and pooled over the years. Hence, high magnitude of it indicates the reliability with which a genotype can be recognized by its phenotypic expression (Lush, 1940).

Rai *et al.* (2009) and Upadhayay and Mehta (2010) reported that high estimates of broad sense heritability was observed for all the characters under study this might be possible due to low impact of environment on these traits. Days to last pod harvest had high heritability in spite of low GCV, which might be due to introduction of replication into the system (Burton and Devane, 1953). Dahiya *et al.* (2000) provided information on heritability and genetic advance on 16 quantitative traits in 48 genotypes of French bean grown. Days to first flowering, days to 50% flowering, days to pod initiation, plant height, primary branches per plant and secondary branches per plant were characterized by high genetic advance combined with high heritability, indicating that additive gene effects.

Raffi and Nath (2004) conducted the performance, as well as the genetic heritability of yield and yield contributing characters viz., days to 50% flowering, days to maturity,

plant height, number of pods per plant, pod length, number of seeds per plant and 20-seed weight of 31 bean genotypes, all the characters showed high heritability with high genetic advance. Singh *et al.* (2007) revealed heritability of different characters of Forty-five varieties of French bean (*Phaseolus vulgaris*) originating from different ecogeographical regions of the country. Estimated Heritability and expected genetic advance were high for 100-seed weight, number of pods per plant and seed yield, suggesting that these are more useful traits for varietal improvement program.

Mishra and Dash (1991) studied heritability among 11 genotypes of French bean. Very high heritability was estimated for yield and pod girth and these 2 characters also showed high genetic advance, as did pod length. Singh *et al.* (1994) revealed heritability on 5 characters in 7 genotypes of French bean. High values for heritability and genetic advance were observed for yield/plant, pod length and pods/plant. Nandi *et al.* (1998) conducted a field experiment with advanced brown seeded pole French bean mutants during winter 1995-96. Seeds were gamma irradiated with 30 kR and grown as bulk populations subsequently subjected to single plant selection. Data revealed that pod weight had high heritability. Both pods/plant and green pod yield/plant showed moderately high heritability and genetic advance as a percentage of the mean. Thus, selection of high yielding lines may be effective if based on these parameters.

Shah *et al.* (1999) studied on thirty exotics, as well as, indigenous accessions of Kidney bean (*P. vulgaris*) to know genetic variability and high estimates of heritability was recorded in six agro-economic traits. Three traits showed additive gene effects by way of high heritability and genetic advance. Rai *et al*. (2006) studied on fifty-two genotypes of pole type French bean were done. The characters namely, pod yield/plant, number of pods/plant, seed weight and pod weight showed high heritability along with high genetic advance revealing that these characters are controlled by additive gene. Junaif (2010) studied on twenty-six genotypes of French beans (*Phaseolus vulgaris* L.) to estimate the heritability of different traits. High heritability along with high genetic gain was observed for green pod yield plot-1, followed by green pod yield plant-1 and number of pods per plant indicating that these traits could be exploited for further improvement through selection procedures.

Makhdoomi and Dar (2011) carried out an experiment to know the heritability of different traits, using thirty-five genotypes of common bean. All the characters showed high heritability with high genetic advance. Kamaluddin (2011) used ten common bean genotypes to study their performance, heritability and genetic advance for yield and yield contributing characters plant height, 100-seed weight and days to 50% flowering showed high heritability with high genetic advance. Patil *et al.* (1993) reported that high genetic advance associated with high heritability values for the characters yield per plant, 100 seed weight and plant height followed by number of seeds per pod and number of branches per plant revealed additive gene action.

Lush (1949) defined heritability in "Narrow sense" as the ratio between the genotypic variance as a whole and that due to phenotype. Later, Hanson *et al*., (1956) suggested heritability in "Broad sense" as the ratio of genotypic variance to the total variance. But, broad-sense heritability does not give a clear picture of transmissibility of variation from one generation to the next. Its utility in plant improvement program was limited since the genetic variation included is fixable additive effect and non-fixable dominance and epistatic effect. Thus, heritability in the "Narrow- sense" was defined as the ratio of additive genetic variance to the phenotypic variance (Lush, 1949). Selection for traits having high heritability would be very effective as there would be a close correspondence between genotype and phenotype. Kapila and Pawar (1997) reported that days to maturity, plant height, and 100 seed weight and pod length had high heritability in combination with genetic advance which is attributed to additive gene action. Dikshit *et al*. (1999) studied genetic variability in 59 genotypes of French bean and reported variability for yield and yield related traits, high heritability for plant height, pods per plant, primary branches and yield per plant. High heritability coupled with high genetic advance was observed for 50 per cent flowering, yield per plant, pods per plant and plant height.

2.3 CORRELATION COEFFICIENT ANALYSIS

In plant breeding, correlation coefficient measures the mutual relationship between various plant characters and determines the component characters on which selection can be done for genetic improvement in yield. Among the types of correlation,

genotypic correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement in one character by selecting the other character of a pair, if that is genetically correlated in desirable direction. This type of correlation may be either due to pleiotropic action of genes or due to linkage or more likely both but the pleiotropic effect is considered to be more important which refers to manifold effect of gene (Falconer, 1960).

Correlation coefficient measures the association between any two characters. These, however, may not give the information about the direct and indirect effect of one variable on the other. Wright (1921); originally developed the concept of path analysis to find out the direct and indirect causes of association while Dewey and Lu (1959) first used the technique of path coefficient analysis for plant breeding program. Frake *et al.* (1961) also indicated the utility of path coefficient analysis in the selection of plants.

Narsinghani and Saxena (1991) presented information on genetic parameters and correlations for 7 characters studied in a diverse collection of indigenous and exotic *Phaseolus vulgaris* genotypes. Yield was most strongly associated with 100-seed weight. Singh *et al.* (1994) observed correlation of 5 characters in 7 genotypes of French bean. Study showed that yield was highly correlated with pod length and pod weight at the genotypic level. Coimbra *et al*. (1998) evaluated twenty-five French bean genotypes for the influence of 7 characters of agronomic importance on seed production per unit area. Number of pods per plant and 1000-seed weight has high phenotypic correlation with seed yield. Shah *et al*. (1999) studied on thirty exotics, as well as, indigenous accessions of French bean (*P. vulgaris*) to know correlation among the characters. Correlation studies revealed that pod yield had positive correlations with plant height, pod length and pods per plant. Generally high genotypic coefficient of correlation was observed in all the agro-economic traits. Yadav *et al.* (2001) reported correlation coefficient analysis for test weight, seed length, seed breadth, seed thickness, seed germination, root length, collar diameter, number of leaves per plant, and shoot length on 20 French bean (*Phaseolus vulgaris*) cultivars. Test weight was positively correlated with seed length, seed breadth, seed thickness, collar diameter, number of leaves per plant, and shoot length at phenotypic and genotypic levels. At the phenotypic level only, significant positive correlation was recorded between seed length and seed thickness, collar diameter, and shoot length; between seed thickness

and collar diameter, number of leaves per plant, and shoot length; and between shoot length and germination percentage, root length, collar diameter, and number of leaves per plant.

Shinde and Dumbre (2001) studied on Fifty genotypes of French bean (*Phaseolus vulgaris*) for 11 characters, Seed yield per plant was positively and significantly correlated with days to first flower, days to maturity, plant height, plant spread, number of branches per plant, number of pods per branch and number of seeds per pod. It showed positive but non-significant correlation with pod breadth, while negative non-significant correlation with pod breadth, pod length and 100seed weight both at genotypic and phenotypic levels. Kurek *et al.* (2001) conducted an experiment to determine the relationship between grain yield and yield components in 15 bean (*Phaseolus vulgaris*) genotypes. Observations were recorded for grain yield, grain medium weight, number of grains per pod and number of pods per plant. Grain yield was correlated with the 3 yield traits, mainly with number of pods per plant.

Amini *et al*. (2002) reported correlation analysis in common bean (*P. vulgaris*) on 576 accessions. In general, correlation analysis of biological yield indicated that number of nodes on the main stem was highly and directly effective in increasing yield. Raffi and Nath (2004) investigated the performance, as well as the correlation in yield and yield contributing characters viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, pod length, number of seeds per plant and 20-seed weight of 31 bean genotypes were determined in a field experiment conducted in Bangladesh. Grain yield was positively correlated with number of pods per plant, pod length, number of seeds per plant and 20-seed weight. Subhadeep and Korla (2004) studied twenty-eight dwarf Kidney bean (*Phaseolus vulgaris*) genotypes for correlation coefficient. Number of pods per plant and pod length had significant positive correlation with pod yield per plant.

Rai *et al.* (2006) studied on fifty-two genotypes of pole type French bean were done. Association studies revealed that pod yield/plant exhibited significant positive correlation with pod length, pod weight and seed weight at both genotypic and phenotypic levels. Mishra *et al.* (2008) conducted an experiment on thirty-three genotypes (including check variety "Lakshmi") of pole type French bean (*Phaseolus vulgaris* L.) to find out the correlation among different yield contributing characters. A

positive correlation of green pod yield per plant was observed with days to first flowering, number of pods per plant, pod length and days to first marketable maturity.

Bhushan *et al*. (2008) evaluated Simple correlation coefficient for seven characters with four hundred forty-one exotics French bean germplasm lines during 2005. Seed yield per plant showed positive and significant correlation with number of pods per plant, pod length and seed index (100 seed weight). However, number of pods per plant exhibited positive and significant correlations with pod length, days to maturity and plant height. Sabokdast and Khyalparast (2008) conducted the study in order to determine the relationship between grain yield and yield components, using 30 common bean cultivars in a randomized complete block design with four replications in the field at the Faculty of Agriculture, Tehran University. The results showed that the grain yield had a positive and significant genotypic correlation with number of seed/pod, pod weight, number of pod/plant, biological yield, days to flowering and maturity.

Rai *et al.* (2010) while conducted on experiment the association studies revealed that pod yield per plant exhibited significant positive correlation with number of pods/plant, % fruit set per cluster and 100 seed weight at both genotypic and phenotypic level. Singh *et al.* (2011) studied correlation in 18 genotypes of French bean (*Phaseolus vulgaris* L.) Number of pods/plant had strong positive correlation with pod girth and pod yield and demonstrated ample scope for pod yield through selection of this trait. Makhdoomi and Dar (2011) carried out to elucidate the correlation among the various parameters. Grain yield was found to be positively correlated with number of pods/plant, pod length, number of seeds/pod, and 100 seed weight. Kamaluddin (2011) used ten common bean genotypes to study their correlation for yield and yield contributing characters. Seed yield was found to be positively correlated with days to 50% flowering, plant height and number of seeds/pod.

Siddique and Gupta (1991) observed a significant correlation of seed yield per plant with days to 50 per cent flowering, days to maturity, number of clusters per plant and number of pods per plant. In 1992, Oseni *et al*., revealed that there is a positive correlation between seed yield and pods per plant, between days to flowering and seed yield and between 100 seed weight, seed yield, days to flowering, days to pod filling and pod length were the major components contributing to yield. Altinabas and Sepetoglu (1993) concluded that correlation with pods per plant, seeds per plant and

number of branches per plant. Both days to flowering and maturity had no influence on seed yield, 100 seed weight was negatively and significantly associated with pods per plant and seeds per pod. Sawant (1994) found that the seed yield was significantly and positively related with branches per plant, inflorescence per plant, pods per plant, pod length, seeds per pod, 100 seed weight and harvest index.

Tamilselvan and Das (1994) reported that the number of clusters, number of pods per plant and 100 seed weight should be used as a selection criterion in the development of high yielding genotypes of cowpea. In a study involving three F2 populations, Biradar *et al*. (1996) reported a strong correlation between pod weight per plant and seed yield, pod length and number of seeds per pod, number of clusters and number of pods per plant and pod weight per plant. Twenty-two diverse pole type of French bean (*Phaseolus vulgaris*) cultivars were studied for green pod yield and eight other component traits (Mishra *et al*. 1996). Characters such as pods per plant, pod weight, pod length and seeds per pod showed significant positive correlations with yield.

Rangaiah *et al*. (1999) reported that total seed weight was positively and significantly associated with all the traits except plant height and pod weight. Hundred seed weight made the greatest contribution towards yield per plant in both crosses. The characters such as plant height, number of pods per plant and number of seeds per pod showed significant and positive association with 100 seed weight indicating that more number of pods gives more number of seeds and also observed a positive association of pod length with plant height, number of branches per plant and number of pods per plant. Zeven *et al.* (1999) reported positive and strong correlation of 100 seed weight with pod length and plant height; but a negative correlation with number of pods per plant was reported by Nienhuis and Singh (1986).

Shinde and Dumbre (2001) evaluated 50 genotypes of French bean (*Phaseolus vulgaris*) for 11 characters. Seed yield per plant was positively and significantly correlated with days to first flower, days to maturity, plant height, plant spread, number of branches per plant, number of pods per branch and number of seeds per pod. It showed positive but non-significant correlation with pod breadth, while negative nonsignificant correlation with pod breadth, pod length and 100-seed weight both at genotypic and phenotypic levels.

2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis permits the separation of direct and indirect effect through the other related characters by portioning the correlation coefficients. The review of the work done utilizing path coefficient analysis in Kidney bean is presented below. The method of path coefficient analysis provides an effective means of finding out direct and indirect causes of association of various component characters. This technique was originally developed by Wright (1921) it was first used for plant selection by Dewey and Lu (1959). To use this technique, it requires cause and effect situation among the variables. In any crop, grain yield has been associated with a number of yield contributing characters and these characters themselves are inter related.

Duarte and Adams (1972) reported that pods per plant exerted a predominant effect upon green pod yield. Pande *et al*. (1975) revealed that primary branch, pod length, days to flowering and pods per plant had the highest direct effect on green pod yield.Shettar *et al.* (1975) reported that more importance should be given to number of pods per plant in selection programs while studying path analysis of pod yield components of 50 genotypes of snap beans. Direct influence of number of pods on pod yield was very high while its indirect influence on pod yield through pod length was negligible and negative. The direct influence of pod length on pod yield was shown to be moderate while its indirect influence through pod number was not significant. Prakash and Ram (1981) reported that the number of green pod per plant had highest direct effect on green pod yield. Thus, green pod number could be considered as an important primary yield component and selection should be primarily for this trait. Pod weight had negligible direct effect on green pod yield but contributed substantially indirectly via pod length, thus pod number and length of green pods were more important in increasing green pod yield.

Coimbra *et al.* (1998) evaluated twenty-five bean genotypes for the influence of 7 characters of agronomic importance on seed production per unit area. Path analysis showed the importance of number of pods per plant and 1000-seed weight. Yadav *et al.* (2003) done path coefficient analysis for test weight, seed length, seed breadth, seed thickness, seed germination, root length, collar diameter, number of leaves per plant, and shoot length on 20 French bean (*Phaseolus vulgaris*) cultivars. Path coefficient analysis revealed that seed length, seed weight, root length, collar diameter, seed

thickness, and seed breadth had the greatest effect on vigor and growth, indicating that these characters should be considered for selection.

Shinde and Dumbre (2001) studied on fifty genotypes of French bean (*Phaseolus vulgaris*) for 11 characters. Path analysis showed that characters 100seed weight and number of seeds per pod showed strong positive direct effects, while number of pods per plant and number of branches per plant showed moderate direct effects. The direct negative effects on yield were observed for pod length and days to first flower. Amini *et al.* (2002) observed path analysis in common bean *(P. vulgaris*) on 576 accessions. In path analysis for seed yield, the weight and number of pods had high direct effect on yield while the direct effects of biological yield and seed number per plant were negligible. Thus, the highest impact was due to their indirect effect through pod weight. In path analysis for pod weight, number of pods had the highest direct effect (0.79). Harvest index and seed number per pod had indirect effects through pod number on pod weight.

Furtado *et al.* (2002) evaluated path analysis for grain yield and its primary components in common bean. Among the components studied, only the number of pods per plot showed a good combination of path coefficient. Raffi and Nath (2004) revealed path coefficient analysis in yield and yield contributing characters viz., days to 50% flowering, days to maturity, plant height, number of pods per plant, pod length, number of seeds per plant and 20-seed weight of 31 bean genotypes were determined in a field experiment conducted in Bangladesh. Path coefficient analysis revealed that all the pod and seed characters showed positive and significant direct effects on seed yield. Subhadeep and Korla (2004) investigated twenty-eight dwarf French bean (*Phaseolus vulgaris*) genotypes for correlation and path coefficient analysis. Eight quantitative characters were analyzed for their path coefficients in relation to pod yield. Number of pods per plant had the highest direct effect, while harvest index and pod length had the highest indirect effects through pod numbers.

Dahiya *et al.* (2006) conducted the study to determine the direct and indirect effects of the different yield attributing characters on seed yield of 48 French bean genotypes. Path coefficient analysis of yield attributes and seed yield in 48 French bean genotypes representing wide agro-climatic regions of the world revealed that in selection program,

maximum weight age should be given to biological yield, days to pod initiation, number of clusters per plant, seeds per pod and secondary branches per plant since their direct influence on seed yield was highly significant, while their indirect influence via most of the other component characters was negligible. Bhushan *et al.* (2008) calculated path analysis for seven characters with four hundred forty-one exotics French bean germplasm lines during 2005. Path coefficient analysis revealed that number of pods per plant, pod length and seed index was most important traits contributing towards seed yield. It could, therefore, be suggested that these characters were dependable for selection of yield in French bean.

Mishra *et al.* (2008) have done path coefficient analysis using thirty-three genotypes observed that days to first flowering, number of pods per plant and pod length showed maximum direct effect on pod yield. Rai *et al.* (2006) maximum direct effect was observed in pod weight followed by seed length, seed thickness and number of pods/plant towards yield indicated that these characters are very important while making selection for high yielding genotypes. Sabokdast and Khyalparast (2008) conducted the study in order to determine the relationship between grain yield and yield components, using 30 common bean cultivars in a randomized complete block design with four replications in the field at the Faculty of Agriculture, Tehran University. The results of path analysis showed that the highest direct effect, being positive, was related to number seed/plant and the lowest direct effect, which was related to number pod/plant.

Rai *et al*. (2010) conducted an experiment on 66 pole type French bean genotypes. Association studies revealed that pod yield per plant exhibited significant positive correlation with number of pods/plant, % fruit set per cluster and 100 seed weight at both genotypic and phenotypic level. Maximum direct effect was observed in number of pods/plant followed by % fruit set/cluster, number of seeds/pod towards yield. Hence, these characters have significant effect on yield, while making selection for high yielding genotypes. Ahmed (2011) used ten common bean genotypes to study path analysis for yield and yield contributing characters. Path coefficient analysis revealed that day to 50% flowering, no. of pods/plant, pod length and 100-seed weight showed positive direct effects on seed yield. Hence, selection for these traits for improving seed yield in French bean is suggested. Makhdoomi and Dar (2011) reported path coefficient

analysis on thirty-five genotypes of common bean. Path coefficient analysis revealed the importance of plant height, pods/plant, and pod length, seeds/pod and 100-seed weight as the major yield components in this crop. Kamaluddin (2011) used ten common bean genotypes to study their path analysis for yield and yield contributing characters. Path coefficient analysis revealed that days to 50% flowering, No. of pods/plant, pod length and 100-seed weight showed positive direct effects on seed yield.

2.5 GENETIC DIVERGENCE

For a successful plant breeding program, genetic divergence is very much essential to classify the experimental material, based on the extent of similarity, into close and divergent types. Genetic improvement in any crop mainly depends upon the amount of genetic variability present in the population. Mahalanobis (1936) developed a statistic known as D^2 statistic to measure the distance between two populations. Fisher (1936) suggested that Mahalanobis' D^2 would be more useful when the number of groups happened to be more than two.

Murthy and Pavate (1962), in taxonomic studies, suggested that D^2 analysis could be extended to the situations where overlapping species need to be discriminated, since the technique of Mahalanobis D^2 statistic has been applied widely to resolve genetic divergence at intervarietal, sub-species and species levels in several crops. Mahalanobis technique is in the form of a generalized distance, which considers the variation produced by any character and their conjoint effect that it bears on other character. Mahalanobis also pointed out that D^2 would be remain constant when samples were drawn from two different population irrespective of the size of the representative sample. This indicates that D^2 provided a measure of actual magnitude of divergence between two individuals under comparison. McClean *et al.,* (1993) grouped 143 North American commercial dry bean cultivars by using coefficient of parentage and cluster analysis. The analysis identified 16 clusters, with 13 entries unassigned, but listed with the most closely related clusters. Cluster analysis identified three major clusters, corresponding to the small (navy, small white and black), medium (pinto, GN, red Mexican and pink), and large (kidney) seed size groups. Prasad (1995) revealed that

towards the total divergence of genotypes, the contribution of green pod length was at the greater extent followed by green pod breadth and reproductive branches per plant.

Dikshit *et al*. (1999) measured the genetic divergence by Mahalanobi's D^2 statistics in 59 genotypes and grouped them into six cluster based on D^2 values. One of the clusters had both indigenous and exotic germplasm, which indicated no association clustering pattern and eco-geographical distribution and added that there was no parallelism between geographical and genetic diversity. They suggested that the parents should be selected on basis of total divergence for the character used for an overall improvement in the yield. Zeven *et al*. (1999) studied phenotypic variation in a core collection of common bean in the Netherlands using 14 quantitative and qualitative traits. Considerable variation among the accessions was recorded for each of the fourteen characters. Principal component (PC) analysis indicated that the first three PCs express 89 per cent of the variation. The first PC separates the accessions mainly on seed (weight, height and length) and pod (height and length, colour intensity, beak curve and length) characteristics, whereas the second PC separates mainly on growth habit, pods/plant and seed length. The third PC separates mainly on flowering time, pods/plant, pod length, seeds/pod and seed width.

The analysis of genetic distance through D^2 statistic in French bean was studied by Kalia *et al*. (2001) they grouped 44 genotypes into six different clusters, cluster I had the maximum number of genotypes (11) whereas cluster IV had only one genotype. Inter cluster distance was maximum (8.094) between cluster IV and V. whereas minimum inter cluster distance (2.355) was observed between cluster III and V. There is only one genotype i.e. HPR-230 in cluster IV which is at significant distance from the other genotypes. They reported that genotypes of heterogeneous origin were grouped together in some of the major cluster. Govanakoppa *et al*. (2002) grouped 62 genotypes into 11 clusters and reported that number of green pods per plant, 100 seed weight, plant height and reproductive branches contributed more than 99 per cent to the total divergence.

Barelli *et al*. (2005) used 35 landraces of common bean from Brazil to study the divergence among them. They evaluated traits like, number of days to emergence, number of days to flowering, height of the insertion of the first pod, longitudinal length

of the pods, total number of pods/plant, number of total seeds/plant, number of seeds/pod and seed weight. The genetic distance measurements using generalized Mahalanobsis D^2 demonstrated greater dissimilarity between genotypes from Mesoamerica and Andean gene pools. Cluster analysis grouped the genotypes into nine clusters; with the most similar cultivars grouped in cluster I. Cluster I to V contained landraces from Mesoamerican origin, whereas clusters VII to IX only possess Andean origin genotypes. Thirty-three genotypes of pole type French beans obtained from India and abroad were evaluated by Sharma *et al.* (2009); based on Mahalanobis D^2 statistics, 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 programme. They suggested that further hybridization between cluster IV and V could be utilized for getting the superior recombinants or transgress segregants in segregating generations

2.6 NUTRIENT COMPONENT ANALYSIS

Beans have been known to be a source of complex carbohydrates, including dietary fibre and resistant starch (Aykroyd, 1982). Fat content of the beans were generally low. Beans and legumes in general are low in fat and cholesterol. Nutritional data, calculated as a percentage of the whole seed, indicates that most of the ash, protein and lipid are found in the cotyledon, while up to 80-93% of the crude fiber is found in the seed coat (Deshpande & Damodaran, 1990). The protein content of kidney beans varies from 20-25% based on dry weight. The moisture content was 9.94 ±0.12%. (Lu and Chang, 1996). The range of 20.43 to 23.62 g of protein content obtained by Bhatty *et al.* (2001) and Siddiq *et al.* (2010), but shown a higher protein variation in bean seeds. The protein variation in the Madeiran bean seeds was greater than 17.96 to 27.45 g for the Northern Portuguese bean (Coelho *et al.* 2009) and 17.96 and 22.07 g for the improved Ethiopian beans (Shimelis *et al.* 2005). Ash content is an indication of the mineral nutrients present in a food material. In seed of *Phaseolus vulgaris* significant correlation ($r = 0.77$, $P<0.01$) between calcium content and ash content was revealed. Even though the calcium content accounts for only 3% of the total ash content in raw beans, the data

predicted that a possible ratio relationship between the two values might exist (Lu & Chang, 1996). The variation of starch content among the Madeiran beans was higher than 37.6 to 45.9 g detected by Rodiño *et al.* (2001), 40.1 to 49.5 g Rodiño *et. al.* (2003). Fat content of the Madeiran beans was lower than 2.45 to 3.62 g range reported by Bhatty *et al.* (2001) and Siddiq *et al.* (2010). The Madeiran beans showed a relatively high ash content. While trait variation was greater than 2.86 and 4.26 g reported by (Shimelis *et al.* 2005).

Chapter III

Methods and Materials

CHAPTER III
METHODS AND MATERIALS

The present investigation entitled **"**Phenotypic evaluation of genotypes based on agro-morphological and nutritional traits of Kidney bean **(***Phaseolus vulgaris* L**.)"** was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. This experiment was conducted during Rabi season 2016-2017. The detail information regarding the materials and methodology of this experiment is discussed below:

3.1. Location of Experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University, Dhaka-1207 from November 2016 to February 2017. The experimental area was situated at 23°46'16" N latitude and 90°22'46" E longitude at an altitude of 4 meter above the sea level (Digital Globe, Google). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (www.banglapedia.com). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.2 Climate characteristics of the experimental area

The area possesses subtropical climate, which is characterized by high temperature, relative humidity and heavy rainfall in Kharif season (April-September) and relatively low rainfall associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.3 Soil Characteristics

Soil of the experimental site belongs to the general soil type, Shallow red brown terrace soils under Tejgaon Series. Top soils were clay loam in texture, the pH ranged from 6.0-6.6 and had organic matter 0.84%. Experimental area was flat which facilitated irrigation and drainage system easily. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in Appendix III.

3.4 Plant materials

The research was conducted with 18 genotypes of Kidney beans which were collected from local areas of Sylhet and Bandarban**.** Three released varieties were collected from Plant Genetic Resource Centre **(**PGRC**)** of Bangladesh Agricultural Research Institute **(**BARI**).** The origin of the genotypes is shown in Table 1**.**

3.5 Experimental layout

The field experiment was designed in Randomized Complete Block Design (RCBD) with three replications**.** The plot size was 200m^2**.** A distance of 30 cm from row to row and 15 cm from plant to plant was maintained**.** The genotypes were randomly distributed to each row within each line**.** Two irrigation channels were built among three replications**.**

3.6 Operational practice

3.6.1 Soil and field preparation

The experimental field was irrigated to have optimum level of moisture condition**.** Deep and light ploughing were done with tractor and power tiller to bring about to good tilth**.**

3.6.2 Fertilizer application

Fertilizer was applied at the rate of 92**.**16 kg/ha nitrogen, 80 kg/ha phosphorus, 75 kg/ha potassium (Table 2)**.** The entire quantity of nitrogen, phosphorus and potassium had applied as basal dose**.** Urea, and MOP were used as fertilizer and Cowdung was used as manure**.** Half of the Urea, and full doses of T**.**S**.**P, MOP and Cowdung were was used during land preparation**.** Rest half of the Urea was applied after 15 and 30 days by foliar application**.**

3.6.3 Selection of seed and sowing time

Pure and healthy seeds of each genotype were collected before sowing**.** The seeds were treated with Vitavax 200 and soaked in water for 12 hours to get good germination**.** The distance between the plants is 15 cm and rows are 30 cm**.** The sowing was carried out on 16 November 2016**.**

Table 1: Name of the genotypes/accession/variety of Kidney bean used in the study

Sl No	Name	Genotype/Accession/Variety	Source
1	G1 (used as Check variety)	BARI Jharseem-1	BARI
2	G2 (used as Check variety)	BARI Jharseem-3	BARI
3	G3	Local	Sylhet
4	G4	Local	Sylhet
5	G5	Local	Sylhet
6	G6	Local	Sylhet
7	G7	Local	Sylhet
8	G8	Local	Sylhet
19	G9	BARI Jharseem-2	BARI
10	G10	Advanced Line (Accession no. BD- 4502)	BARI
11	G11	Advanced Line (Accession no. BD- 7360)	BARI
12	G12	Advanced Line (Accession no. BD-10198)	BARI
13	G13	Local	Bandarban
14	G14	Local	Bandarban
15	G15	Local	Bandarban
16	G16	Local	Bandarban
17	G17	Local	Bandarban
18	G18	Local	Bandarban

Table 2: Doses of manures and fertilizers used in the study

Sl. No.	Fertilizers/ Manures	Dose	
		Applied in the plot	Quantity/ha
1.	Urea	4 kg	200 kg
2.	TSP	4 kg	200 kg
3.	MOP	3 kg	150 kg
4.	Cow dung	100 kg	5 ton

3.6.4 Intercultural operations

When the seedlings emerged, 1st weeding were done (7 DAS) uniformly in all replications of the whole plot. Second weeding was done after 15 DAS (days after sowing) of the first one. Gap filling was done by resowing within a week after germination. During early stages of growth, thinning was done by removing of some closely germinated plants to allow plants more sunlight and to reduce the self-shading and incidence of increased insect infestation.

3.6.4.1 Staking and tagging

When the plants were well established, staking was done using bamboo sticks to keep the plants erect. Tagging of each genotype of all replication was done after a week of sowing (Plate1)

3.6.4.2 Weeding and mulching

Several weeding and mulching were done as per requirement. At the very first stage weeding was done (20 DAS) for ease of aeration and less competition seedling growth and mulching was provided after an irrigation to prevent crust formation and facilitate good aeration. Weeding was done four times according to the requirement of maintain uninterrupted growth of the crop**.**

3.6.4.3 Irrigation and after-care

The experimental plot was irrigated during the cropping period with light irrigation**.** The field was irrigated every two days interval according to the soil condition of the field. During irrigation, special care was taken of plants that the water pressure might not break the shoots.

3.6.4.4 Pesticide application

During the cropping period, Sevin Dust, Ripcord, Malathion 57EC were used for 6 times at an interval of 14 days till pod maturation.

3.6.5 Harvesting

Harvesting continued for about one month because seeds of different lines matured progressively at different dates and over long time. Seeds were picked on the basis of horticultural maturity, size, colour and age being determined for the purpose of

consumption. Harvesting was started from 1 February and completed by 15 February. The fruits per entry were allowed to ripe and then seeds were collected for future use. Photograph showing different stages of plant in Plate 2, one replication in Plate 3, entire field view in Plate 4 and field view during maturity of Kidney bean in Plate 5.

3.6.6 Selection of plants for observation

In a field experiment, detail study of the entire population is rather difficult**.** Since all the plants get identical environment**.** Five plants from each replication were randomly selected for detailed investigation avoiding border plants and tagged for identification**.**

3.7 Observation recorded

The technique of random sampling was adopted for recording the observations of various quantitative characters of Kidney bean**.** Five plants of each treatment from each replication were selected at random at the time of recording the data on various characters**.** Data of five plants were averaged replication wise and mean data was used for statistical analysis**.** The observations were recorded on following characters given below**.**

3.7.1 Days to 5-leaves stages

Numbers of days were counted from the date of sowing to the day 100**%** flower blooming of plants in each plot and in each genotype**.**

3.7.2 Days to 1st flowering and

Numbers of days were counted from the 1st day of flowering in the plants of a plot at each genotype in each of the replication and the value is averaged**.**

3.7.3 Days to 50% flowering

Numbers of days were counted from the day of 50**%** flowering in the plants of a plot at each genotype in each of the replication and value is averaged**.**

3.7.4 Days to pod maturity

It was recorded as the number of days taken from sowing to peaking of mature pods in each replication in each genotype**.**

3.7.5 Pod length (cm)

Randomly five pods were selected from each selected plant in every replication and their length was measured in cm**.** The average was worked out for recording the value**.**

Plate 1*:* Tagging of each genotype of entire field

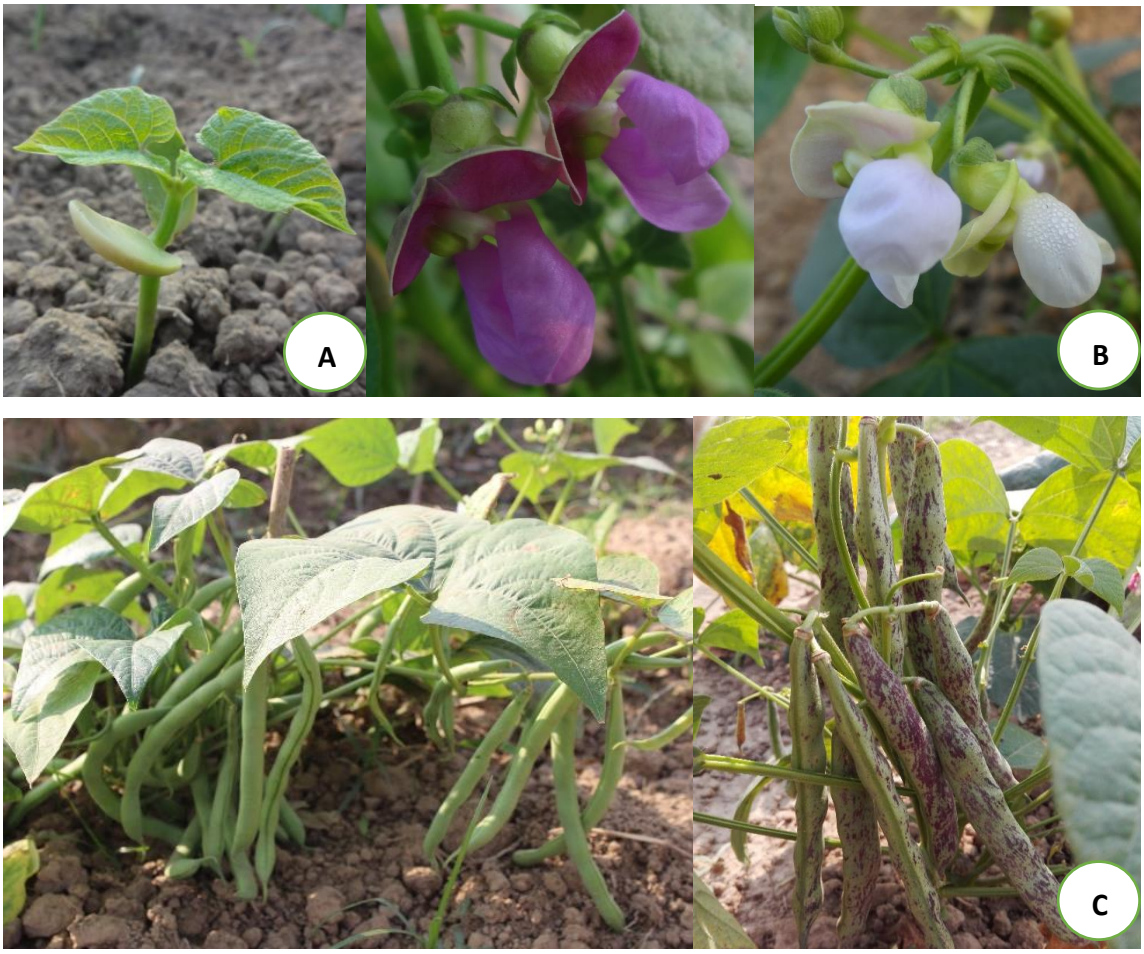


Plate 2: A. Seedling stage, B. Flowering stage, C. Fruiting stage

Plate 3: One replication view of the experimental field

Plate 4: The entire view of the experimental field during growth stage

Plate 5: View of the experimental field of matured plants

3.7.6 Pod width (cm)

Randomly five pods were selected from each selected plant in every replication and their width was measured in cm**.** The average was worked out for recording the pod width**.**

3.7.7 Number of leaves

The numbers of leaves of five selected plants were counted and recorded at the time of final harvesting**.**

3.7.8 Plant height (cm)

Five plants were randomly selected then height of the main stem of the plants from the ground level to the growing tip **(**terminal bud**)** was measured with the help of a meter scale in cm at the time final harvesting**.**

3.7.9 Leaf area (cm^2)

Leaves were collected from five tagged plants and leaf area was measured by leaf area meter in the central laboratory of Sher-e-Bangla Agricultural University and the average value was worked out for recording the leaf area**.**

3.7.10 Dry weight of pod (g)

Dry pods were collected from plants of each genotype of each replication which were weighed and its average was calculated**.**

3.7.11 Number of seeds per pod

The number of seed per pod from selected plants were harvested and threshed separately and counted**.**

3.7.12 Seed weight per plant (g)

The seed weight of fives pods of each replication of each genotype were weighed and its average was calculated**.**

3.7.13 Number of pods per plant

The numbers of pods from each of the five tagged plants were counted and their average value was calculated**.**

3.7.14 1000 seed weight (g)

Weights of 1000 dry seeds from mature pod of each genotype were calculated and average value was recorded**.**

3.7.15 Seed yield per hectare (t/ha)

The seed yield per plot was divided by plot area to obtain seed yield multiplied by 1hectare area to obtain seed yield per hectare**.**

3.7.16 Nutrient Content

50g Kidney bean of all genotypes of each replication was grinded and the analysis below was done**:**

3.7.16.1 Estimation of protein

Standard micro Kjeldahl procedure of AOAC **(**1995**)** was used for the determination of nitrogen and crude protein was estimated by multiplying the nitrogen content by a factor 5**.**95**.** About 0**.**2 g bean sample was taken into 100 mL Micro Kjeldahl flasks and then about 0**.**5**-**0**.**6 g of the catalyst mixture **(**for digestion**)** and 5**.**0 mL concentrated H_2SO_4 were added**.** Then the micro Kjeldahl digestion flask was heated for about 1 hour until the mixture becomes clear**.** After cooling the digested mixture, a minimum amount of water was added to the flask to dissolve the solids**.** Then the flask was connected to the distillation set**-**up, placing a 250 mL Erlenmeyer flask containing 25 mL of 4**%** boric acid solution plus one drop of the mixed indicator under the condenser with the tip of the condenser extending below the surface of the solution**.** Then 9 mL NaOH solution **(**40**%)** was slowly added to the digested solution**.** The distillation flask was connected to a steam source to distill the solution until about 75 mL distillate was collected **(**within 10**-**12 minutes**).** The tip of the condenser was washed with distilled water into the receiver**.** The distillated solution was immediately titrated with standard HCl solution to the first appearance of the violet reddish color**.** A blank was simultaneously run to calculate the percent N in the sample**.**

Calculation

$$\text{Nitrogen } \textbf{(\%)} = \frac{\{(\text{mL HCl for sample} - \text{mL HCl for Blank}) \times N_{HCl} \times 0.014\} \times 100}{\text{Weight of sample (g)}}$$

where, N_{HCl} = Normality of HCl

Protein **(%)** = Nitrogen **(%)** × 5**.**71

3.7.16.2 Estimation of crude fiber

It was estimated by the method of the Association of Official Agricultural Chemists **(**AOAC, 1995**).** Sulphuric acid 0**.**26 N, Sodium hydroxide 0**.**30 N, Ethanol 95**%** reagents were used**.** About 2 g bean sample was taken into a 250mL beaker and 200 mL hot solution sulphuric acid **(**0**.**26 N**)** was added**.** Then placed the beaker on a preheated hot plate of the digestion apparatus and digested the sample for 30 minutes,

rotating the beaker periodically to keep the solids or material from adhering to the sides**.** After digestion, the sample was filtered by a California modified Buchner funnel using a vacuum pump**.** The residues were washed with hot water until those were free from acid **(**Litmus paper used for that test**).** Transferred the residue **(**sample**)** backed into the beaker with 200 mL hot sodium hydroxide **(**0**.**30 N**)** solution**.** The beaker was placed on a preheated heater and digested the sample for 30 minutes as mentioned above**.** Then filtered the sample through California modified Buchner funnel and washed the residue with hot water until the washings were free from alkali **(**Litmus paper used for that test too**).** Finally, the residue was washed with alcohol **(**about 25 mL**).** Then the residue was transferred into a clean porcelain crucible and dried at 100^{o}C overnight**.** The crucible was transferred in desiccators and cooled at room temperature and weighed **(**W_1**).** Then the residue was ignited in a muffle furnace at 600^{o}C for 30 min**.** After that the crucible was transferred into the desiccators and cooled at room temperature and weighed **(**W_2**).**

Calculation

Weight of the crude fiber = **(**$W_1 - W_2$**)** – Blank

$$\text{Crude fiber } \textbf{(\%)} = \frac{\text{Weight of the crude fiber}}{\text{Weight of the sample}} \times 100 = \frac{(W1-W2)-\text{Blank}}{\text{Weight of the sample}} \times 100$$

3.7.16.3 Estimation of fat

It was extracted from the grounded seed samples with Chloroform**:** Methanol **(**2**:**1**)** solution**.** Fat was determined from the extract by the method of Choudhury and Juliano **(**1980**)** by Chloroform, Methanol**.** About 40 g bean powder was soaked with 100 mL of chloroform**:** methanol (2:1) mixture for overnight. Then the sample was filtered through Whatman filter paper No. 42 into a conical flask. The solvent was evaporated and transferred into a screw cap Pyrex test tube of known weight. Then the test tube was heated until the whole solvent was evaporated and dried completely under nitrogen. After that the weight of the test tube was taken again. The process was repeated until a constant weight was observed. Fat content was reported on a dry basis of the grain sample.

Calculation

$$\text{Fat (\%)} = \frac{(\text{Final weight of the test tube} - \text{Initial weight of the test tube})\ \text{g} \times 100}{\text{Weight of sample (g)}}$$

3.7.16.4 Estimation of ash

The sample is ignited at 550°C to burn off all organic materials**.** The inorganic material which does not volatilize at that temperature is called ash**.** The temperature of the muffle furnace was set to 550°C and the crucibles were heated for half an hour and then cooled in a desiccator and weighed (W_1). Then about 2 g of the sample was taken into the crucible (which has previously been heated and cooled) and weighted (W_2). The samples were incinerated at 550°C for 5 hours. The crucible was then cooled in a desiccator and weighted (W_3). For the prevention of moisture absorption weight had been taken immediately. To ensure completion of ashing, the crucible was again heated in the muffle furnace for an hour, cooled and weighed. This was repeated till two consecutive weights were the same, and the ash was almost white or grayish white in color.

Calculation

$$\text{Ash (\%)} = \frac{\text{Weight of ash (g)}}{\text{Weight of the sample (g)}} \times 100 = \frac{(W_3 - W_1)}{(W_2 - W_1} \times 100$$

where, $(W_2 – W_1)$ = weight of the sample, $(W_3 - W_1)$ = weight of the ash.

3.7.16.5 Estimation of moisture

Moisture content of bean flour sample was determined by drying at 105°C for overnight in an electric oven**.** About 2 g of flour was weighted into a weighted glass dish and dried in an oven at 105°C overnight and again in the morning till the weight of the dish became constant. Each time before weighing, the dish was cooled in a desiccator.

Calculation

$$\text{Moisture (\%)} = \frac{W_2 - W_3}{W_2 - W_1} \times 100$$

3.7.16.6 Estimation of carbohydrate

The carbohydrate content of a sample was calculated by subtracting the percentage of other components of that sample **(**moisture, ash, fat, protein and fiber**)** from 100**.** Percentage of carbohydrate = 100 **- (**moisture + ash + fat + protein + fiber**).**

Calculation

Percentage of carbohydrate = 100 - (moisture + ash + fat + protein + fiber).

3.8 Statistical analysis

The mean values of five randomly selected plants used for recording observations were computed for each of seventeen traits for each genotype in each replication and were subjected to statistical analysis**.** Duncan**'**s Multiple Range Test **(**DMRT**)** was performed for all the characters to test the differences between the means of the genotypes**.** Mean, range and co**-**efficient of variation **(**CV**%)** were also estimated using MSTAT**-**C**.** Multivariate analysis was done by computer using GENSTAT 5**.**13 and Microsoft Excel 2016 software through four techniques viz**.**, Principal Component Analysis **(**PCA**)**, Principal Coordinate Analysis **(**PCO**)**, Cluster Analysis **(**CA**)** and Canonical Vector Analysis **(**CVA**).**

3.8.1 Analysis of variance

The analysis of variance for different characters was carried out using mean data in order to assess the genetic variability among genotypes as given by Cochran and Cox **(**1957**).** The level of significance was tested at 5**%** and 1**%** using F test**.** The model of ANOVA used is presented in table 3

Table 3. Analysis of variance (ANOVA)

Sources of variation	**Degrees of freedom (df)**	**Mean sum of squares (MSS)**	**Expected MSS**
Replication	**(**r**-**1**)**	Mr	$g\sigma^2_r + \sigma^2_e$
Genotypes	**(**g**-**1**)**	Mg	$r\,\sigma^2_g + \sigma^2_e$
Error	**(**g**-**1**) (**r**-**1**)**	Me	σ^2_e
Total	**(**rg**-**1**)**		

Where,

r = number of replications

g = number of treatments **(**genotypes**)**

σ^2_r = variance due to replications**.**

σ^2_g = variance due to treatments **(**genotypes**)**

σ^2_e = variance due to error

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

$$S.E = \sqrt{\frac{2\,Ee}{r}}\,(1+\frac{rqu}{q+1})$$

Where, S. E = Standard error of mean

Ee = Mean sum of squares for error (Intra block)

r = Number of replications

q = Number of genotypes in each sub-block

u = Weightage factor computed

3.8.2 Study of variability parameters in Kidney bean genotypes

The variability among the genotypes for traits related to seed yield in Kidney bean were estimated as mentioned below.

3.8.2.1 Genotypic variance and phenotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{R}$$

Phenotypic variance = Genotypic variance $(\sigma^2 g)$ + Error variance $(\sigma^2 e)$

3.8.2.2 Co-efficient of variability

Both phenotypic and genotypic co-efficient of variability for all characters were estimated using the formula of Burton (1952).

$$\text{Phenotypic Co efficient of Variability (PCV\%)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$\text{Genotypic Co efficient of Variability (GCV\%)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$$

PCV nd GCV were classified into three following categories as suggested by Sivasubramanian and Madhamenon (1973).

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

3.8.2.3 Heritability in broad sense (h^2)

The broad sense heritability (h^2_{bs}) was estimated for all characters as the ratio of genotypic variance to the total of phenotypic variance as suggested by Lush (1949) and Hanson *et al.* (1956).

$$h^2 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability estimates in cultivated plants could be placed in the following categories as suggested by Robinson *et al***. (**1966**).**

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

3.8.2.4 Genetic advance (GA):

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson *et al***. (**1955**).**

$GA = h^2_{bs} \times б_p \times K$

Where,

h^2_{bs} = Heritability estimate in broad sense

$б_p$ = Phenotypic standard deviation of the trait

K = Standard selection differential which is 2**.**06 at 5% selection intensity**.**

Categories High (>20%) Moderate (10**-**20%) Low (<10%)

Further the Genetic advance as per cent of mean was computed by using the following formula:

$$\text{GA as per cent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent mean was categorized into following groups as suggested by Johnson *et al.* **(**1955**).**

Categories Low **-** <10% Moderate **-**10-20% High **-** >20%

3.8.3 Correlation coefficient analysis

To determine the degree of association of characters with yield and also among the yield components, the correlation coefficients were calculated**.** Both genotypic and phenotypic coefficients of correlation between two characters were determined by using the variance and covariance components as suggested by Al-Jibouri *et al***. (**1958**).**

$$r_g(xy) = \frac{Cov_g xy}{\sqrt{б^2_x} \cdot \sqrt{Б^2_y}}, \qquad r_p(xy) = \frac{Cov_p xy}{\sqrt{б^2_x} \cdot \sqrt{б^2_y}}$$

Where, $r_g(xy)$, $r_p(xy)$ are the genotypic and phenotypic correlation coefficients respectively**.**

Cov_g, Cov_p are the genotypic and phenotypic covariance of xy, respectively**.**

$б^2_g$ and $б^2_p$ are the genotypic and phenotypic variance of x and y, respectively**.**

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

3.8.4 Path coefficient analysis

Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software packages called OPStat. These values were obtained by solving the following set of 'p' simultaneous equation using above package.

$P_{01} + P_{02}\ r_{12} + \ldots\ldots\ldots\ldots\ldots + P_{0p}\ r_{1p} = r_{01}$

$P_{01} + P_{12}\ r_{02} + \ldots\ldots\ldots\ldots\ldots + P_{0p}\ r_{2p} = r_{02}$

$P_{01} + r_{1p} + P_{02}\ r_{2p} + \ldots\ldots\ldots\ldots + P_{0p} = r_{0p}$

Where, P_{01}, P_{02}, ……. P_{0p} are the direct effects of variables 1, 2……P on the dependent variable 0 and r_{12}, r_{13},.....r_{1p}……$r_{p(p+1)}$ are the possible correlation coefficient between various independent variables and r_{01}, r_{02}, r_{03}..... r_{0p} are the correlation between dependent and independent variables. The indirect effects of the i^{th} variable via j^{th} variable was attained as (P_{0j} * r_{ij}). The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below.

$P_{ox}^2 = 1 - (P_{01}^2 + 2P_{01}P_{02}r_{12} + 2P_{01}P_{03}r_{13} + \ldots\ldots + P_{02}^2 + 2P_{02}P_{03}r_{13} + \ldots\ldots\ldots + P_{0P}^2)$

Residual factor = $v\ (P_{ox}^2)$

Categories

Negligible - 0.00 to 0.09; Low- 0.10 to 0.19; Moderate 0.20 to 0.29;
High – 0.30 to 1.0; Very High- >1.00

3.8.5 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 programme 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, Principal Coordinate analysis, 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:

3.8.5.1 Principal Component analysis (PCA)

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

3.8.5.2 Principal Coordinate analysis (PCA)

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.

3.8.5.3 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.

3.8.5.4 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 is 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.

3.8.5.5 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 Caudhury (1987). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

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

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.

3.8.5.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh *et al.* (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.

3.8.5.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh *et al.* (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.

3.8.5.8 Contribution of individual characters towards genetic divergence

The character contribution towards genetic diversity was calculated following the method suggested by Singh and Caudhary (1977). In all combinations, each character is ranked on the basis of $d_i = Y_i^j - Y_j^k$ values

Where,

d_i = Mean deviation

Y_i^j = Mean value of the jth genotype for ith character and

Y_j^k = Mean value of kth genotype for ith character

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

3.8.5.9 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 Caudhury (1977). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

Chapter IV

Results and Discussions

CHAPTER IV
RESULTS AND DISCUSSIONS

In the present study the data was collected from 18 diverse genotypes of Kidney bean on seventeen characters related to vegetative, reproductive and nutrient components parameters emphasizing growth, yield, and nutrition. The data were subjected to biometrical analysis and results obtained are presented below under the following headings:

4.1 Mean performance and genetic parameters

4.2 Correlation analysis

4.3 Path co-efficient analysis

4.4 Genetic diversity through D^2 statistics

4.5 Nutrient components analysis by mean separation method

4.1 MEAN PERFORMANCE AND GENETIC PARAMETER

The success in any crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability, and to select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather, 1949). Therefore, it is necessary to have prior information on both PCV and GCV, so that the estimate of heritability that helps the breeder to predict the expected GA possibly by selection for a character can be computed.

The results are pertained to mean values grand mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GA) for all the fifteen characters are furnished in Table 4. Genotypic and phenotypic variability is shown in figure 1; Heritability and genetic advance as per cent of mean is shown in figure 2. Out of the seventeen characters studied, plant heights, number of leaves, leaf area, petiole length are considered as growth attributing characters. Days to 1st flowering, days to 50% flowering and days to pod maturity, days to 1st pod setting were regarded as earliness attributes. Pods per plant, pod length, pod width, dry weight of pod, number of seed per

pod and 1000 seed weight were considered as reproductive traits. Yield per plant and yield per hectare were the economic traits. The character wise details of these variability parameters are presented below of the genotypes evaluated for 17 characters are presented in Appendix IV and V**.**

4.1.1 Days to 5-leaves stage

The mean sum of square of days to 5-leaves Stage was 15.34, which was significant in Kidney bean indicating existence of considerable variation for this character. The mean ranged from 7.00 to 13.67 DAS (days after sowing). Highest duration for days to 5-leavs stage was recorded in G1- BARI Jharsheem -1 (13.67) and lowest in G11 (7.00) from DAS (Appendix IV and V). It was observed that BARI Jharsheem-1 took the shortest time to attain 4 leaves stage (17.33 days), whereas the genotype BB-3 took the longest (23.00 days) by Noor *et al.* (2014). These results concur with the findings of Roy (Roy, 2004) who also observed marked variation (15.00 to 21.67 days) among the genotypes in respect of days required to attain 4 leaves stage of Kidney bean genotypes.

The genotypic variance and phenotypic variance for this trait were 4.91 and 5.52 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The difference between the genotypic co-efficient of variation (24.00) and phenotypic co-efficient of variation (25.46) indicated presence of considerable variability among the genotypes for this trait. The minimum difference shows that there is less influence of environment. Mishra *et al.* (1995), Kumar (1997) found moderate to high genotypic coefficient of variation were observed for the trait.

The heritability (88.80%) estimates for this trait was high, low genetic advance (4.30) and high genetic advance over percentage of mean (46.58) (Table 4), indicated that this might be controlled by non-additive genes. Thus, the selection will be rewarding for improving this trait. High heritability of this trait is being exhibited due to favorable environment rather than genotype. Chakraborty and Mukherjee (2001); Mandal and Dana (1998) found similar result in rice bean.

Table 4: Estimation of mean performance and genetic parameters in seventeen characters of eighteen genotypes of Kidney bean

Traits	Mean	Min	Max	Mean	CV	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA
Days to 5 leaves stage	15.34**	7.00	13.67	9.20	8.53	4.91	0.62	5.52	24.00	8.52	25.46	88.80	4.30	46.58
Days to 1st flowering	29.53**	30.00	38.67	32.41	3.47	9.41	1.30	10.71	9.33	3.47	9.96	87.84	5.92	18.02
Days to 50% flowering	24.83**	33.00	42.00	35.56	3.16	7.85	1.29	9.14	7.79	3.16	8.40	85.87	5.35	14.86
Days to Maturity	39.57**	78.00	89.33	81.33	3.27	10.80	7.17	17.97	4.02	3.27	5.18	60.12	5.25	6.42
Days to 1st Pod Setting	22.05**	36.67	47.00	39.44	3.48	6.71	1.92	8.63	6.51	3.48	7.38	77.78	4.71	11.82
Plant Height (cm)	94.66**	20.53	36.59	29.23	9.55	28.80	8.27	37.06	17.82	9.55	20.22	77.69	9.74	32.36
No of Leaves	28.38**	7.93	21.93	14.41	7.94	9.03	1.30	10.33	20.88	7.94	22.34	87.38	5.79	40.20
No of Pod/Plant	94.11**	10.67	30.68	19.37	10.66	29.92	4.35	34.27	27.97	10.66	29.93	87.32	10.53	53.83
Leaf Area (cm^2)	2609.06**	83.80	169.67	125.50	4.14	860.30	28.16	888.46	22.88	4.14	23.25	96.83	59.46	46.39
Petiole Length (cm)	16.26**	5.43	12.67	8.44	4.73	5.36	0.17	5.53	26.53	4.73	26.94	96.92	4.70	53.79
Pod Length (cm)	6.46**	6.53	12.38	9.78	9.05	1.89	0.79	2.68	14.05	9.05	16.71	70.65	2.38	24.32
Pod Diameter (cm)	0.72^{NS}	7.03	8.92	7.92	8.47	0.09	0.45	0.54	3.74	8.46	9.25	16.37	0.25	3.12
Dry Weight of Pod	0.61^{NS}	1.00	2.75	1.81	5.88	0.20	0.01	0.21	24.53	5.87	25.22	94.59	0.89	49.14
No of Seeds/Pod	0.94^{NS}	3.23	5.50	4.20	5.06	0.30	0.05	0.34	13.00	5.06	13.95	86.86	1.05	24.96
1000 Seed Weight	9355.92**	213.64	443.33	301.10	20.21	1907.79	3632.54	5540.33	14.65	20.21	24.96	34.43	52.80	17.70
Seed Yield (g/Plant)	1748.91**	35.85	120.43	79.51	17.75	517.43	196.63	714.06	28.79	17.75	33.83	72.46	39.89	50.49
Yield	0.86**	0.80	2.68	1.77	17.77	0.26	0.10	0.35	28.72	17.72	33.75	72.42	0.89	50.34

** = Significant at 5% level, * = Significant at 1% level, NS = Non-significant, CV = Coefficient of variation, σ^2_g = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_e = Environmental variance, GCV = Genotypic co-efficient of variance, PCV = Phenotypic co-efficient of variance, h^2_b = Heritability in broad sense, GA = Genetic advance, GA (% of mean) = Genetic advance as per cent of mean

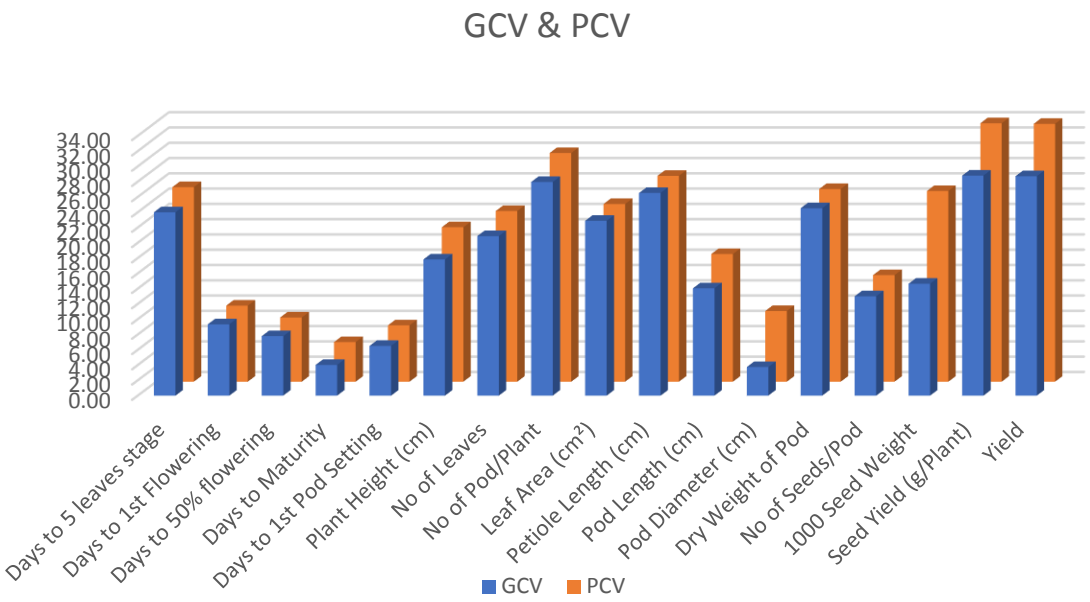


Figure 1: Genotypic and phenotypic variability in Kidney bean

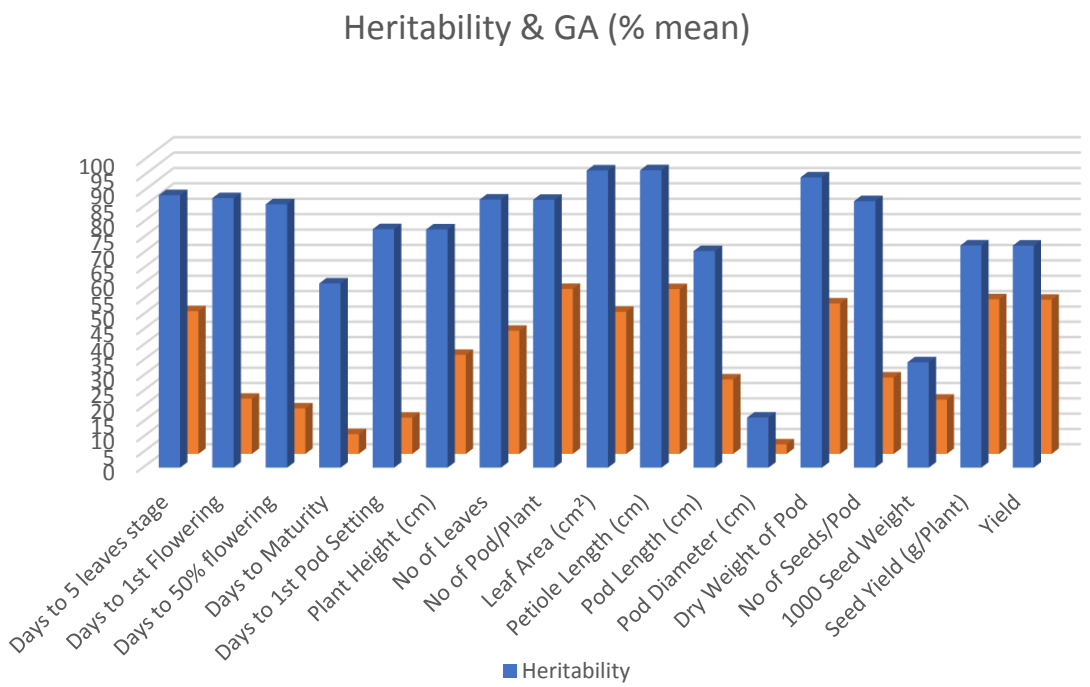


Figure 2: Heritability and genetic advance as percent over mean in Kidney bean

4.1.2 Days to 1st flowering

Days to 1st flowering was ranged from 30.00 to 38.67 DAS with mean value of 32.41 (Table 4). The mean sum of square of days to 1st flowering was 29.53 which showed considerable significant differences among the genotypes. Highest duration was recorded in G9 (38.67) and lowest in G3 (30.00), G5 (30.00), G6 (30.00), G8 (30.00), G11 (30.00), G13 (30.33) and G15 (30.00) (Appendix IV and V). Neupane *et al*. (2003) reported that the number of days required for flowering in Kidney bean was influenced by the genotype varying from 40 to 84 depending on the genotype.

The phenotypic variance (10.71) was higher than genotypic variance (9.41) revealing that the apparent variation was not only due to genotypes but also due to influence of environment. The genotypic co-efficient of variance and phenotypic co-efficient of variance were 9.33 and 9.96 respectively (Table 4). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on the expression of this character. Singh *et al.* (1994) reported that days to 1st flowering showed lowest phenotypic and genotypic coefficients of variation. The low PCV and GCV value for days to 1st flowering indicated less scope to selection for this trait. Dahiya *et al*. (2000) observed the highest GCV and PCV for days to first flowering. The heritability (87.84%) estimates for this trait was high. Most likely the high heritability is due to additive gene effects. Scully *et al.* (1991) observed high heritability value for days to 1st flowering. Low genetic advance (5.92) and moderate genetic advance over percentage of mean (18.02) were found in (Table 4). High heritability coupled by low genetic advance was noticed for days to 1st flowering. This low value may be due to non-additive gene action and selection will not be beneficial.

4.1.3 Days to 50% flowering

Significant mean sum of square was observed in days to 50% flowering with the value of 24.83. The maximum duration to days to 50% flowering was found in G9 with 42.00 DAS and the minimum in G3 with 33.67 DAS, G8 with 33.33 DAS, G11 with 33.33 DAS, G17 with 33.67 DAS, G18 with 33.00 DAS (Appendix IV and V). The mean value was 35**.**56**.** Singh *et al***. (**1993**)** reported significant differences for days to 50 per cent flowering and recommended the selection based on these traits**.** Devi *et al.* **(**2012**)** reported that the genotypes of Kidney bean showed considerable variation in days to

50 per cent flowering which varied from 40.0 days to 46.7 days. According to Prakash and Ram (2014), considerable variation had been expressed in days to 50 per cent flowering which varied from 36.0 days to 48.5 days.

The genotypic variance (7.85) is lower than phenotypic variance (9.14). Thus, genes controlling this trait possessed considerable influence of environment on the expression of the character. The GCV (Genotypic co-efficient of variation) and PCV (Phenotypic co-efficient of variation) were low with value of 7.79 and 8.40 per cent respectively, along with high heritability of 85.87% with moderate genetic advance as per cent mean of 14.86%` and low genetic advance (5.35) (Table 4). This moderate value may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). The flowering trait of the plant is very much sensitive and influenced by the environmental temperature fluctuation which is reflected in the present study. High heritability and low genetic advance indicating that the traits were being exhibited due to favorable influence of environment rather than genotype. Thus, it is indicative that non-additive gene action might be controlling the trait of expression and selection for this trait may not be rewarding. In the contrast to the present results, High heritability was being exhibited due to favorable influence of environment rather than genotype. Thus, selection for this trait may not be rewarding. Raffi and Nath (2004) reported that days to 50 per cent flowering showed high heritability with high genetic advance.

4.1.4 Days to maturity

The average of 81.33 days with a range of 78.00 to 89.33 days ranges was recorded for days to maturity. The G6 and G12 required least number of days to maturity (78.00 days) followed by G14 (78.67 days), whereas required maximum number of days to maturity was observed in the genotype G9 (89.33 days) followed by G10 (86.00 days) (Appendix IV and V). The shortest time required for first pod maturity in BARI Jharsheem-1 (81.5 days) and longest time from BB-3 (96.0 days) as reported by Hussain (2005).

Days to maturity exhibited low GCV and PCV of 4.02 and 5.18percent respectively, along with moderate heritability of 60.12 per cent, low genetic advance 5.25 and low genetic advance as per cent mean of 6.42 per cent. This moderate heritability with low

genetic advance indicative of non-additive gene action. Moderate heritability is being exhibited due to favorable influence of environment rather than genotype. Thus, selection for such trait may not be rewarding. The genotypic and phenotypic variance were recorded as 10.80 and 17.97 respectively. As phenotypic variance is larger than genotypic variance proving that considerable influence of environment is present in the expression of genes for this trait. Raffi and Nath (2004) reported that highest genotypic and phenotypic variations were observed for days to maturity, while Scully *et al.* (1991) observed high heritability value for days to maturity,

4.1.5 Days to 1st pod setting

A general observation is that if less time taken for days to pod maturity is directly proportion to the yield. Early pod maturity genotypes are presumed to have high yield. Hence less days to taken from sowing to pod maturity are considering into account for early pod production genotypes. In present study days to pod maturity in different genotypes ranged from 36.67 to 47.00 days with mean value of 39.44days. The genotypes G11 recorded earliest in pod production (36.67days) followed by genotypes G5 (37.33 days). On other hand maximum days for pod maturity were found in genotypes G9 (47.00 days) followed by G10 (42.00 days), and the mean sum of square was recorded for this character was 22.05 days (Appendix IV and V).

The genotypic variance and phenotypic variance for this trait were 6.71 and 8.63 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested presence of influence of environment on the expression of the genes controlling this trait. Low genotypic co-efficient of variation (6.51) and phenotypic co-efficient of variation (7.38) were close to each other (Table 4) in dictating minor influence of environment. High PCV and GCV were observed in 38 genotypes of cowpea by Kumari *et al.* (2003).

The heritability (77.78%) estimates for this trait was high, low genetic advance (4.71) and genetic advance in per cent of mean (11.82) which was found moderate (Table 4). High heritability coupled with low genetic advance is indicative of non-additive genes. Thus, selection may not be rewarding. Dahiya *et al.* (2000) reported for days to 1st pod setting characterized by high genetic advance combined with high heritability. This

indicated that additive gene effects were more important in the inheritance of these characters.

4.1.6 Plant height (cm)

Plant height was observed highest in G1 (BARI Jharsheem-1) (36.59 cm) followed by in G9 (36.38 cm) and lowest in G12 (20.53 cm). The mean value was recorded as 29.23 cm and mean of sum of square was 94.66 indicating significant differences among the genotypes for this trait (Appendix IV and V). Moniruzzaman *et al.* (2009) found that the plant height of French bean was significantly higher in BARI Jharsheem-1 (45.3 cm) as compared to BARI Jharsheem-2 (41.8 cm). According to Noor *et al.* (2014) plant height varied enormously from genotype to genotype. It ranged from 25.61 to 60.83 cm. This might be due to genetic configuration and environmental effect. It was studied by Hussain (2005) for ten genotypes of Kidney bean who found the tallest plant 40.78 cm and the shortest 20.50 cm.

Genotypic and phenotypic variance was observed 28.80 and 37.06 respectively for plant height with large environmental influence. The plant height exhibited moderate genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) of 17.82 and 20.22 per cent respectively (Table 4). PCV and GCV were found high in plant height (Patil *et al*. 1993). High PCV was found by Prakash *et al.* (2015). High heritability of 77.69 per cent, low genetic advance 9.74 along with high genetic advance as per cent mean (32.36%) was recorded. High heritability with low genetic advance shows that it is controlled by non-additive gene effects and the selection maybe ineffective for improvement of Kidney bean. But Raffi and Nath **(**2004**)** and Prakash *et al***. (**2015**)** reported that plant height showed high heritability with high genetic advance**.**

4.1.7 Number of leaves

The mean of sum of square for number of leaves was significantly recorded as 28.38. Maximum number of leaves were found in G6 (21.93) and minimum number of leaves were found in G18 (7.93) followed by G17 (9.17) with mean value 14.41 (Appendix IV and V). The maximum number of leaves 21.67, and the minimum was 9 found by Noor *et al.* (2014). These variations might be due to difference in genetical constituents as well as environmental effects.

The genotypic and phenotypic variance was recorded as 9.03 and 10.33 respectively. Moderate genotypic co-efficient of variation (GCV) and high phenotypic co-efficient of variation (PCV) of 20.88 and 22.34 per cent were observed respectively (Table 4). Medium GCV (14.15%) was also observed for number of leaves by Alemu *et al.* (2013). And the variation is caused not only due to genotypes but also the influence of environment but the influence is little. Findings of Ahmed *et al*. (2005), Dahiya *et al*. (2007) were also in agreement with this result. High heritability 87.38% and high genetic advance as per cent mean 40.20% shows that additive gene effects were present, making selection effective for this trait. But according to Alemu *et al.* (2013) found moderate heritability of number of leaves (35.75%). The genetic advance was recorded as 5.79. Coyne (1968), Dahiya (2006), Deepak (1999) also found similar findings.

4.1.8 Number of pods per plant

Number of pods per plant ranged from 10.67 to 30.68 with mean value 19.37 in different genotypes. The maximum number of pods per plant was noticed in genotype G6 (30.68) followed by genotype G11 (22.00). The genotype G18 recorded minimum number of pods per plant (12.50) followed by genotype G17 (10.67) (Appendix IV and V). The mean sum of square reported significantly for this trait was 94.11 (Table 4). Prakash and Ram (2014) reported considerable variation in number of pods per plant which varied from 10.46 to 30.22 in Kidney bean.

The phenotypic variance (34.27) is higher than genotypic variance (29.92). this indicates high influence of environment on this character. The high phenotypic coefficient of variation (27.97%) and genotypic coefficient of variation (29.93%) (Table 4) indicated presence of considerable variability among the genotypes. Similar result was also reported by Devi *et al*. (2014), Reddy *et al.* (2004). The heritability (87.32%) estimates for this trait was high, moderate genetic advance (10.53) and very high genetic advance in per cent of mean (53.83) were found (Table 4), revealed that High heritability coupled by moderate genetic advance may be due to moderate values for phenotypic standard deviation as the heritability is high for these characters and selection differential is always constant (Nadarajan and Gunasekaran, 2005). Scully *et al.* (1991) observed high heritability value for days to 1st flowering.

So, these traits could be exploited for further improvement through selection procedures. It was also reported by Rai *et al*. (2010), Junaif *et al*. (2010) and Devi *et*

al. (2014). Singh *et al.* (1994) reported that pods per plant had moderately high GCV and genetic advance and high heritability. But Mishra and Dash (1991) found moderate heritability and high genetic advance in number of pods per plant.

4.1.9 Leaf area (cm^2)

The mean of sum of square for this trait was found 2609.06 which was significant among the genotypes. Leaf area was ranged from 83.80 to 169.67 and the mean value was 125.50. In the present study highest value was recorded in G6 (169.67) and lowest was observed in G7 (83.80) (Appendix IV and V) while the mean value was 125.50. Noor *et. al* (2014) reported genotypic differences in leaf area as he found the maximum leaf area 2165.26 cm^2 and the minimum was 855.18 cm^2 (Table 4).

The genotypic variance and phenotypic variance were recorded 860.30 and 888.46 respectively, showing little influence of environment on this character. The GCV and PCV were found respectively 22.88 and 23.25. Kamaluddin (2011), Ahmed (2011), Angadi *et al*. (2011) observed similar facts in their findings. The heritability, genetic advance and genetic advance in per cent of mean was recorded as 96.83%, 59.46, 46.39% respectively. High heritability with high genetic advance is the indicative of additive gene action, thus selection for this trait would be effective. Ahmed (2011), Rai *et al*. (2010), Prasad (1995) also reported in consonance.

4.1.10 Petiole length (cm)

Petiole length of different genotypes ranged from 5.43 cm to 12.67 cm. The maximum petiole length was observed in genotype G6 (12.67 cm) followed by genotype G9 (12.48 cm). However minimum plant height was found in genotype G18 (5.43 cm) (Appendix IV and V). The grand mean reported for this trait was 8.44 cm (Table 4).

The genotypic variance and phenotypic variance were recorded 5.36 and 5.53 respectively. High GCV and PCV were found respectively 26.53 and 26.94 showing very little influence of environment on this character. Similar observations were found by Mishra (1996), Mittal (2005), Narsinghani (1991). The heritability, genetic advance and genetic advance in per cent of mean was recorded as 96.92%, 4.70, 53.79% respectively. High heritability with low genetic advance indicates of non-additive gene action. Thus, the selection would not be benificial for the improvement of Kidney bean. Similar observations were reported by Dahiya *et al*. (2000), Raffi and Nath (2004), Singh *et al.* (2007), Junaif (2010), Makhdoomi and Dar (2011).

4.1.11 Pod length (cm)

The mean of pod length was 9.78 cm and ranged from 6.53 to 12.38 cm. The G6 had long pods of 12.38 cm followed by G5 (11.18 cm). The pods were shorter in G18 (6.53 cm) followed by G17 (6.67 cm) and G9 (8.00 cm) (Appendix IV and V). The mean sum of square was significant (6.46) which indicated considerable amount of variation for this trait in the genotypes (Table 4). The experimental findings of Sarangi and De (2010) revealed that the pod length of Kidney bean variety varied from16.35 cm to 15.86 cm.

The genotypic and phenotypic variance for pod length were seen as value of 1.89, 2.68 respectively. Pod length exhibited moderate GCV (14.05%) and PCV (16.71 %) values. Similar result was seen by Junaif (2010), Seth *et al*. (1972), Nandi *et al.* (1996) and Rai *et al*. (2004). As PCV is higher than GCV thus we can conclude that the trait is controlled by its genotype as well as influence of environment. Raffi and Nath (2004) reported that highest genotypic and phenotypic variations were observed for pod length. A high heritability estimates of 70.65%, low genetic advance 2.38 and a high genetic advance as per cent of mean of 24.32% were observed. High heritability with combination of low genetic advance as per cent of mean allow us to speculate the presence of non-additive gene effects on this trait. Singh *et al*. (1994) reported that pod length had moderately high GCV and genetic advance and high heritability. Presence of high variability for this character is also in agreement with the results obtained by Patil *et al* (1993), Singh *et al*. (1994), Kapila and Pawar (1997), Dikshit *et al.* (1999), Reddy *et al*. (2004). Plate 6 is presented showing length variation in green pods of different genotypes of kidney bean.

4.1.12 Pod diameter (cm)

Highest pod diameter was noticed in G18 (8.92 cm) followed by G13 (8.40 cm) and lowest in G6 (7.03cm) among all genotypes. The mean value was calculated as 7.92. (Appendix IV and V). The phenotypic variance (0.54) appeared to be very high than the genotypic variance (0.09). The low genotypic co-efficient of variation (3.74) and phenotypic co-efficient of variation (9.25) suggested influence of environment on the expression of this character ((Table 4). Therefore, selection based upon phenotypic expression of this character would be ineffective for the improvement of this crop. The heritability (16.37%) estimates for this trait was very low, genetic advance (0.25) was low and

Plate 6: Length variation in green pods of different genotypes of Kidney bean

genetic advance in per cent of mean (3.12) was very low (Table 4), revealed that this character was governed by non-additive gene. This reveals that the character is highly influenced by the environmental effects and selection would be ineffective. Singh *et al*. (2007) reported that pod diameter showed low to moderate heritability and genetic gain. Angadi *et al*. (2011) reported that pod diameter exhibited high heritability and genetic advance over mean.

4.1.13 Dry weight of pod (g)

The range observed for dry weight of pod was from 1.00g to 2.75g with average 1.81. The high dry weight of pod was observed in G6 (2.75 g) followed by G5 (2.50 g) and G4 (2.33 g) (Appendix IV and V). There was any significant varication observed among the genotypes for this trait (Table 4).

The genotypic variance (0.20) is closely related with phenotypic variance (0.21) indicating that minor influence of environment. High GCV (24.53) and PCV (25.22) were estimated as and respectively were close to each other (Table 4), indicating minor environmental influence on this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Dahiya *et al*. (2007), Padi and Ehlers (2008) reported in consonance. High heritability (94.59%), low genetic advance (0.89), high genetic advance as per cent of mean (49.14%) were observed. Thus, the selection would be ineffective as the heritability was most likely due to favorable environmental effects. There is similarity with the report of Makhdoomi and Dar (2011) and Kamaluddin (2011).

4.1.14 Number of seed per pod

Number of seeds per pod ranged from 3.23 to 5.50 in different genotypes. The maximum number of seeds per pod was recorded in genotype G6 (5.50) followed by genotype G5 (5.04). However, minimum number of seeds per pod exhibited in genotype G18 (3.23) followed by genotype G17 (3.37) (Appendix IV and V). The mean observed for this trait was 4.20.

The genotypic variance (0.30) and phenotypic variance (0.34) were very close to each other. Moderate GCV and PCV were observed as 13.00 and 13.95 respectively (Table 4). This indicates very little influence of environment upon the character. According to Angadi *et al.* (2011) assessed that number of seeds per pod exhibited low genotypic and

phenotypic coefficient of variation. Whereas, it showed high heritability (86.86%), low genetic advance (1.05) and high genetic gain as per cent of mean (24.96%) for this trait. It was also reported as Patil *et al.* (1993). High heritability with low genetic advance indicates that high heritability occurs due to environmental effects. Thus, selection is ineffective for the improvement of the crop.

4.1.15 1000 Seed Weight

1000 seed weight of different genotypes ranged from 213.64 g to 443.33 g. The genotype G12 was exhibited maximum 1000 Seed Weight (4.54g) followed by genotype G2 (370.11g). Whereas, the genotype G15 was recorded minimum seed weight of (213.64 g) followed by genotype G18 (225.32 g). The grand mean found for this trait was (301.10 g) (Appendix IV and V). The mean sum of square was significant (9355.92) in Kidney bean which allows to show the presence of considerable variation for this trait. Significant variations in 1000 seed weight were observed by Noor *et al*. (2014). The highest seed weight was recorded 368.50 g and the lowest 116.38 g by him.

1000 seed weight was recorded moderate PCV (24.96 %) and GCV (14.65%) (Table 4). As PCV is greater than GCV, there is considerable influence of environment on this trait (Table 4). PCV and GCV were high for 100 seed weight according to Patil *et al*. (1993). High phenotypic coefficient variation for 100-seeds weight (43.22%) was found by Prakash *et al.* (2015). While it recorded moderate heritability (34.43%), high genetic advance (52.80) and moderate genetic gain as percent of means (17.70%) was found for this trait. High heritability with high genetic advance suggests that the character is governed by the additive gene action. Thus, selection may be effective in this trait for the improvement of the crop. High heritability coupled with high genetic advance in 100 seed weight was observed by Kamaluddin (2011) and Prakash *et al*. (2015). Sarafi (1978) also reported high heritability value for 100-seed weight.

4.1.16 Seed Yield per Plant (g)

Seed yield ranged from 35.85g to 120.43g, with a mean value of 79.51g. Maximum yield was recorded by the genotype G6 (120.43g) followed by G5 (115.07g) and G4 (112.03g). The lowest yield was recorded by the genotype G18 (35.85g) followed by G17 (38.55g) and G16 (51.30g) (Appendix IV and V). The mean sum of square was significant (1748.91).

Seed yield per plant exhibited high estimates of PCV (33.83%) and GCV (28.79%) in Table 4. It was also shown by Singh *et al*. (1994). Whereas, it also recorded high heritability (72.46%), high genetic advance (39.89) and high genetic gain as per cent of mean (50.49) for this trait. Similar result was also found by Raffi and Nath **(**2004**).** Selection would be effective for this trait as there is additive gene effects on the gene controlling this trait. Patil *et al*. (1993) reported that high genetic advance associated with high heritability values for the characters yield per plant. According to Singh *et al*. (1994) yield per plant had high GCV, genetic advance and heritability. reported that seed yield per plant showed high heritability with high genetic advance**.** Low heritability for seed yield per plant was observed in F3 generation of cowpea by Padi and Ehlers (2008).

4.1.17 Seed Yield (t/ha)

Seed yield per hectare of different genotypes ranged from 0.80 ton to 2.68 ton. The maximum seed yield per hectare was exhibited in genotype G6 (2.68 t/ha) followed by genotype G5 (2.56 t/ha) and genotype G4 (2.49 t/ha). The genotype G18 given minimum seed yield per hectare (0.80 t/ha) followed by genotype G17 (0.86 t/ha). The mean noticed for this trait was (1.77) (Appendix IV and V). The mean of sum of square was significant (0.86) which indicated variation among the genotypes for the trait (Table 4).

Seed yield (t/ha) also recorded high estimates of PCV (33.75%) and GCV (28.72%). Higher PCV shows apparent variation is not only due to genotypes but also due to effect of environment. Angadi *et al.* (2011) reported that both genotypic and phenotypic coefficient of variations was generally high for total yield per hectare. While, it showed high heritability (72.42%), low genetic advance (0.89) and high genetic gain as per cent of mean (50.34) observed for this trait. Thus, it reveals that this trait might be controlled by non-additive gene effects and selection would be ineffective. Omoigui *et al.* (2006) calculated heritability in selected varieties of cowpea and noted that yield had high heritability. Plate 7 and 8 represents the variation which were found in dry pod and seeds in case of color, shape and size.

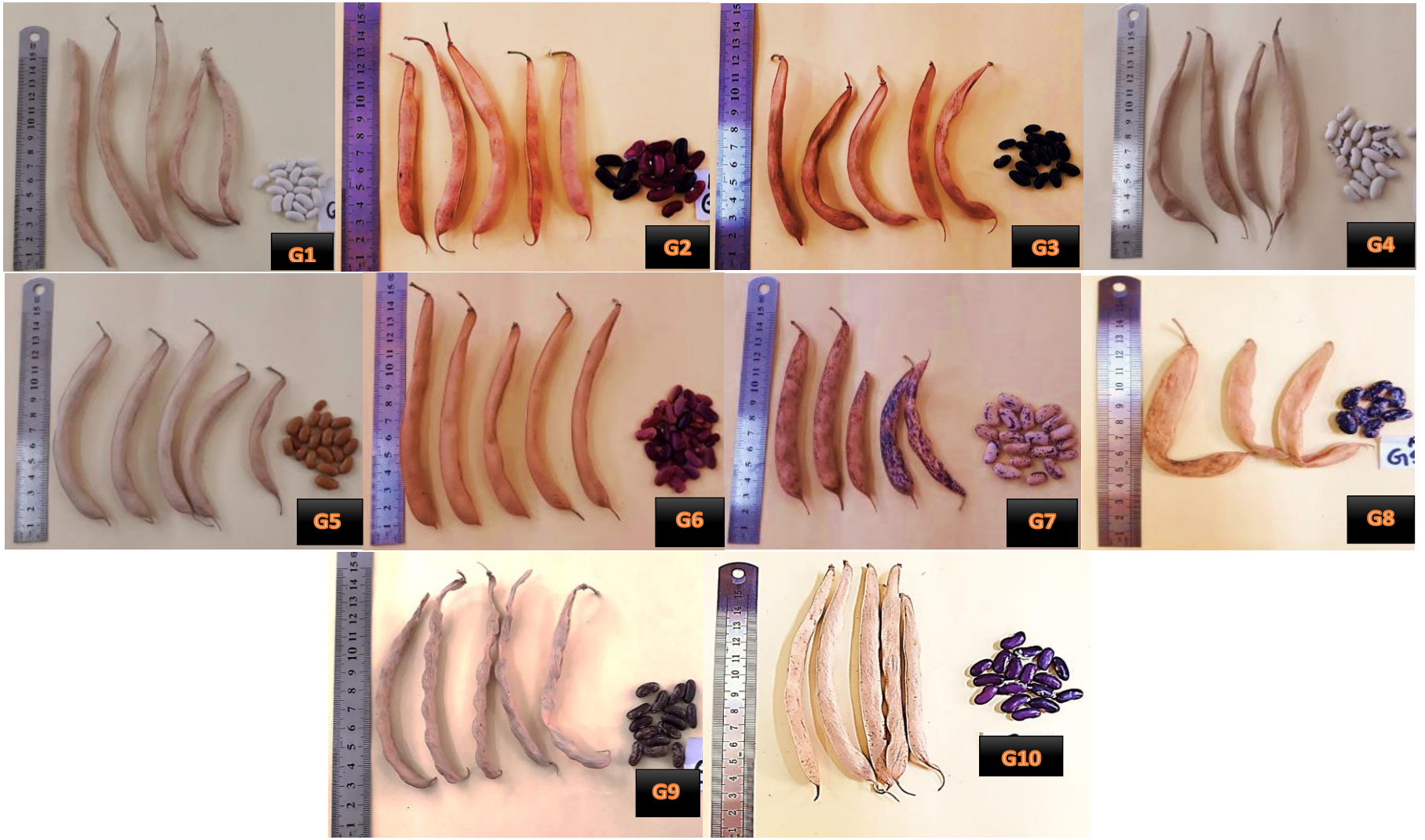


Plate 7: Variation in dry pod and seed color, size and shape

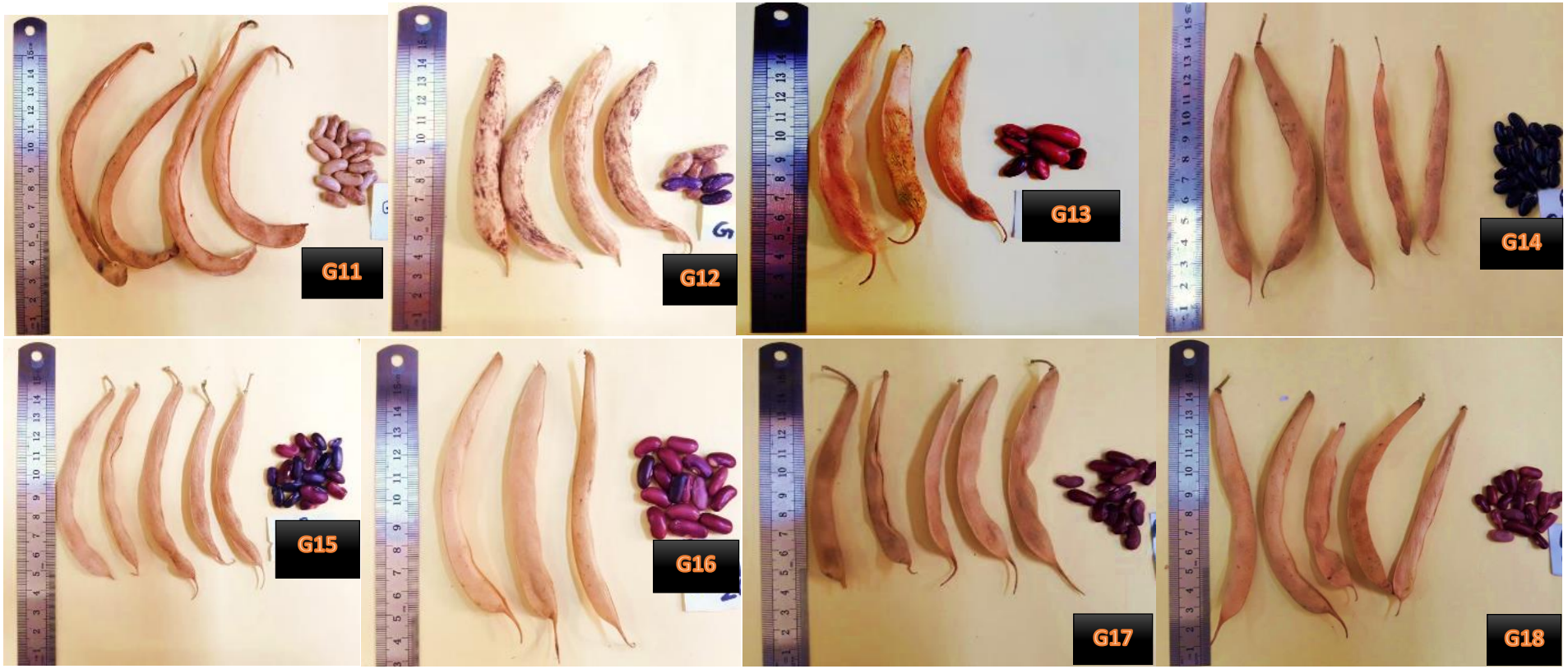


Plate 8: Variation in dry pod and seed color, size and shape

4.2 CORRELATION ANALYSIS

Improvement of a target character in all the breeding programs can be achieved by indirect selection via other characters. This needs a good understanding of the association of different characters with the target character and among the different characters themselves. It is necessary to have the estimates of correlation of yield with other characters for which the genotype could be assessed visually. The phenotypic and genotypic correlation reveals the extent of association between different characters, thus, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. A positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling different traits. No correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes. Yield being a complex character, is governed by a large number of genes. The influence of each character on yield could be known through correlation studies with a view to determine the extent and nature of relationships prevailing among yield and yield attributing characters.

So, the genotypic and phenotypic correlation co-efficient values for 17 characters in 18 Kidney bean genotypes studied are presented in Table 5 and 6 respectively and figure 3**.**

4.2.1 Days to 5- leaves stage

Association of days to 5- leaves stage is negatively significant with number of leaves -(-0.515, -0.495), pod length (-0.532, -0.494) and seed yield (-0.559, -0.504) and yield (-0.560, -.504) at both genotypic and phenotypic levels respectively (Table 5 & 6). However, the trait is highly significant and positively associated with pod diameter (0.678) at genotypic level but it is non-significant with pod diameter at phenotypic level. Siddique and Gupta (1991) also reported similar positive association among the traits observed. There is positive but non- significant correlation of days to 5- leaves stage with days to 1st flowering, days to 50% flowering, days to maturity, days to 1st pod setting, plant height at both genotypic and phenotypic level. Ahmed (2011), Baisakh (1992), Bhushan *et al.* (2008) observed the similar results. 0.257, -0.244), number of pod per plant (-0.112, -0.095), pod length (-0.193, -0.177), dry weight of pod

Table 5: Genotypic correlation coefficient for seventeen characters of Kidney bean

	FF	50%F	M	FPS	PH	NL	NPP	LA	PL	PdL	PdD	DWP	NSP	1000SW	SY	Y
LS	0.423	0.275	0.176	0.385	0.066	-0.515*	-0.337	-0.017	-0.126	-0.532*	0.678**	-0.417	-0.456	0.087	-0.559*	-0.560*
FF		0.988**	0.699**	0.952**	0.556*	-0.257	-0.112	0.273	0.495*	-0.193	0.435	-0.105	-0.163	-0.139	-0.217	-0.217
50%F			0.773**	0.990**	0.607**	-0.068	0.048	0.417	0.640**	-0.072	0.309	0.023	0.038	-0.202	-0.142	-0.142
M				0.791**	0.703**	-0.288	-0.324	0.227	0.460	-0.559*	0.370	-0.204	-0.247	-0.580*	-0.462	-0.462
FPS					0.557*	-0.127	-0.085	0.386	0.635**	-0.213	0.331	-0.011	-0.067	-0.076	-0.176	-0.172
PH						0.077	0.148	0.601**	0.721**	0.112	0.283	0.090	-0.028	-0.506*	-0.186	-0.185
NL							0.855**	0.469*	0.483*	0.909**	-0.523*	0.848**	0.885**	0.253	0.837**	0.831**
NPP								0.471*	0.428	0.795**	-0.676**	0.802**	0.903**	-0.125	0.793**	0.785**
LA									0.821**	0.536*	0.029	0.616**	0.537*	0.033	0.391	0.391
PL										0.447	0.044	0.559*	0.441	0.093	0.371	0.372
PdL											-0.408	0.816**	0.742**	0.359	0.861**	0.861**
PdD												-0.554*	-0.631**	-0.092	-0.677**	-0.677**
DWP													0.816**	0.352	0.976**	0.976**
NSP														0.083	0.799**	0.798**
1000SW															0.463	0.462
SY																1.000**

** = Significant at 1% * = Significant at 5%

LS =Days to 5 leaves stage FF =Days to 1st Flowering 50%F =Days to 50% flowering M =Days to Maturity FPS =Days to 1st Pod Setting
PH =Plant Height (cm) NS =No of Leaves NPP =No of Pod/Plant LA =Leaf Area (cm²) PL =Petiole Length (cm)
PdL =Pod Length (cm) PdD =Pod Diameter (cm) DWP =Dry Weight of Pod NSP =No of Seeds/Pod 1000SW=1000 Seed Weight
SY =Seed Yield (g/Plant) Y =Seed Yield (g/Plant)

Table 6: Phenotypic correlation coefficient for seventeen characters of Kidney bean

	FF	50%F	M	FPS	PH	NL	NPP	LA	PL	PdL	PdD	DWP	NSP	1000SW	SY	Y
LS	0.410	0.267	0.165	0.379	0.059	-0.495*	-0.330	-0.018	-0.119	-0.494*	0.378	-0.407	-0.423	0.050	-0.504*	-0.504*
FF		0.956**	0.628**	0.902**	0.531*	-0.244	-0.095	0.267	0.481*	-0.177	0.273	-0.109	-0.164	-0.077	-0.196	-0.196
50%F			0.674**	0.940**	0.584*	-0.052	0.057	0.399	0.614**	-0.064	0.203	0.027	0.031	-0.130	-0.096	-0.096
M				0.728**	0.571*	-0.287	-0.279	0.205	0.419	-0.486*	0.273	-0.200	-0.228	-0.383	-0.376	-0.376
FPS					0.498*	-0.105	-0.071	0.367	0.611**	-0.201	0.232	-0.015	-0.070	-0.041	-0.139	-0.139
PH						0.072	0.144	0.572*	0.676**	0.102	0.107	0.082	-0.049	-0.407	-0.156	-0.155
NL							0.821**	0.451	0.468	0.827**	-0.266	0.825**	0.844**	0.195	0.781**	0.781**
NPP								0.462	0.419	0.732**	-0.361	0.769**	0.845**	-0.065	0.734**	0.735**
LA									0.810**	0.499*	-0.008	0.604**	0.520*	0.024	0.366	0.367
PL										0.423	0.024	0.551*	0.429	0.081	0.349	0.349
PdL											-0.236	0.759**	0.682**	0.300	0.767**	0.767**
PdD												-0.322	-0.344	0.133	-0.411	-0.411
DWP													0.804**	0.288	0.902**	0.902**
NSP														0.074	0.720**	0.720**
1000SW															0.348	0.348
SY																1.000**

** = Significant at 1% * = Significant at 5%

LS =Days to 5 leaves stage FF =Days to 1st Flowering 50%F =Days to 50% flowering M =Days to Maturity FPS =Days to 1st Pod Setting
PH =Plant Height (cm) NS =No of Leaves NPP =No of Pod/Plant LA =Leaf Area (cm²) PL =Petiole Length (cm)
PdL =Pod Length (cm) PdD =Pod Diameter (cm) DWP =Dry Weight of Pod NSP =No of Seeds/Pod 1000SW=1000 Seed Weight
SY =Seed Yield (g/Plant) Y =Seed Yield (g/Plant)

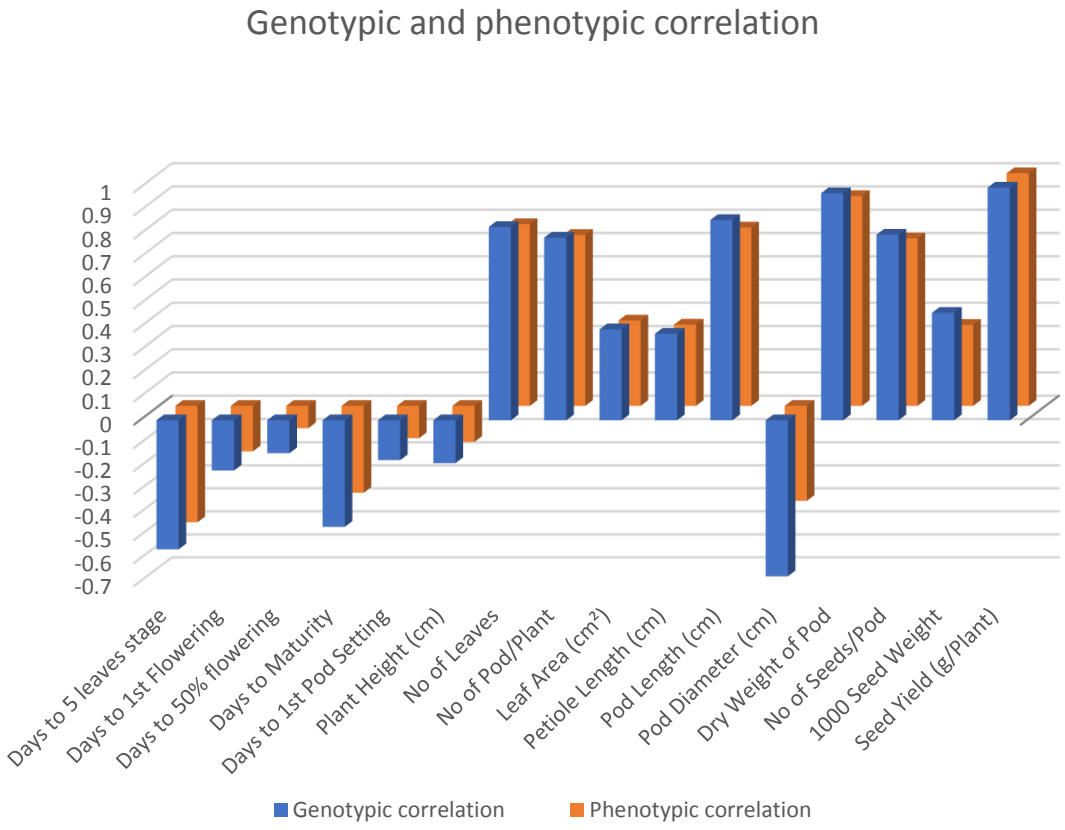


Figure 3: Genotypic and phenotypic correlation of Kidney bean

4.2.2 Days to 1st flowering

Days to 1st flowering is highly significant and positively correlated with days to 50% flowering (0.988, 0.956), days to maturity (0.699, 0.628), days to first pod setting (0.952, 0.902) at both genotypic and phenotypic levels (Table 5 & 6). Similarly, it was found positively and significantly correlated with (genotypic and phenotypic) with days to 50% flowering (0.990; 0.879) by Prakash *et al.* (2015). Days to first flowering exhibited highly significant and positive correlation with days to 50 percent flowering (0.781) (Topwal *et al.*, 2016).

There is also significant and positive correlation with plant height (0.556, 0.531) and pod length (0.495, 0.481). This also had positive and significant correlation with plant height (0.556, 0.531) and pod length (0.481, 0.495) at genotypic and phenotypic level. However, it showed non- significant and negative association with number of leaves (-(-0.105, -0.109), number of seeds per pod (-0.163, -0.164), 1000 seed weight (-0.139, -0.077), seed yield (-0.217, -0.196), yield (-0.217, -0.196) at both levels. On other hand, Sabokdast and Khyalparast (2008) found seed yield to be significant and positively correlated with days to 1st flowering.

4.2.3 Days to 50% flowering

At genotypic and phenotypic levels days to 50% flowering showed highly significant and positive association with days to 1st flowering (0.988, 0.956), days to maturity (0.773, 0.674), 1st pod setting (0.990, 0.940), plant height (0.607, 0.584), pod length (0.640, 0.614). Association of days to 50 per cent flowering was significant and positive with days to maturity in the findings of Baisakh (1992) in Rice bean and Immaculee in Kidney bean (2011). But Bhushan *et al.* (2007) found days to 50% flowering had negative non- significant correlation with number of pods per plant, pod length and significant negative correlation with 100 seed weight and seed yield per plant.

The association with other characters was non-significant. At genotypic level it showed negative non- significant correlation with number of leaves (-0.068), pod length (-0.072), 1000 seed weight (-0.202), seed yield (-0.142), yield (-0.142) (Table 5 & 6). The association with other characters was non-significant as well in phenotypic level. Days to 50 per cent flowering was found significant negative association with seed yield to at phenotypic level and pods per plant, 100 seed weight at genotypic level observed by Immaculee (2011).

4.2.4 Days to maturity

At genotypic level days to maturity (0.459) displayed a high significant positive association with days to1st flowering (0.699), days to 50% flowering (0.773), days to first pod setting (0.791) and plant height (0.703) and negative significant association with pod length (-0.559) and 1000 seed weight (-0.580). At phenotypic level, significant negative correlation was recorded with pods length (-0.486). It showed positive and significant association with days to 1st flowering (0.628), days to 50% flowering (0.674), 1st pod setting (0.728) and plant height (0.571) at phenotypic level (Table 5 & 6). Similarly, days to maturity was found significant negative association with seed yield to at both genotypic and phenotypic level by Immaculee (2011). These results were in conformity with the findings of Venkatkrishnakishore *et al*. (2002) and Mittal and Paramjit Singh (2005) in Mung bean. On the contrary, Sharma *et al.* (1998) also obtained significant positive association of days to maturity with all the characters at genotypic level in rice bean. Agarwal and Singh (1973) recorded significant positive correlation of seed yield with number of days to maturity.

4.2.5 Days to 1st pod setting

The correlation of days to first pod setting with days to 1st flowering (0.952, 0.902), days to 50% flowering (0.990, 0.940), days to maturity (0.791, 0.728), plant height (0.557, 0.498) and pod length (0.635, 0.611) was positive and highly significant at the genotypic and phenotypic levels (Table 5 & 6). Aggarwal *et al*. (1973), Chand (1999), Coimbra *et el*. (1998) found similar results. The association with other characters was negative and non-significant.

4.2.6 Plant height (cm)

At genotypic level plant height had positive and high significant correlation with 1st flowering (0.556), days to 50% flowering (0.607), days to maturity (0.703), and days to 1st pod setting (0.557), leaf area (0.601) and petiole length (0.721). However, 1000 seed weight (-0.506) had negative significant association with plant height.

At phenotypic level, plant height was significant and positively correlated with leaf area (0.572) and petiole length (0.676). It was also positively associated with significant correlation with days to 1st flowering (0.531), days to 50% flowering (0.584), days to maturity (0.571), and days to 1st pod setting (0.498) (Table 5 & 6). The rest of the association were non- significant and most likely negative. It was reported that positive

correlation of architectural traits such as plant height with seed yield was found by Chand (1999), Nienhuis and Singh (1986) and Vasic *et al*. (1997). But according to Siddique and Gupta (1991) plant height exhibited significant positive association with pods per plant, pod length and negative association with days to 50 per cent flowering and days to maturity at both levels.

4.2.7 Number of leaves

At genotypic level number of leaves were positive and highly significant with number of pods per plant (0.855), pod length (0.909), dry weight of pod (0.848), seed yield (0.837) and yield (0.831). Number of leaves was also positively correlated with significant association with leaf area (0.469) and plant height (0.483) but negatively significant with pod diameter (-0.523).

At phenotypic level number of leaves was highly significant and positive with almost all parameters e.g. days to 5-leaves stage (0.495), number of pods per plant (0.821), pod length (0.827), dry weight of pod (0.825), number of seeds per plant (0.844), seed yield (0.781) and yield (0.781) (Table 5 & 6). At phenotypic level, leaf number per plant showed positive and significant correlation with plant height and at genotypic level, there was positive and significant correlation of number of green pods per plant with leaf area per plant and leaf number per plant (Alemu *et al.,* 2017). Prakash *et al.* (2015) also found plant height was positively and significantly correlated (genotypic and phenotypic) with number of leaves per plant (0.810; 0.733).

4.2.8 Number of pod per plant

Number of pods per plant displayed high significant and positive correlation with number of leaves (0.855, 0.821), pod length (0.795, 0.732), dry weight of pod (0.802, 0.769), number of seeds per pod (0.903, 0.845), seed yield (0.793, 0.734) and yield (0.785, 0.735) at both genotypic and phenotypic levels (Table 5 & 6). But it showed negatively significant association with pod diameter (-0.676) at genotypic level. It showed negative and non- significant association with 1000 seed weight (-0.125, -0.065) at both genotypic and phenotypic levels which is consonance with the findings of Immaculee (2011). The positive and significant association of pod per plant with seeds per pod has also been reported by Mishra *et al*. (1996), Singh (2000) and Prasad (1995).

4.2.10 Leaf area (cm^2)

At both levels of genotypic and phenotypic levels leaf area showed positive and significant association with plant height (0.821, 0.810), pod length (0.536, 0.499) dry weight of pod (0.616, 0.604) number of seeds per plant (0.537, 0.520) (Table 5 & 6). Leaf area has significant and positive association with pod length and number of seeds per pod while significant negative correlation with days to 50 per cent flowering. Similar results were observed by Dursum (2007) for pod length and number of seeds per pod. There was positive and significant correlation of number of green pods per plant with leaf area per plant at genotypic level. (Alemu *et al.*, 2017). The rest of the association were not significant.

4.2.11 Petiole length (cm)

Petiole length was reported to show positive and significant association with days to 1st flowering (0.495, 0.481), days to 50% flowering (0.640, 0.614), days to 1st pod setting (0.635, 0.611), plant height (0.721, 0.676), leaf area (0.821, 0.810) and dry weight of pod (0.559, 0.604) at both genotypic and phenotypic levels (Table 5 & 6). Similarly, Coimbra (1998), Dahiya (2006), Kapila *et al.* (1997) also observed similar results. It also showed positive significant correlation with number of leaves (0.483) at genotypic level, but it was non- significant at phenotypic level.

4.2.12 Pod length (cm)

Pod length is one of the main yield components in Kidney bean. Pod length showed similar association in case of both genotypic and phenotypic levels. It was recorded that pod length had positive and high significant correlation with number of leaves (0.909, 0.827), dry weight of pod (0.816, 0.759), number of pods per plant (0.795, 0.732), number of seeds per plant (0.742, 0.682), seed yield (0.861, 0.767) and yield (0.861, 0.767) (Table 5 & 6). Besides, Singh (2000) reported pod length showed significant and positive association with plant height, number of pods per plant. Apart from that, Alemu *et al.* (2017) reported that there was negative and significant association between green pod width and green pod length. Pod length was also negatively correlated with days to 5- leaves stage (-0.532, -0.494) and maturity (-0.559, -0.486) at both genotypic and phenotypic levels. However, pod length was negatively associated with seed yield observed by Immaculee (2011) in Kidney bean, Venkatkrishnakishore *et al.* (2002) and

Mittal and Singh (2005) in Mung bean. Pod length had non-significant correlation with days to maturity in the investigation confirmed by Narsinghani and Saxena (1991).

4.2.13 Pod diameter (cm)

Pod diameter had positive and significant correlation with days to 5- leaves stage (0.678), number of seeds per pods (0.631) and seed yield (0.677) at genotypic level. It was also negatively significant with number of leaves (-0.523), number of pods per plant (-0.676) and dry weight of pods (-0.554). There was no significant association at phenotypic level (Table 5 & 6). But Singh *et al.* (2011) found that number of pods per plant had strong positive correlation with pod diameter. Pod diameter exhibited strong positive significant association with yield per plant at both genotypic and phenotypic level (Saha *et al*., 1990). Kumar Swamy (1990) also reported days to 50% flowering to be negatively associated with green pod width and green pod breath. On the other hand, Shinde and Dumbre (2001) reported that seed yield had positive but non-significant correlation with pod diameter at genotypic level, while negative non-significant correlation with pod diameter phenotypic levels.

4.2.14 Dry weight of pod (g)

At both genotypic and phenotypic level high significant and positive association were recorded of dry weight of pod with number of seeds per plant (0.816, 0.804), number of pods per plant (0.802, 0.769), number of leaves (0.848, 0.825), leaf area (0.616, 0.604) and pod length (0.816, 0.759) and seed yield (0.976, 0.902). It was also positively significant with petiole length (0.559, 0.551)) at genotypic and phenotypic levels (Table 5 & 6). Alemu *et al.* (2017) found pod dry weight (0.333) had significant positive association with green pod yield at genotypic level only and green pod width and length showed positive and significant correlation with dry pod weight at genotypic level.

4.2.15 Number of seeds per pod

Number of seeds per pod was found in significant and positive association with number of leaves (0.885, 0.844), Number of pods per plant (0.903, 0.845), pod length (0.742, 0.682), dry weight of pods (0.816, 0.804), seed yield (0.799, 0.720) and yield (0.798, 0.720). This also had significant and positive correlation with leaf area (0.537,

0.520). All these associations were observed at both genotypic level and phenotypic levels. Significant and negative correlation with pod diameter (-0.631) was in genotypic level (Table 5 & 6). Seeds per pod were recorded significant and positive association with pod length in accordance with Sharma *et al.* (1998). Similarly, the significant association of seeds per plant with pod length was reported by Singh *et al*. (1994), Kumara *et al*. (1997) in Rice bean and Chauhan *et al*. (2003) in cowpea.

4.2.16 1000 seed yield

1000 seed yield had negative and significant correlation with days to maturity (-0.580) and plant height (-0.506) at genotypic levels. It showed negative and non- significant association with days to 1st flowering (-0.077), days to 50% flowering (-0.130), days to maturity (-0.383), days to first pod setting (-0.041), plant height (-0.407) and number of pods per plant (-0.065). Interestingly, was non- significant and positively correlated with petiole length (0.081), pod length (0.300), pod diameter (0.133), dry weight of pod (0.288), number of seeds per pod (0.074) and seed yield (0.348) in present study (Table 5 & 6). On the contrary, Zeven *et al*. (1999) found 100 seed exhibited significant, positively correlated with pod length, number of seeds per pod and number of pods per plant in *Phaseolus vulgaris*. With an agreement similar result was seen with number of pods per plant and pod length in cowpea by Biradar *et al.* (1996). A positive correlation of seed yield with 100 seed weight was reported by Chand (1999) and Coimbra *et al*. (1998).

4.2.17 Seed yield per plant

Seed yield was highly significant and positively correlated with number of leaves (0.837, 0.781), number of pods per plant (0.793, 0.734) pod length (0.861, 0.767) dry weight of pod (0.976, 0.902) number of seeds per pod (0.799, 0.720) and yield (1.000, 1.000) at both genotypic and phenotypic levels (Table 5 & 6). Thus, these traits having positive association with seed yield may contribute in improving the seed yield trait of kidney bean. However, it recorded that it had significant and negative association with pod diameter (-0.677) at genotypic level. Similar result was found by Immaculee (2011). Similar results were also observed in several correlation studies conducted in Kidney bean, both number of pods per plant and number of seeds per pod have been positively associated with seed yield (Atuahene-Amankwa and Michaels, 1997; Chand,

1999; Coimbra *et al.,* 1998; Coyne, 1968; Duarte and Adams, 1972; Nienhuis and Singh, 1986; Samal *et al*., 1995).

4.2.18 Seed yield (t/ha)

Seed yield was highly significant and positively correlated with number of leaves (0.831, 0.781), number of pods per plant (0.785, 0.735) pod length (0.861, 0.767) dry weight of pod (0.976, 0.902) number of seeds per pod (0.798, 0.720) and yield (1.000, 1.000) at both genotypic and phenotypic levels. However, it was also observed that it showed significant and negative association with pod diameter (-0.677) at genotypic level (Table 5 & 6). Similar result was found by Immaculee (2011). Correlation of yield with number of days to flowering (Aggarwal and Singh, 1973), number of pods per plant (Aggarwal and Singh, 1973; Pande *et al.,* 1975 and pod length (Prakash and Ram, 1981) were found to be positive thus indicating the feasibility of selection based on these traits. However, 100 seed weight was positively correlated with number of pod per plant and number of seeds per pod (Aggarwal and Singh, 1973; Patil *et al*., 1993; Samal *et al*., 1996). These character association studies suggest that number of pods per plant, pod length, number of seeds per pod may be the most important yield attributes in Kidney bean. Based on phenotypic and genotypic correlation between yield and yield attributing characters, it is suggested that selection should made for the characters, which are having positive significant association to improve the seed yield per plant in Kidney bean. Raffi and Nath (2004) reported that yield was positively correlated with number of number pods per plant, pod length, number of seeds per plant and 20-seed weight.

The inter-correlations estimated for the yield components indicate the probability of simultaneous improvement of these traits by selection. If the correlation existing between the characters is positive, simultaneous improvement of these traits by a single selection program is possible, but when negative association exists, it would be difficult to exercise simultaneous selection of these characters in developing a variety (Newell and Eberhart, 1961). Since the characters are inter correlated among themselves, selection in any one of these traits will result in the improvement of other character thereby, resulting in increasing in seed yield.

4.3 PATH COEFFICIENT ANALYSIS

Simple correlation does not consider the complex relationships between the various traits related to the dependent variable. Correlation coefficients show relationships among independent variables and the linear relationship between these variables. But it is not sufficient to describe these relationships when the causal relationship among variables is needed. It has been suggested that yield components have either a direct or an indirect effect on seed yield, or both. Therefore, it was essential to determine the effects of yield components on seed yield. Consequently, path coefficient analysis is the most common statistical method used for this purpose. Thus, it is possible to calculate both direct and indirect effects of yield components on seed yield through the other components. Genotypic and phenotypic paths were worked out in the present study (Table 7) considering yield per hectare as dependent character and its attributes as independent characters viz, days to 5- leaves stage, days to 1st flowering, days to 50% flowering, days to maturity, days to first pod setting, pod length (cm), pod diameter (cm), number of leaves, leaf area (cm^2), petiole length, plant height (cm), dry weight of pod, number of seeds per pod, number of pods per plant, 1000 seed weight (g), seed yield per plant. Each component has two path actions viz, direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.3.1 Days to 5 leaves stage

Days to 5- leaves stage recorded negligible negative direct effect (-0.036) towards yield per hectare. Further, it showed negligible positive indirect effect towards days to 1st flowering (0.015), days to maturity (0.009), plant height (0.007), petiole length (0.011), pod diameter (0.006), number of pods per plant (0.010), number of seeds per plant (0.001) (Table 7). However, it was negligible negative indirect effect towards yield per hectare via, days to 50 % flowering (-0.029), Days to 1st pod setting (-0.011), number of leaves (-0.019), leaf area (-0.022), pod length (-0.032), dry weight of pod (-0.020) and 1000 seed weight (-0.022). It showed high negative indirect effect through seed yield (-0.429). Days to 5 leaves stage was highly correlated with yield per hectare with significant association. Alemu *et al.* (2017), Angadi *et al.* (2012), Bhushan *et al.* (2008) reported similar indirect effects on yield per hectare.

Table 7: Path coefficient analysis showing direct and indirect effects of different characters on yield of Kidney bean

Characters	Direct effect	Indirect effect															Genotypic correlation with yield
		LS	FF	50%F	M	FPS	PH	NS	NPP	LA	PL	PdL	PdD	DWP	NSP	1000SW	SY
LS	-0.036		0.015	-0.029	0.009	-0.011	0.007	-0.019	0.010	-0.022	0.011	-0.032	0.006	-0.020	0.001	-0.022	-0.429	-0.560*
FF	0.031	-0.020		-0.032	0.019	0.004	0.019	-0.012	0.018	-0.014	0.010	-0.020	0.015	-0.013	0.013	-0.013	-0.222	-0.217
50%F	-0.040	-0.022	0.025		0.015	0.001	0.018	-0.017	0.013	-0.018	0.003	-0.021	0.012	-0.017	0.013	-0.018	-0.087	-0.142
M	0.016	-0.023	0.015	-0.030		-0.009	0.010	-0.019	0.011	-0.021	0.006	-0.031	0.008	-0.019	0.005	-0.023	-0.358	-0.462
FPS	0.004	-0.026	0.020	-0.037	0.013		0.011	-0.019	0.011	-0.020	-0.001	-0.026	0.008	-0.020	0.008	-0.019	-0.080	-0.172
PH	0.026	-0.028	0.003	-0.033	0.002	-0.027		-0.029	0.001	-0.029	-0.009	-0.024	0.000	-0.029	0.000	-0.030	0.021	-0.185
NS	-0.010	0.003	0.023	-0.003	0.025	-0.006	0.030		0.023	-0.004	0.013	0.011	0.028	-0.007	0.043	-0.002	0.663**	0.831**
NPP	0.020	0.000	0.022	-0.003	0.023	-0.010	0.027	-0.010		-0.006	0.016	0.008	0.028	-0.009	0.041	-0.004	0.641**	0.785**
LA	-0.016	-0.013	0.016	-0.018	0.015	-0.011	0.025	-0.017	0.013		-0.003	-0.005	0.017	-0.018	0.027	-0.013	0.393	0.391
PL	-0.012	-0.014	0.017	-0.024	0.015	-0.006	0.024	-0.020	0.012	-0.018		-0.008	0.014	-0.019	0.024	-0.014	0.401	0.372
PdL	0.021	0.006	0.026	0.003	0.027	-0.006	0.035	-0.004	0.027	-0.001	0.019		0.031	-0.004	0.041	0.002	0.636**	0.861**
PdD	-0.037	-0.052	-0.019	-0.051	-0.020	-0.047	-0.018	-0.050	-0.020	-0.050	-0.020	-0.052		-0.050	-0.023	-0.047	-0.120	-0.677**
DWP	-0.005	0.006	0.028	0.001	0.029	-0.001	0.032	-0.005	0.027	-0.001	0.015	0.014	0.033		0.046	0.003	0.756**	0.976**
NSP	0.053	0.007	0.030	0.001	0.031	0.000	0.030	-0.003	0.028	0.001	0.020	0.013	0.035	-0.002		0.003	0.549*	0.798**
1000SW	0.003	-0.006	0.024	-0.005	0.022	-0.004	0.018	-0.008	0.023	-0.007	0.019	-0.002	0.018	-0.008	0.024		0.351	0.462
SY	1.000	-0.009	0.011	-0.013	0.013	-0.017	0.015	-0.019	0.012	-0.016	0.005	-0.002	0.017	-0.019	0.026	-0.012		1.000**

Residual Effect= 0.11597014

** = Significant at 1% * = Significant at 5%

LS =Days to 5 leaves stage FF =Days to 1st Flowering 50%F =Days to 50% flowering M =Days to Maturity FPS =Days to 1st Pod Setting
PH =Plant Height (cm) NS =No of Leaves NPP =No of Pod/Plant LA =Leaf Area (cm²) PL =Petiole Length (cm)
PdL =Pod Length (cm) PdD =Pod Diameter (cm) DWP =Dry Weight of Pod NSP =No of Seeds/Pod 1000SW =1000 Seed Weight
SY =Seed Yield (g/Plant) Y =Seed Yield (g/Plant)

4.3.2 Days to 1st flowering

Days to 1st flowering recorded negligible positive direct effect (0.031) towards yield per hectare (Table 7). Faisal *et al.* (2007) stated that the days to flowering had the maximum direct contribution to soybean yield. This relationship indicates that a late genotype usually has higher grain yield than an early genotype. In contrast, Arshad *et al*. (2006) reported that the days to flowering had a negative direct effect on grain yield of soybean.

Further, it showed negligible positive indirect effect towards yield per hectare via, days to maturity (0.019), days to 1st pod setting (0.004), plant height (0.019), number of pods per plant (0.018), petiole length (0.010), pod diameter (0.015), and number of seeds per pod (0.013). However, it was negligible negative indirect effect towards yield per hectare via, days to 5- leaves stage (-0.020), days to 50% flowering (-0.032), number of leaves (-0.012), leaf area (-0.014), pod length (-0.020), dry weight of pod (-0.013), 1000 seed weight (-0.013) and moderate negative effect through seed yield per plant (-0.222). Days to 1st flowering was negative and non- significantly correlated with yield per hectare. Devi *et al.* (2014) showed that pods/plant had maximum indirect contribution on days to 1st flowering, which resulted into significant positive correlation of the trait with pod yield/plant of Kidney bean.

4.3.3 Days to 50% flowering

Days to 50% flowering showed negligible negative direct effect (-0.040) towards yield per hectare. It was observed by Acharya (2013) that days to 50% flowering had negligible positive direct effect toward the yield. Days to 50% flowering exhibited high positive direct effect on yield per plant at genotypic level (Kumar *et al.*, 2014). Further, it showed negligible positive indirect effect towards yield per hectare via, days to 1st flowering (0.025), days to maturity (0.015), days to 1st pod setting (0.001), plant height (0.018), number of pods per plant (0.013), petiole length (0.003), pod diameter (0.012), number of seeds per pod(0.013) (Table 7).However, it was recorded negligible negative indirect effect yield per hectare via, days to 5- leaves stage (-0.022), number leaves (-0.017), leaf area (-0.018), pod length (-0.021), dry weight of pod (-0.017), 1000 seed weight (-0.018) and seed yield (-0.087). It showed negative and non-significant genotypic correlation (-0.142) with yield per hectare. Karasu and Oz (2010) reported

that days to 50% flowering exhibited low positive indirect effects towards yield per hectare via number of pods per plant, and high negative indirect effect pod weight.

4.3.4 Days to maturity

Days to maturity found negligible positive direct effect (0.016) towards yield per hectare. Further, it recorded negligible positive indirect effect towards yield per hectare via, days to first flowering 0.015, plant height (0.010), number of pod per plant (0.011), petiole length (0.006), pod diameter (0.008) and number of seeds per plant (0.005) (Table 7). However, it was recorded negligible negative indirect effect towards yield per hectare via, days to 5 leaves stage (-0.023), days to 50% flowering (-0.030), plant height (-0.010), days to 1st pod setting (-0.009), number of leaves (-0.019), leaf area (-0.021), pod length (-0.031), dry weight of pod (-0.019), 1000 seed weight (-0.023) and high negative indirect effect towards seed yield per plant (-0.358). It showed negative and non-significant genotypic correlation (-0.462) with yield per hectare. However, days to pod maturity observed moderate positive indirect effect toward pod yield per hectare via number of pods per plant and high negative in direct effect pod weight (Acharya, 2013).

4.3.5 Days to 1st pod setting

Days to 1st pod setting recorded negligible positive direct effect (0.004) towards yield per hectare. Further, it recorded negligible positive indirect effect towards yield per hectare via, days to first flowering (0.020), days to maturity (0.013), plant height (0.011), number of pod per plant (0.011), pod diameter (0.008) and number of seeds per plant (0.008) (Table 7). However, it was recorded negligible negative indirect effect towards yield per hectare via, days to 5 leaves stage (-0.026), days to 50% flowering (-0.037), number of leaves (-0.019), leaf area (-0.020), petiole length (-0.001), pod length (-0.026), dry weight of pod (-0.020), 1000 seed weight (-0.019), seed yield per plant (-0.080). This is in agreement with Fisher (1918), Pande *et al* (1975), Shinde *et al.* (2001) and Tamilselvan *et al.* (1994). The genotypic correlation of days to 1st pod setting was negative and non-significant (-0.172) with yield per hectare.

4.3.6 Plant height

Plant height recorded negligible positive direct effect (0.026) towards yield per hectare. Acharya (2013) found the result in accordance. On the contrary, Karasu (2010) reported

that plant height provided high and positive direct effect on seed yield per hectare (0.301) and the correlation between seed yield and plant height recorded as 0.490. Whereas, in the present study the correlation was negative and non- significant (-0.185) with yield per hectare (Table 7). Again, Mehra *et al.* (2016) reported that plant height (-0.003) showed the negative direct effect on the seed yield. Further, it was recorded low positive indirect effect towards yield per hectare via. days to first flowering (0.003), days to maturity (0.002), number of pods per plant (0.001) and seed yield per plant (0.021). It did not have any effect through pod diameter and number of seeds per plant. However, it was found negligible negative indirect effect towards yield per hectare via, days to 5- leaves stage (-0.028), days to 50% flowering (-0.033), days to 1st pod setting (-0.027), number of leaves (-0.029), leaf area (-0.029), petiole length (-0.009), pod length (-0.024), dry weight of pod (-0.029), 1000 seed weight (-0.030).

Devi *et al.* (2014) found that pods/plant had maximum indirect effect of plant height which resulted into significant positive correlation of the trait with pod yield/plant. Plant height showed low direct effect on seed yield but the indirect effects were high through pods per plant, seeds per pod and 100 seed weight (Immaculee, 2011). Plant height also showed moderate negative indirect effects towards pod yield per hectare via number of pods per plant (Acharya, 2013).

4.3.7 Number of leaves

Number of leaves recorded negligible negative direct effect (-0.010) towards yield per hectare. Further, it was recorded negligible positive indirect effect towards yield per hectare via. days to 5- leaves stage (0.003), days to 1st flowering (0.023), days to maturity (0.025), plant height (0.030), number of pods per plant (0.023), petiole length (0.013), pod length (0.011), pod diameter (0.028), number of seeds per pod (0.043) and significant high positive indirect effect toward seed yield per plant (0.663) (Table 7). However, it was found negligible negative indirect effect towards yield per hectare via, days to 50% flowering (-0.003), days to 1st pod setting (-0.006), leaf area (-0.004), dry weight pod (-0.007) and 1000 seed weight (-0.002). This proves in the conformity with the findings of Oseni *et al*. (1992), Altinabas and Sepetoglu (1993). The correlation of number of leaves was highly significant (0.831) with yield per hectare.

4.3.8 Number of pods per plant

Number of pods per plant recorded negligible positive direct effect (0.020) towards yield per hectare. Relating to this result, Kasaru (2010) also found number of pods per plant had low direct effect on seed yield per hectare. On the other hand, Kumar *et al.* (2014) found number of pods per plant showed high positive indirect effect through number of seeds per pod. Mishra *et al*. (1996) reported high positive direct effect of pods per plant on seed yield which was an indication of improvement of high pod yield through selection of these characters. Further, it was recorded negligible positive indirect effect towards yield per hectare via. days to 1st flowering (0.022), days to maturity (0.023), plant height (0.027), petiole length (0.016), pod length (0.008), pod diameter (0.028), number of seeds per pod (0.041) and significant, high, positive indirect effect toward seed yield per plant (0.641) (Table 7). Number of pods per plant did not have any significant effect on yield per hectare through days to 5- leaves stage. However, it was found negligible negative indirect effect towards yield per hectare via, days to 50% flowering (-0.003), days to 1st pod setting (-0.010), number of leaves (-0.010), leaf area (-0.006), dry weight pod (-0.009) and 1000 seed weight (-0.004). The correlation of number of leaves was highly significant (0.785) with yield per hectare. Positive indirect effect of pod per plant was recorded high through seed per pod whereas indirect effects of seeds per pod through other character were negligible (Immaculee, 2011).

4.3.9 Leaf area

Leaf area observed negligible negative direct effect (-0.016) towards yield per hectare. It was also recorded negligible negative indirect effects to yield per hectare via. days to 5-leaves stage (-0.013), days to 50 % flowering (-0.018), days to 1st pod setting (-0.011), number of leaves (-0.017), petiole length (-0.003), pod length (0.005), dry weight of pod (-0.018) and 1000 seed weight (-0.013) (Table 7). On the other hand, it was found negligible positive indirect effect toward yield per hectare through days to first flowering (0.016), days to maturity (0.015), plant height (0.025), number of pods per plant (0.013), pod diameter (0.017), number of seeds per plant (0.027) and high positive indirect effect via. seed yield (0.393). The genotypic correlation of leaf area (0.391) with yield per hectare was positive and non- significant. Angadi *et al.,* (2012) found that leaf area had positive correlation with yield and the same had high indirect contribution through leaf area.

4.3.10 Petiole length

Petiole length observed negligible negative direct effect (-0.016) towards yield per hectare. It was also recorded negligible negative indirect effects to yield per hectare via. days to 5-leaves stage (-0.014), days to 50 % flowering (-0.024), days to 1st pod setting (-0.006), number of leaves (-0.020), leaf area (-0.018), pod length (-0.008), dry weight of pod (-0.019) and 1000 seed weight (-0.014) (Table 7). On the other hand, it was found negligible positive indirect effect toward yield per hectare through days to first flowering (0.017), days to maturity (0.015), plant height (0.024), number of pods per plant (0.012), pod diameter (0.014), number of seeds per plant (0.024) and high positive indirect effect via. seed yield (0.401). Similar findings can be related with Narsinghani (1991), Nienhuis (1986), Patil (1993), Sabokdast and Khyalparast (2008). The genotypic correlation of leaf area (0.372) with yield per hectare was positive and non-significant.

4.3.11 Pod length

Pod length observed negligible positive direct effect (0.031) towards yield per hectare. However, Ulukan *et al.* (2003) and Sharifa (2014) found out pod length had high positive direct effect on seed yield per plot in broad bean. It was also recorded negligible negative indirect effects to yield per hectare via. days to days to 1st pod setting (-0.006), number of leaves (-0.004), leaf area (-0.001), dry weight pod (-0.004) (Table 7). On the other hand, it was found negligible positive indirect effect toward yield per hectare via. days to 5- leaves stage (0.006), days to 1st flowering (0.026), days to 50% flowering (0.003), days to maturity (0.027), plant height (0.035), number of pods per plant (0.027), petiole length (0.019), pod diameter (0.021), number of seeds per pod (0.041) 1000 seed weight (0.002) and high positive indirect effect of seed yield per plant (0.636). The genotypic correlation of leaf area (0.861) with yield per hectare was positive and significant. Pod length recorded low positive indirect effects towards pod yield per hectare via pod weight (Acharya, 2013). It also showed negligible positive direct effect on toward the yield.

4.3.12 Pod diameter

Pod diameter exhibited negligible negative direct effect (-0.037) towards yield per hectare. Pod diameter had positive direct effect on yield per plant but its negative effect

through number of seeds per pod and number of pods per plant made its association with yield per plant significantly negative (Verma *et al.* 2014). However, it showed negligible negative indirect effect towards yield per hectare via, days to 5- leaves stage (-0.052), days to 1st flowering (-0.019), days to 50% flowering (-0.051), days to maturity (-0.020), days to 1st pod setting (-0.047), plant height (-0.018), number of leaves (-0.050), number pods per plant (-0.020), leaf area (-0.050), petiole length (-0.020), pod length (-0.052), dry weight of pod (-0.050), number of seeds per pod (-0.023), 1000 seed weight (-0.047), and low negative indirect effect of seed yield (-0.120) (Table 7). The genotypic correlation of pod diameter (-0.677) with yield was negative and significant. Pod diameter exhibited high positive indirect effects towards pod yield per hectare via pod weight (Acharya, 2013).

4.3.13 Dry weight of pod

Pod weight exhibited negligible negative direct effect (-0.005) towards yield per hectare. But according to Amini *et al*., 2002 and Dursun, 2007 dry pod weight had highest and positive direct effect on seed yield. It was the lowest negative direct effect on yield per hectare. Further, it was recorded negligible positive indirect effect towards yield per hectare via, days to 5- leaves stage (0.006), days to first flowering (0.028), days to 50% flowering (0.001), days to maturity (0.029), plant height (0.032), number or pods per plant (0.027), petiole length (0.015), pod length (0.014), number of seeds per pod (0.046), pod diameter (0.003), 1000 seed weight (0.003) and seed yield per plant (0.756). However, it showed negligible negative indirect effect towards yield per hectare via, days to 1st pod setting (-0.001), number of leaves (-0.005), leaf area (-0.001) (Table 7). The genotypic correlation of dry weight of pod (0.976) was positive and significant with yield per hectare.

4.3.14 Number of seeds per pod

Number of seed per pod showed negligible positive direct effect (0.053) towards yield per hectare. In previous studies, it was reported that seed number per pod had highest and positive direct effect on seed yield (Amini *et al*., 2002; Dursun, 2007). Shinde and Dumbre (2001) also found it on consonance. Further, it was recorded negligible positive indirect effect towards yield per hectare via, days to 5- leaves stage (0.007), days to first flowering (0.030), days to 50% flowering (0.001), days to maturity (0.031), plant height (0.030), number or pods per plant (0.028), leaf area (0.001), petiole length

(0.020), pod length (0.013), pod diameter (0.035), 1000 seed weight (0.003) and high positive indirect effect of seed yield per plant (0.549) (Table 7). It also found negligible negative indirect effect towards yield per hectare via, number of leaves (-0.003) and dry weight pod (-0.002). It had significant and positive genotypic correlation (0.79) with yield per hectare. Dursun (2007) found that number of seeds per pod showed the highest indirect effect on yield via wet pod weight. Number of seed per pod exhibited high positive indirect effects towards pod yield per hectare via pod weight and moderate negative indirect effect number of pods per plant observed by Acharya (2013).

4.3.15 1000 Seed Weight

1000 seed weight found negligible positive direct effect (0.003) towards yield per hectare. It was found the lowest positive direct effect of 1000 seed weight on yield per hectare. But it was determined by Karasu (2010) that 1000 seed weight had a positive direct effect (0.185) on seed yield per hectare. Further, it was recorded negligible positive indirect effect towards yield per hectare via, days to first flowering (0.024), days to maturity (0.022), plant height (0.018), number or pods per plant (0.023), petiole length (0.019), pod diameter (0.018), number of seeds per pod (0.024), seed yield per plant (0.351) (Table 7). It also reported negligible negative indirect effect towards yield per hectare via, days to 5- leaves stage (-0.006), days to 50% flowering (-0.005), days to 1st pod setting (-0.004), number of leaves (-0.008), leaf area (-0.007), pod length (-0.002), dry weight pod (-0.008). Interestingly, 1000-seed weight gave low and insignificant indirect effects on seed yield per hectare observed by Kasaru (2010). The trait was genotypically positive and non- significant (0.462) correlated with yield per hectare.

Shinde and Dumbre (2001) reported high positive indirect effect of 100 seed weight on yield per hectare. Acharya (2013) observed that 100 seed weight exhibited high positive indirect effects towards pod yield per hectare via pod weight. It suggested that for selecting genotypes with higher yield the indirect influence of different traits should be given due weight age along which exerted direct effects.

4.3.16 Seed yield per plant

High positive direct effect was found in seed yield (1.000) towards yield per hectare. It was recorded as the highest positive effect on yield per hectare. However, Immaculee (2011) found pods per plant having the highest direct effect on yield per hectare.

Further, it was recorded negligible positive indirect effect towards yield per hectare via, days to first flowering (0.011), days to maturity (0.013), plant height (0.015), number or pods per plant (0.012), petiole length (0.005), pod diameter (0.017), number of seeds per pod (0.026). It also reported negligible negative indirect effect towards yield per hectare via, days to 5- leaves stage (-0.009), days to 50% flowering (-0.013), days to 1st pod setting (-0.017), number of leaves (-0.019), leaf area (-0.016), pod length (-0.002), dry weight pod (-0.019), 1000 seed weight (-0.012) (Table 7). The genotypic correlation (1.000) with yield was positive and significant. Karasu and Oz (2010) found high positive direct effect of seed yield per plant with yield per hectare. He also found positive significant correlation between the traits. It was reported by Acharya (2013) that seed weight had negligible positive direct effect on toward the yield. He also reported high positive indirect effects towards pod yield per hectare via pod weight. Seeds per plant (0.442) exhibited highest positive direct effect on seed yield found by Mehra *et al.* (2016). Previous studies indicated that seed yield per hectare in the bean was positively correlated with number of pods per plant, number of seeds per pod and seed yield per plant (Duarte and Adams, 1972; Westerman and Crothers, 1977; Prakash and Ram, 1981)

From the foregoing investigation, it can be concluded that seed yield per plant and number of seeds per pod are considered to be vital traits in selection of desirable genotypes of Kidney bean.

4.3.17 Residual effect

The magnitude of residual effect (0.12) indicated that traits included in the path analysis explained about 88% of the variation in green pod yield. However, the remaining variation in green pod yield (12%) can be attained by incorporating other yield related traits in the path analysis as far as studies involving association of traits is concerned. Devi *et al.* (2015) found residual effect 0.19 in case of seed yield. Alemu *et al.* (2017) found 0.21 in case of pod yield.

4.4 GENETIC DIVERSITY ANALYSIS

4.4.1 Mahalanobis' generalized distance (D^2)

Conservation of genetic diversity is an essential prerequisite for developing new cultivars with desirable agronomic traits. Although a large number of germplasm

collections have been established worldwide, many of them face major difficulties due to large size and a lack of adequate information about population structure and genetic diversity. The development of new varieties is mainly governed by the magnitude of genetic variability in the base material and extent of variability for the desired characters. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. D^2 analysis is a may be useful tool in identifying the best parents and their combinations for generating variability with respect to various traits under study. The results of D^2 analysis may be useful tool in identifying the best parental combination for generating variability with respect to various traits under study. Progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability providing greater scope for isolating high yielding segregants in the succeeding generations. The genetic diversity among 18 genotypes was measured by employing D^2 statistics. The contribution of each character towards total diversity is present in Table 8.

4.4.2 Principal component analysis (PCA)

Principal component analysis was carried out with 18 genotypes of Kidney bean. The first three Eigen values for three principal coordination axes of genotypes accounted for 74.8% variation (Table 8). Out of 17 characters studied, Component I contributed maximum towards the total diversity with the value 42.9%, followed by Component II 22%, Component III 9.9%, and Component IV 7%. Govanakoppa *et al.* (2002) reported high contribution of pods per plant, 100 seed weight, plant height and reproductive branches towards divergence in Kidney bean. Manivannan and Nadajarajan (1996) noticed maximum contribution of plant height towards divergence followed by pod length, pods per plant and seeds per pod in Mung bean. Important characters with greater weightings in principal component axis I include yield (q/ha), average pod weight, number of pods per plant and number of seeds per pod. Important characters with greater weightings in principal component axis II include dry matter content, days to 50% flowering (Verma *et al.* 2014).

4.4.3 Clustering of the genotypes

The correlated unstandardized mean values (X) for all genotypes for 17 characters under consideration were transferred to the uncorrelated standardized value

(Y). The D^2 value which being the sum of squares for each (Y) value was calculated for all combinations. Based on D^2 values the genotypes were grouped into four clusters using Tocher's methods given by Rao (1952). Clustering of genotypes are presented in the Table 9. Among four clusters, cluster I was the largest comprising of 7 genotypes followed by cluster II and Cluster IV with 5 genotypes, and Cluster III is the solitary cluster.

Cluster I was composed of G1 (BARI Jharseem -1), G3, G4, G5, G6, G9 and G10. The genotype G10 was an advanced line collected from BARI and the rest of them were local genotypes collected from Sylhet. Cluster II comprised of two local varieties from Sylhet (G7, G8), G2 (BARI Jharseem 3) and G13 which was advanced line collected from BARI. Cluster III possesses only one genotype which was also an advanced line collected from BARI (G12). Cluster IV consists of local varieties collected from Bandarban (G14, G15, G16, G17, and G18).

The present investigation shows that there is no perfect relationship between genetic diversity and geographical diversity. This may be attributed since the genotypes of the present study were indigenous, landraces, local types and released varieties collection from BARI. The genotypes have overlapped in different clusters with some distinctness. The absence of correlation between genetic diversity and geographic diversity has also been supported by the previous work of Dikshit *et al*. (1999), whereas Zeven *et al* (1999) and Barelli *et al*. (2005) reported correlation between genetic diversity and geographic diversity. The random pattern of distribution of genotypes into various clusters from different eco-geographic regions suggests that forces other than geographic influence such as exchange of breeding material, genetic drift, natural and artificial selections are responsible for diversity as reported earlier (Murthy and Arunachalam, 1966).

4.4.4 Cluster mean analysis

Cluster means were computed for all the 17 characters studied and presented in Table 10. Genotypes grouped within cluster II were relatively early to days to 5 leaves stage (7.8 days) whereas; genotype grouped under cluster III were relatively late (13.33 days). Genotypes grouped within cluster II were relatively early to flower (31.4 days) whereas; genotype grouped under cluster III were relatively late in flowering (34.33 days).

Table 8: Eigen values and yield percent contribution of each character toward genetic divergence

Principal Component Axis	Eigen values	Percent variation	Cumulative % of Percent variation
I	7.29	42.9	42.9
II	3.73	22.0	64.9
III	1.69	9.9	74.8
IV	1.19	7.0	81.8
V	0.84	4.9	86.7
VI	0.66	3.9	90.6
VII	0.59	3.5	94.1
VIII	0.35	2.1	96.2
IX	0.28	1.7	97.8
X	0.13	0.8	98.6
XI	0.12	0.7	99.3
XII	0.04	0.3	99.6
XIII	0.04	0.2	99.8
XIV	0.03	0.2	100.0
XV	0.01	0.0	100.0
XVI	0.00	0.0	100.0
XVII	0.00	0.0	100.0

Table 9: Distribution of genotypes in different clusters

Cluster	Number of population	Genotypes
I	7	G1, G3, G4, G5, G6, G9 and G10
II	5	G2, G7, G8, G11 and G13
III	1	G12
IV	5	G14, G15, G16, G17 and G18

Table 10: Cluster mean values of 17 different characters of 18 genotypes of Kidney bean

Parameter	Clusters			
	I	II	III	IV
Days to 5 leaves stage	9.29	7.8	13.33	9.67
Days to 1st Flowering	32.95	31.4	34.33	32.27
Days to 50% flowering	36.43	34.46	36.67	35.2
Days to Maturity	81.67	80.93	78	81.93
Days to 1st Pod Setting	40.14	38.53	41.33	39
Plant Height (cm)	30.14	29.3	20.53	29.64
No of Leaves	16.13	14.36	14.67	12.01
No of Pod/Plant	23.61	16.41	19.17	16.44
Leaf Area (cm^2)	146.24	120.71	114.67	103.42
Petiole Length (cm)	9.51	8.75	7.33	6.86
Pod Length (cm)	10.37	10.19	9.99	8.5
Pod Diameter (cm)	7.78	8.03	8.33	7.95
Dry Weight of Pod	2.21	1.86	1.62	1.25
No of Seeds/Pod	4.66	3.95	4.19	3.82
1000 Seed Weight	291.27	346.15	443.33	241.36
Seed Yield (g/Plant)	95.14	83.17	81.15	53.64
Yield	2.12	1.85	1.8	1.19

In case of 50% flowering similarly genotypes of cluster II (34.46 days) was early and genotypes under cluster III (36.67 days) followed by cluster (36.43 days) were relatively late. Early maturing genotypes were grouped into cluster III (78 days) comprising whereas late maturity genotypes were grouped under the cluster IV (81.93 days) with one genotype. Early pod setting was recorded in cluster II (38.53 days) and and late pod setting in cluster III (41.33 days). Cluster III exhibited the highest mean for plant height with 30.14 cm, whereas the cluster I had the lowest average of plant height 20.53cm followed by cluster IV (29.64 days). Highest number of leaves was found in cluster I (16.13) and the lowest number of leaves was observed in both cluster II (14.36). Maximum number of pods per plant was found in both cluster I (23.61) whereas the minimum number of pods was found in cluster II (16.41) followed by cluster IV (16.44). In respect of leaf area, cluster I had the maximum value of 146.24 while cluster IV had the minimum mean value of 103.42 was recorded. Genotypes grouped under cluster I recorded highest mean value for petiole length (9.51) and the lowest by the genotypes of cluster VI (6.86). Cluster I comprised of genotypes with long pods (10.37) while cluster IV consisted of genotype with shorter pod (8.5). The highest mean value for pod diameter was exhibited by the genotypes grouped under cluster III (8.33) and the lowest (7.78) by the genotypes under the cluster I. Cluster I with five genotypes exhibited the highest mean for dry weight of pod (2.21g), whereas the cluster IV had the lowest average (1.25g). Cluster I with five genotypes exhibited the highest mean for number of seeds per pod (4.66), whereas the cluster IV had the lowest average (3.82). Cluster III with five genotypes exhibited the highest mean for 1000 seed weight (443.33g), whereas the cluster IV had the lowest average (241.36g). Genotypes grouped under cluster I recorded highest mean value for seed yield per plant (95.14g) and the lowest by the genotypes of cluster VI (53.64g). Seed yield was highest in genotypes grouped under cluster I (2.12g) and lowest (1.8) in the cluster IV.

4.4.5 Canonical variate analysis

4.4.5.1 Inter and intra cluster distances

Genotypes grouped into the same cluster presumably diverge little from one another. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or segregants. However theoretically, a general notion exists that

the larger is the divergence between the genotypes, higher will be the heterosis (Falconer, 1981).

From table 11 it is observed that cluster I showed the maximum inter-cluster distance with the cluster III (23.742), followed by cluster II (11.014); and it has minimum distance with the cluster IV (8.595). Figure 4 is shown to present different clusters. Cluster II showed the maximum inter-cluster distance with cluster III (15.644) and it was nearest to cluster IV (8.652). Cluster III showed more distanced from the cluster IV (15.783). All clusters showed intra cluster distances except cluster III which constitute one genotype. Intra cluster distance was highest in the cluster VI (0.900) followed by the cluster I (0.858). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses. But heterosis cannot be exploited in a highly self-fertilized crop like Kidney bean.

Table 11: Intra (Bold) and inter cluster distances (D^2) for 18 genotypes

Cluster	1	2	3	4
1	**0.858**	11.014	23.742	8.595
2		**0.651**	15.644	8.652
3			**0.000**	15.783
4				**0.900**

However, the crosses involving parents from clusters with high inter cluster distance are likely to yield desirable recombinants in the advanced generations which could be developed as traditional homozygous varieties. The lowest intra cluster was recorded in cluster II (0.651).The highest inter cluster distance (23.742) was observed between cluster I and cluster III. This high intra- cluster distance indicated the wider genetic diversity among the genotypes, which could be used in yield improvement of bean. The lowest inter cluster distance (8.595) was seen between Cluster II and cluster IV. The genotypes from distant clusters exhibit wide diversity. So, genotypes from divergent clusters (I and III) can be selected for hybridization program in order to achieve novel

recombinants. Gangadhar (2014) found the highest intra cluster distance and lowest intra cluster distance was found in the cluster I (D^2 = 122.419) and cluster II (D^2 = 86.14) respectively. He also found maximum inter cluster distance between Cluster I and II (D^2 = 148.84). Similar results were given by Thaware *et al.* (1997) and Chaubey *et al.* (2003) in Kidney bean. In this experiment, inter cluster distance was always higher than intra-cluster distance. Similar result was found by Nandi *et al*. (2000), Sureja and Sharma (2001), Singh and Mishra (2008) and Savitha (2008).

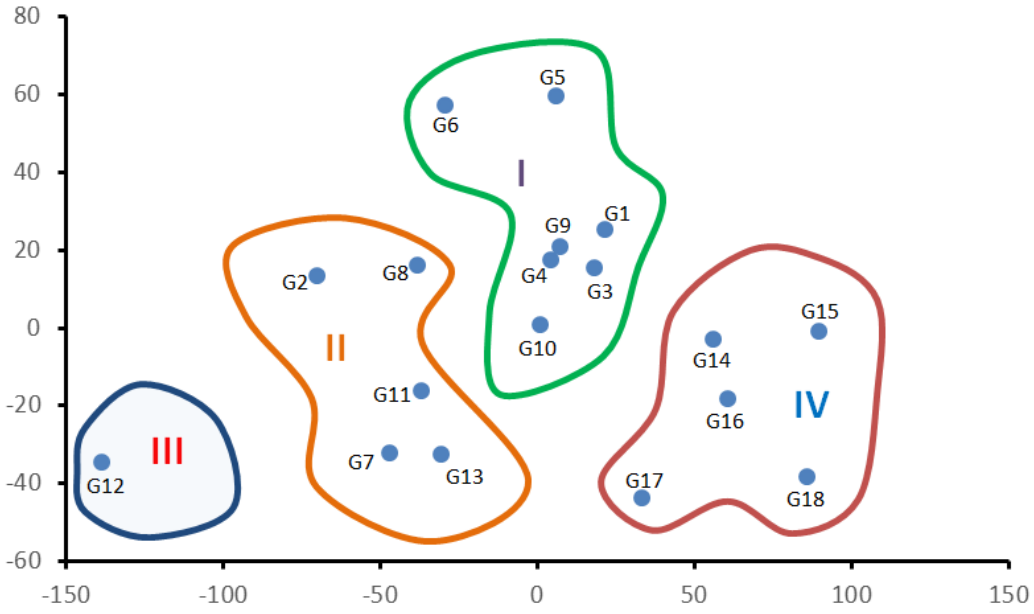


Figure 4: Cluster of the different genotypes of Kidney bean

4.4.5.2 Nearest and farthest cluster

Cluster I consist of nearest cluster with D^2 values cluster IV (8.595) & farthest cluster with D^2 values cluster III (23.742) (Table 12). Cluster II consist of nearest cluster with D^2 values cluster IV (8.652) & farthest cluster with D^2 values III (15.644). Cluster III consist of nearest cluster with D^2 values cluster II (15.644) & farthest cluster with D^2 values I (23.742). Cluster IV consist of nearest cluster with D^2 values cluster I (8.595) & farthest cluster with D^2 values III (15.783) (Figure 5).

Table 12: Nearest and farthest cluster in Kidney bean genotypes

Cluster	Nearest with D^2 values	Farthest with D^2 values
I	IV (8.595)	III (23.742)
II	IV (8.652)	III (15.644)
III	II (15.644)	I (23.742)
IV	I (8.595)	III (15.783)

4.4.5.3 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 13. Vector I obtained from PCA expressed that days to 5 leaves stage (0.477), days to 50% flowering (1.046), plant height (0.151), pod length (0.016), number of seeds per pod (0.781), 1000 seed weight (0.097), seed yield per plant (0.101), yield (4.152) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation.

In vector II days to 1st flowering (1.822), days to maturity (0.126), days to first pod setting (0.674), number of leaves (0.885), number of pod per plant (0.764), leaf area (0.110) showed their important role toward genetic divergence. The value of Vector I and Vector II revealed that both Vectors had positive values for days to maturity and number of leaves per plant indicating the highest contribution of these traits towards the divergence among 18 genotypes of Kidney bean. Negative values in both vectors for dry weight of pod had lower contribution towards the divergence.

In the present study, eighteen genotypes of Kidney bean were grouped into four clusters. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. Days to 5 leaves stage, days to 1st flowering, days to 50% flowering, days to maturity were the maximum contributors for divergence in the present study should be given utmost importance for selecting the genotypes for crossing program. Cluster I, III and IV which have extreme values for days to 5 leaves stage, days to 1st flowering, days to 50% flowering, days to maturity. Singh *et al*. (1997) reported the importance of cluster mean of a character within the

Table 13: Relative contributions of 17 characters of 18 genotypes of Kidney bean to the total divergence

Parameters	Vector-1	Vector-2
Days to 5 leaves stage	0.477	-0.290
Days to 1st Flowering	-1.196	1.822
Days to 50% flowering	1.046	-1.863
Days to Maturity	0.095	0.126
Days to 1st Pod Setting	-0.511	0.674
Plant Height (cm)	0.151	-0.342
No of Leaves	0.749	0.885
No of Pod/Plant	-0.043	0.764
Leaf Area (cm^2)	-0.015	0.110
Petiole Length (cm)	0.067	-0.801
Pod Length (cm)	0.016	-0.997
Pod Diameter (cm)	0.149	-1.304
Dry Weight of Pod	-24.087	-10.215
No of Seeds/Pod	0.781	-1.225
1000 Seed Weight	0.097	-0.011
Seed Yield (g/Plant)	0.101	-0.028
Yield	4.152	-0.938

different clusters and its significance for improvement of Kidney bean, which is in agreement with the present result.

The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that seed yield per hectare ranked first days to 5-leaves stage which contributed maximum towards the total diversity with the value 42.9%, followed by days to 1st flowering 22%, days to 50% flowering 9.9%, suggesting that these are potent factors in differentiating the germplasm of dolichos bean. Apart from the high divergence, the performance of the genotypes (cluster I- G1, G3, G4, G5, G6, G9, G10 and cluster III- G12) and the characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion for improvement in Kidney bean. Here, it is worthy to note that in calculating cluster means, the superiority of a particular genotype in respect of a given character get diluted by other genotypes that are related and grouped in the same cluster which are inferior or intermediary for that character in question. Hence apart from selecting lines from clusters which have high inter cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence in respect of trait of interest. Plate 9 represents the diverse seeds of Kidney bean in respect of color, shape and size.

4.5 NUTRIENT COMPONENTS ANALYSIS IN KIDNEY BEAN DRY SEEDS

Carbohydrates, lipids and proteins, which are stored during the later stages of seed formation, are considered the major reserves in most seeds (Lima *et al*. 2008). Legumes are unique foods because of their rich nutrient content including starch, protein dietary fibre. (Borade *et al.*, 1984). Most of the research on Kidney beans has been related to varietal selection. The criteria for selection have always been done for resistance to diseases or yields but not for nutritional quality (Oboh *et al.*, 1998). A study of the composition and nutritive quality of Kidney beans would therefore be of great interest, because the knowledge provided would help to orient the work of investigators involved in varietal selection. Here, we estimated different nutrient components e.g., protein, carbohydrate, fat, fiber, ash and moisture content in different genotypes of Kidney beans collated from local and BARI. The analysis of variance showed the nutrient components were significantly varied among the genotypes (Appendix VI).

Plate 9: Variation in seed color, shape, and size in Kidney bean genotypes

In the present investigation, significant differences (P< 0.01) of protein (10.50), carbohydrate (11.107), fat (0.267%), fiber (0.336), ash (0.386) and moisture (1.41) and was found in 18 genotypes of Kidney bean (Appendix VI and Table 14). Genotype G10 (23.76%) possessed significantly high protein content that was statistically different to other genotypes. Genotype G4 (17.76%) had the lowest amount of protein content. Variations in protein content apparently were due to differences of genetic heterogeneity among Kidney bean cultivars. Variations in the protein content of azuki bean due to the growing region were also observed on by Yoshida *et al.* (1988). Carbohydrate content in the genotypes of Kidney bean ranged from 57.96% (G10) – 64.03% (G4). The highest value was also statistically similar with G2 (59.5%), G3 (58.43%), G5 (60.24%), G10 (57.96%), G13 (58.63%), G15 (58.09%), G16 (58.71%), G7 (%59.31%) and G18 (59.69%). G4 was also found statistically similar with G1 (61.52%), G7 (61.94%), G8 (61.54%), G9 (63.39%), G11 (63.51%) and G12 (62.04%). Similar results were also found by Hseih *et al.* (1992) and Salunkhe *et al.* (1989). Significant fat content was also found which ranged from 2.2-3.11%. Genotype G7 had lowest moisture content which were statistically similar with the genotypes viz. G4, G8, G10 and G11. They all contained 2.5% of fat. Hseih *et al.* (1992) found 1.5% fat in Kidney bean. The highest fat possessing genotype was G1 which was also statistically similar genotype G2 (3%), G3(3.1%), G9(3.1%), G15(3.1%), G17 (3.1%) and G18(3.1). The highest value of fiber was found in genotype G8 (2.46%) and lowest in G4 (1.14%).

Genotype G2 was observed to have lowest amount of ash (1.79%) which was statistically similar with G7 (1.87%), G9 (1.76%), G11 (1.78%) and G17 (1.84%). While the highest value of fat (2.95%) was found in G8 which can also be categorized with G3 (2.94%) and G8 (2.95%) in same class. But Hseih *et al.* (1992) observed 4.5% ash in Kidney bean. The moisture content was ranged from 10.18- 12.68% which were possessed by genotype G1 and G11 respectively. The values were not statistically similar with moisture content of other genotypes. Similar moisture content (10.8%) was found in mature Kidney bean by Hseih *et al.* (1992). When protein is provided from kidney beans, the blood sugar gets stabilized by this versatile legume (www.whfoods.com). In the present study, protein content was found higher in local genotypes collected from Bandarban (G13- 23.11%, G15- 23.05%, G16-23.09%, G17-22.44%, G18- 21.92%) and advanced line (G10- 23.76%) than check variety (G1-21.62% and G2- 22.41%). In case of carbohydrate content, local varieties of Sylhet

Table 14: Analysis of nutrient components in Kidney bean genotypes

Genotypes	Protein		Carbohydrate		Fat		Fiber		Ash		Moisture	
G1	21.62	d	61.52	abcd	3.11	a	1.5	ef	2.08	cde	10.18	i
G2	22.41	c	59.5	cdef	3	ab	1.39	f	1.79	gh	11.91	de
G3	21.93	d	58.43	ef	3.1	a	2.08	c	2.94	a	11.52	f
G4	17.76	h	64.03	a	2.5	de	1.17	g	2.31	b	10.23	hi
G5	21.97	d	60.24	cdef	2.7	bcd	1.39	f	1.71	h	11.99	cd
G6	21.84	d	60.89	bcde	2.6	cd	1.49	ef	1.98	ef	11.2	g
G7	19.93	f	61.94	abc	2.2	e	1.8	d	1.87	fgh	12.26	b
G8	20.14	f	61.54	abcd	2.5	de	2.46	a	2.95	a	10.41	h
G9	18.2	g	63.39	ab	3.1	a	1.78	d	1.76	gh	11.77	e
G10	23.76	a	57.96	f	2.5	de	1.77	d	2.18	bcd	11.83	de
G11	17.78	h	63.51	a	2.5	de	1.75	d	1.78	gh	12.68	a
G12	20.01	f	62.04	abc	2.6	cd	1.53	e	1.92	efg	11.9	de
G13	23.11	b	58.63	ef	2.7	bcd	1.47	ef	1.93	efg	12.16	bc
G14	20.54	e	60.68	cde	2.6	cd	2.25	b	2.21	bc	11.72	ef
G15	23.05	b	58.09	f	3.1	a	1.85	d	2.2	bc	11.71	ef
G16	23.09	b	58.71	ef	2.9	abc	1.44	ef	2.01	def	11.85	de
G17	22.44	c	59.31	def	3.1	a	1.43	ef	1.84	Fgh	11.88	de
G18	21.92	d	59.69	cdef	3.2	a	1.42	ef	1.94	Efg	11.84	de
Lsd 0.05	0.389		2.57		0.362		0.112		0.181		0.211	
CV **(%)**	0.599		1.39		4.25		2.2		2.85		0.594	

(G4- 64.03%, G5- 60.24%, G6- 60.89%, G7- 61.94%, G8- 61.54%) and advanced line (G11- 63.51%, G12- 62.04%) were higher than Bandarban local varieties. Most of the local varieties of both Sylhet and Bandarban along with all three advanced lines had showed lower fat content than check varieties. Kidney beans are a very good source of cholesterol-lowering fiber which prevents heart disease, cancer and rising of blood sugar. Which can be a good choice for individuals with diabetes, insulin resistance or hypoglycemia (www.whfoods.com). Maximum amount of fiber was found in local varieties of Sylhet (G3- 2.08%, G8- 2.46%) and advanced line (G14- 2.25%) among all genotypes. Kidney beans' contribution to heart health lies not just in their fiber, but in the significant amounts of ash (minerals) from Kidney beans. Minerals lessens resistance of veins and arteries and improves the flow of blood, oxygen and nutrients throughout the body (www.whfoods.com). Higher amount of ash was found in local varieties of Sylhet (G3- 2.94%, G4- 2.31%, G8- 2.95%), and advanced line (G10- 2.18%) than check variety (G1- 2.08%, G2- 1.79%). Two of the Bandarban varieties (G14- 2.21%, G15- 2.2%, G16- 2.01%) also possessed high ash content. Figure 6 and 7 is presented showing relative content of protein and ash percentage.

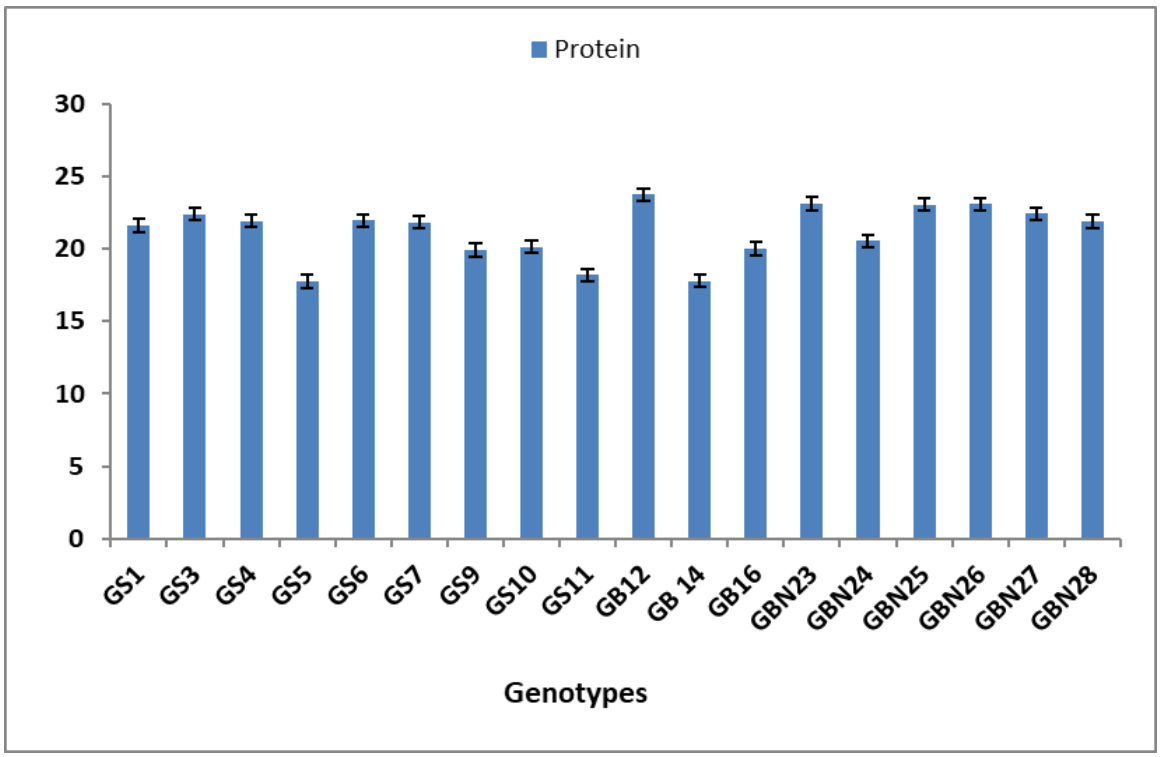


Figure 5: Protein content among the Kidney bean genotypes

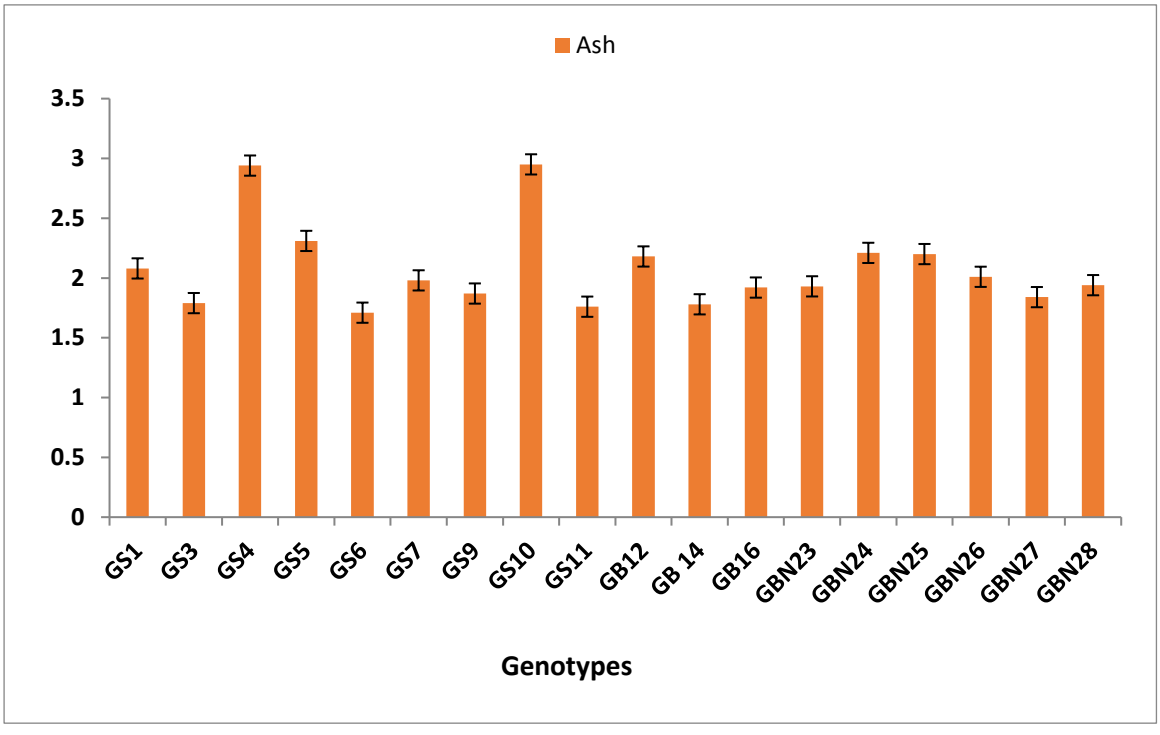


Figure 6: Ash content among the Kidney bean genotypes

Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

Kidney bean has several good features which help the breeders and geneticists to have quick genetic results. These features such as its growing habits, short life span and adaptability to wide range of soil and climatic conditions are highly desirous for developing a high yielding variety. It has many improved varieties in developed countries to its credit suitable for various agro-ecological conditions. However, Bangladesh has only three Kidney bean varieties released from BARI. The crop is relatively less cultivated especially for disease infestation (the leaf curl and mosaic virus) and lack of popularity in consumers and vegetable markets in our country compared to many of the developed countries.

The genetic variability is the raw material of vegetable breeding industry on which selection acts to evolve superior genotypes. The wide genetic variability that exists in the available genotypes provides ample scope for further improvement. Yield being a complex quantitative character, direct selection for yield may not result in successful improvement. Therefore, it is necessary to partition the observed variability into heritable and non-heritable components by calculating genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic gain.

The present study was envisaged to study the nature and magnitude of genetic variability, the pattern of character association among the characters, the direct and indirect effects of component characters on seed yield, the degree of genetic divergence in germplasm accessions and comparison of nutrient components among the genotypes of Kidney bean. The material for the present study comprised of 18 genotypes collected from Sylhet and Bandarban regions and BARI, were evaluated using RCBD design for 17 quantitative characters at Sher-e-Bangla Agricultural University, Dhaka.

The study revealed wide range of variability for most of the characters studied. On the basis of mean performance, genotypes G3, G5, G6, G8, G11 and G15 took minimum number of days to 1st flowering (30.00) while G18 (33.00) followed by G8 (33.33) and G3 (33.67) took minimum days to 50% flowering. Genotype G12 (78.00) followed by

G6 (78.00) required minimum days to mature the seed. Genotype G9 showed maximum days to 1st flowering (38.67), 50% flowering (42.00), maturity (89.33) and 1st pod setting (47.00) whereas the yield (1.61) was comparatively lower than other. G11 (36.67) was observed to take minimum days to 1st pod setting. Highest plant was observed in genotype G1 (36.59cm) (Table 4). Genotype G6 followed by G5 and G4 was recorded to show maximum number of pod per plant (30.68, 27.67, 27.93), pod length (12.38cm, 11.18cm, 11.09cm), seed yield per plant (120.43g, 115.07g, 112.03g) and seed yield per hectare (2.68 t/ha, 2.56t/ha, 2.49t/ha) respectively; G6 in dry weight pod (2.75g) and number of seeds per pod (5.50). Genotype G16 showed highest pod diameter (8.92cm), while genotype G12 had maximum 1000 seed weight (443.33g). So, these genotypes can be used for future breeding program.

The low magnitude of genotypic and phenotypic coefficient of variation (GCV and PCV) was observed for the characters e.g. days to 5 leaves stage (24.00, 25.46) number of leaves (20.88, 22.34), number of pod per plant (27.97, 29.93), leaf area (22.88, 23.25), petiole length (26.53, 26.94), dry weight of pod (24.53, 25.22), seed yield per plant (28.79, 33.83), seed yield per hectare (28.72, 33.75). Except 1000 seed weight (GCV- 14.65% and PCV- 24.96%), seed yield per plant (GCV- 28.79% and PCV- 33.83%) and seed yield per hectare (GCV- 28.72% and PCV- 33.75%) (Table 4). The differences between PCV and GCV for the characters were narrow indicating lesser influence of environment on these characters and could be improved by following phenotypic selection.

High heritability estimates were observed for days to 5 leaves stage (88.80), days to 1st flowering (87.84%), days to 50% flowering (85.87%), days to 1st pod setting (77.78%), plant height (77.69%), number of leaves (87.38%), number of pod per plant (87.32%), leaf area (96.83%), petiole length (96.92%), pod length (70.65%), dry weight of pod (94.59%), number of seeds per pod (86.86%), seed yield per plant (72.46%), seed yield per hectare (72.42%) (Table 4). 1000 seed weight (34.43%) showed moderate heritability. Leaf area (59.46), 1000 seed weight (52.80) and seed yield per plant (39.89) recorded high genetic gain and selection based on these characters may result in development of high yielding genotypes. High heritability coupled with high genetic advance was found in leaf area and seed yield per plant. Moderate heritability with high genetic advance was observed in 1000 seed weight.

In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Association of the character seed yield per hectare was highly significant and positive with number of leaves (0.831, 0.781), number of pods per plant (0.785, 0.735), pod length (0.861, 0.767), dry weight of pod (0.976, 0.902), number of seeds per pod (0.798, 0.720) and seed yield per plant (1.000, 1.000) at both genotypic and phenotypic level (Table 5 and 6). It shows that yield per hectare in Kidney bean can be improved by making direct selection based on these traits. Pod diameter (-0.677) had highly significant negative association at genotypic level and days to 5- leaves stage (-0.560, -0.504) had significant negative association with yield per hectare. Days to 1000 seed weight exhibited no significant association with seed yield.

Path co-efficient analysis for seed yield per hectare revealed that seed yield per plant exerted highest direct effect on seed yield (1.000), followed by number of seeds per pods (0.053). The indirect contribution of component characters viz., number of leaves (0.663), number of pods per plant (0.641), pod length (0.636), dry weight of pod (0.756), number of seeds per pod (0.549) was high through seed yield per plant (Table 7).

Genetic diversity was assessed by using Mahalanobis D^2 statistic. Grouping the genotypes into clusters using Tocher's method resulted in the formation of four clusters, of which cluster I was the biggest with 7 genotypes followed by cluster II and IV with 5 genotypes, cluster III was solitary (Table 9). The inter cluster distances ranged from 8.595 (between clusters I and IV) to 23.742 (between clusters I and III). The highest intra cluster distance (0.900) was in cluster IV (Table 11). The genotypes included under the cluster I (G1, G3, G4, G5, G6, G9 and G10) showed high mean values for the characters plant height (30.14), number of leaves (16.13), number of pods per plant (23.61), leaf area (146.24), petiole length (9.51), pod length (10.37), dry weight of pod (2.21), number of seeds per plant (4.66), seed yield per plant (95.14) and yield per hectare (2.12) (Table 10). The single genotype G12 under cluster III showed high mean value for pod diameter (8.33) and 1000 seed weight (443.33). While the genotypes included in cluster IV showed lowest values for almost characters above.

Both genetic and environmental factors can have an influence on the contents of protein, moisture, fat, fiber, ash, carbohydrate in the seeds of Kidney beans and also on the crop yield. The range of nutrient component of kidney bean was found carbohydrate 57.96%- 64.03%, protein 17.76%- 23.76%, fat 2.2%-3.11%, fiber 1.17%- 2.46%, ash 1.79%- 2.95% and moisture 10.18%- 12.68%. In the present investigation genotype G1 showed highest fat (3.11%) and lowest moisture (10.18%) content. Genotype G4 showed highest carbohydrate (64.03%) content and lowest protein (17.76%) and fiber (1.17%) content. G8 showed highest fiber (2.46%) and ash (2.95%) content while G10 showed highest protein (23.76%) and lowest carbohydrate (57.96%) content (Table 14).

Local genotypes collected from Bandarban (G13- 23.11%, G15- 23.05%, G16-23.09%, G17- 22.44%, G18- 21.92%) and advanced line (G10- 23.76%) were found comparatively higher in protein content. However, local varieties of Sylhet (G4- 64.03%, G5- 60.24%, G6- 60.89%, G7- 61.94%, G8- 61.54%) and advanced line (G11- 63.51%, G12- 62.04%) had higher carbohydrate content than Bandarban local varieties. The highest amount of fiber was found in local varieties of Sylhet (G3- 2.08%, G8- 2.46%) and advanced line (G14- 2.25%) among all genotypes. Similarly, higher amount of ash was found in local varieties of Sylhet (G3- 2.94%, G4- 2.31%, G8- 2.95%) than check variety (G1- 2.08%, G2- 1.79%) (Table 14).

The possibility to make predictions for the nutrient composition of Kidney bean is very limited due to unforeseeable combinatory effects of variety, site (cultivation), and climate (year). It is yet not possible to make predictions with regard to the influence of those combined environmental factors. The effect of the variety is the most certain factor of influence, and is more or less affected by other parameters. But the choice of the variety can be essential with regard to the quality-determining constituents.

Future line of work

Based on the findings of the present investigation, the speculation drawn for further improvement of Kidney bean genotypes is that the genotypes G1 (BARI Jharseem- 1), G3 (local), G4 (local), G5 (local), G6 (local), G9 (BARI Jharseem- 2), G10 (Advanced line) and G12 (Advanced line) showed considerable genetic diversity among them, so

crosses between these genotypes are likely to produce new recombinants with desired traits.

Four genotypes viz., G4 (2.49 t/ha), G5 (2.56 t/ha), G6 (2.68 t/ha) and G11(2.00 t/ha) showed significant high yield over the checks. There is a need to evaluate these high yielding genotypes in large plots and over locations in Bangladesh for their commercial utilization.

Local varieties of Sylhet proved to be high in carbohydrate, fiber and ash content, whereas local varieties of Bandarban was found higher in protein than check varieties. Considering the nutrient component analysis genotype of local varieties of Sylhet G3, G4, G8 and advanced lines G10, G11 and G12 can be a great source of nutritious food as well as a good source of genetic experiments for development of the crop in respect of environment of Bangladesh. Again, local varieties of Bandarban were good source of protein and but still need to be more improved.

As pests and diseases infestation also affected the crop performance, there is a need to systematically test the genotypes for pest and disease reaction especially virus diseases. Breeding program should be undertaken to develop resistant varieties against leaf curl and mosaic virus disease.

References

REFERENCES

Acharya, J.N. (2013). Variability and Correlation Analysis in Diverse Genotypes of French Bean (*Phaseolus vulgaris* L). MS thesis. BHU, India.

Aggarwal, V.D. and Singh, T.P. (1973). Genetic variability and interrelationship in agronomic traits in kidney-bean (*Phaseolus vulgaris* L.). *Indian J. Agric. Sci*. **43**: 845-848.

Ahmed, S., Zargar, M.A. and Tahit Ali. (2005). Genetic variability, heritability, genetic advance for seed yield and component traits in cowpea. *Natl. J. Plant Imprt*. **7**:85-87.

Ahmed, K. S. (2011). Variability, correlation and path analysis for seed yield and yield related traits in common beans. *Indian J. Hort*. **68**(1): 56-60.

Alemu, Y., Alamirew, S. and Dessalegn, L. (2013). Genetic variability in snap bean (*Phaseolus vulgaris* L) genotypes in central rift valley of ethiopia. *Intl. J. Plant. Breed. Genet.* **7**(2): 124-131.

Alemu, Y., Alamirew, S. and Dessalegn, L. (2017). Correlation and path analysis of green pod yield and its components in snap bean (*Phaseolus Vulgaris* L.) genotypes. *Intl. J. Res. Agri. Forest.* **4**(1): 30-36.

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

Ali, M. and Kushwaha, B.L. (1987). Cultivation of rabi rajmash in plains. *Indian J*. **31**(2): 2023.

Ali, M.A., Nawad, N.N., Abbas, A., Zulkiffal, M. and Sajjad, M. (2009). Evaluation of selection criteria in *Cicer arietiunum* L. using correlation coefficients and path analysis. *Australian J. Crop Sci*. **3**(2):65-70.

Angadi, P.K., Patil, M.G., Lokesha, R., Hussain, S.A., Hanchinmani, C.N. and Sreenivas, A.G. (2011). Genetic variability, heritability and genetic advance in french bean (*Phaseolus vulgaris* L.). *Environ. Ecol*. **29**(4): 1922-1925.

Angadi, P.K., Patil, M.G. and Angadi, A. (2012). Path coefficient analysis studies in french bean (*Phaseolus vulgaris* L.), *Asian J. Hort.*, **7**(1): 133-136.

AOAC. (1995). Association of Official Analytical Chemists. Washington, DC.

Arshad, M., Ali, N. and Ghafoor, A. (2006). Character correlation and path coefficient in soybean (*Glycine max* L. Merrill). *Pakistan. J. Bot*. **38**(1): 121-130.

Atuahene-Amankwa, G. and Michaels, T.E. (1997). Genetic variances, heritabilities and genetic correlations of grain yield, harvest index and yield components for common bean (*Phaseolus vulgaris* L.) in sole crop and in maize/bean intercrop. *Canadian J. Plant Sci*. **77**: 533-538.

Altinabas, M. and Sepetoglu, H. (1993). A study to determine components affecting seed yield in French bean (*Phaseolus vulgaris* L.). *Arab Univ.J. Agric.Res*. **17**:775-784.

Amini, A. Ghannadha, M. and Abd-Mishani, C. (2002). Genetic diversity and correlation between different traits in common bean (*Phaseolus vulgaris* L.). (Persian) *Iranian J. Agri. Sci*. **33**(4): 605-615.

Aykroyd, W.R., Doughty, J., Walker, A. (1982). Legumes in human nutrition. FAO and Food Nutrition paper 20 Rome: FAO. Pp:67-78.

Baisakh, B. (1992). Inter-relationship between yield and yield attributes in rice bean (*Vigna umbellate*). *Indian J. Agric. Sci*. **62**(9): 620-622.

Barelli, M.A.A., Gonçalves-Vidigal, M.C., Vidigal Filho, P.S., Amaral Junior, Antonio T. Do and Poletine, J. P. (2005). Characterization of landraces of common bean (*Phaseolus vulgaris* L.) germplasm from Mato Grosso do Sul State. *Bean Improv. Crop*. **48**: 10-11.

Bhatty, N., Gilani, A.H. and Nagra, S.A. (2001). Nutritional Improvement of Lobia (*Phaseolus vulgaris*) by Supplementation with Poultry, Mutton and Beef Meat. *Intl. J. Food Sci. Nutri*. **52**: 521-526.

Bhushan, K.B., Singh, B.P., Dubey, R.PK. and Ram, H.H. (2007). Coreelation analysis for seed yield in French bean (*Phaseolus vulgaris* L). *Patnagar J. Res.* **5**(1): 145.

Bhushan, K.B., Jadli, S., Verma, O. and Goswami, A.K. (2008). Plant characters correlation and path coefficient analysis of seed yield in exotic french bean (*Phaseolus vulgaris* L.) germplasm. *Int. J. Agri. Sci.* **4**(2): 667-669.

Biradar, B.D., Goud, J.V. and Patil, S.S. (1996). Association of grain yield with other characters in three F2 populations of French bean (*Phaseolus vulgaris* L.). *Crop Research*. **11**:179-183.

Borade, V.P., Kadam, S.S. & Salunkhe, D.K. (1984). Changes in phytate, phosphorus and minerals during germination and cooking of horse gram and moth bean. *Qual. Plant. Food Hum. Nutr.* **34**: 151-156.

Burton, G.W. (1952). Quantitative inheritance in grasses Process 6th International. Grassland Cop. **1**:227-283.

Burton, G.W. and Devane, E.M. (1953). Estimating heritability in tall fescue from replicated clonal material. *Agro. J*. **45**: 478481.

Castric, V., Bonney, F., and Bernatchez, L., (2001). "Landscape Structure and Hierarchical Genetic Diversity in the Brook Charr". *Evolution*. **55** (5): 1016-1028.

Chakraborty, M. and Mukharajee, A.K. (2001). Variation and character association in rice bean (*Vigna umbellata*), Birsa Agric.Univ. *J. Res*. **13**(1): 45-49.

Chand, P. (1999). Character association and path analysis in rajmash. *Madras Agric. J.* **85**:188-190.

Chaubey, P.K., Singh, S.P. and Chaubey, T. (2003). Genetic divergence in rajmash (*Phaseolus vulgaris* L.). *Veg. Sci*. **30**(2): 190-191.

Chauhan, R. Kharb, R.P.S. and Sangwan, V.P. (2003). Variability and character association studied for seed yield in fodder cowpea. *Forage Res*. **28**: 233-235.

Choudhury, N.H. and Juliano, B.O. (1980). Effect of amylose content on the lipids of mature rice grain. *Phytochemistry*. **19**:1385.

Cochran, W. G. and Cox, G. M. (1957). Experimental design john Wiley and Sons, in., New York. Pp. 611.

Coelho, R.C., Faria, M.A., Rocha, J., Reis, A., Oliveira, M.B.P.P. and Nunes, E. (2009). Assessing Genetic Variability in Germplasm of *Phaseolus vulgaris* L. Collected in Northern Portugal. *Sci. Hort*. **122**: 333-338.

Coimbra, J.L.M., Coimbra, S.M.M., Carvalho, F.I.F. and de Oliveira, A.C. (1998). Path coefficients, canonical correlations and genetic divergence: II. Among primary and disease characters in black bean (*Phaseolus vulgaris* L.) genotypes. (Portuguese) *Pes. Agro. Gau*. **4**(2): 189-195.

Coimbra, J. L.M., Guidolin, A.F. and Carvalho F. (1998). Path coefficients, canonical correlations and genetic divergence: Among primary and secondary characters of seed yield in black beans (*Phaseolus vulgaris* L.) genotypes. *Pesq. -A grop.-Gaucha*. **4**:183-188.

Coyne, D.P. (1968). Correlation, heritability, and selection of yield components in field beans, *Phaseolus vulgaris* L. *Proc. American Soc. Hort. Sci*. **93**:388-396.

Dahiya, A., Sharma, S.K., Singh, K.P. and Kumar, A. (2000). Variability studies in French bean (*Phaseolus vulgaris* L.). *Annals Bio*. **16**(2): 201-204.

Dahiya, A., Sharma, S.K., Singh, K.P. and Luthra, O.P. (2004). Path analysis of seed yield components in French bean (*Phaseolus vulgaris* L.) *Annals Bio*. **7**(1) 255-257.

Dahiya, A. Sharma, S.K. Singh, K.P. and Luthra, O.P. (2006). Path analysis of seed yield components in French bean (*Phaseolus vulgaris* L.) *Annals Bio*. 7(1) 255-257.

Dahiya, O.P., Mishra, S.K. and Singh, D. (2007). Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp]. *J. Arid Leg*. **4**: 107-109.

Deshpande, S.S., Damodaran, S. (1990). Food legumes: chemistry and technology. *Adv. cereal sci. tech*. **44**(10):147-241.

Deepak S.C.C., Pant and Solanki, S.S. (1999). Studies on agroeconomic traits and genetic parameters in French bean (*Phaseolus vulgaris* L.). *Prog. Hort*. **31**: 194-198.

Devi, J, Sharma, A. and Santra, P. (2012). Performance of French bean genotypes (*Phaseolus vulgaris* L.) for seed yield and related traits under mid hill conditions of north western Himalayas. *J. Crop Weed.* **8**(2): 65-69.

Devi, J., Sharma, A., Singh, Y., Katoch, V. and Sharma, K.C. (2014). Genetic variability and character association studies in French bean (*Phaseolus vulgaris* L.) under North-Western Himalayas. *Leg. Res*. **38**(2) 2015: 149-156

Dewey, D.R. and Lu, K.H. (1959). A correlation and path co-efficient analysis of components of crested wheat grass seed production. *Agron. J*. **25**: 515-518.

Dikshit, H.K., Gupta, S.R., Asthana, A.N., and Devraj. (1999). Genetic parameters and diversity in rajmash. *Leg. Res*. **22**: 198-200.

Duarte, R.A. and Adams, M.W.A. (1972). Path coefficient analysis of some yield components correlations in field beans (*Phaseolus vulgaris* L.). *Crop. Sci*. **12**: 579-582.

Duke, J.A. (1981). Handbook of legumes of world economic importance. Plenum Press, New York.

Dursun, A. (2007). Variability, heritability and correlation studies in bean (*Phaseolus vulgaris* L.) genotypes. *World J. Agril. Sci*. **3** (1): 12-16.

East, E.M. (1916). Studies on size inheritance of *Nicotiana.* Genetics. **1**: 164-167.

Faisal, M., Malik, N., Ashraf, M., Qureshi, A.S. and Ghafoor, A. (2007). Assessment of genetic variability, correlation and path analysis for yield and its components in soybean. *Pakistan J. Bot*. **39**(2). 405-413.

Falconer, D.S. (1960). Introduction to quantitative genetics. Oliver and Boyd. London. 145-143.

Falconer, D.S. (1981). Introducao a genetica quantitativa. Traduçao MA Silva and JC Silva. *Imprensa* Universitária, Viçosa. P. 279.

FAOSTAT. (2017). www.fao.org/faostat/en/#data/QC

Fisher, R.A. (1918). The correlation between relatives on the supposition of Mendelian inheritance. *Trans.Rev. Soc. Edinburgh.* **52**:39-43.

Fisher, R.A. (1936). The use of multiple measured taxonomic problems. *Annals Eugen*. **7**: 179-189.

Frake, R.V., Dans, R.L. and Patterson, F.L. (1961). The Breeding Behavior of yield and related variables in alfalfa. Association between characters, *Crops Sci*. **1**:207-209.

Furtado, M.R., Cruz, C.D., Cardoso, A.A., Coelho, A. D. F. and Peternelli, L. A. (2002). Path analysis of grain yield of common bean and its primary components in monoculture and intercropped with maize. *Ciencia Rural.* **32**:(2) 217-220.

Galton, F. (1889). Natural Inheritance. London.

Gangadhara, K., Jagadeesaha, R.C. and Anushma, P.L. (2014). Genetic divergence studies in french bean (*Phaseolus vulgaris*). **14**(1): 225-227.

Govanakoppa, R.B., Hosamani, R.M. and Salimath, P.M. (2002). Genetic diversity in french bean under moisture stress condition. *Veg. Sci*. **29**(1): 37-39.

Gnanesh, B.N. (2005). Genetic variability and divergence studies by D^2 statistics and RAPD analysis in field bean (*Lablab purpureus* L. Sweet). M. Sc. Thesis, Acharya N. G. Ranga Agril. Uni. S.V. Agri. College, Tirupati.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean Lesedezo. *Agro. J*. **48**:268-272.

Hseieh, H.M., Pomeranz, Y. and Swanson, B.G. (1992). Composition, cooking time and maturation of Azuki (*Vigna angularis*) and common bean (*Phaseolus vulgaris*). **69**(3): 244-248.

Hussain, M.M. (2005). Yield and quality of Bush bean (*Phaseolus vulgaris* L.) genotypes as influenced by date of sowing. M.Sc. Thesis. BSMRAU, Gazipur, Bangladesh.

Immaculee, N. (2011). Genetic diversity in French bean (*Phaseolus vulgaris* L.) germplasm lines. M.Sc. Thesis. UAS, Bengaluru, India.

Johanssen, H.W. (1909). Elements Derexatelons Exblichkeitelahre. Jena Gustar, Fisher.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Genotypic and phenotypic correlation in soyabean and their Implication in selection. *Agron. J.* **45**:477-483.

Junaif, N., Wani, K.P., Khan, S.H., Jabeen, N. and Mushtaq, F. (2010). Genetic variability in dwarf French bean (*Phaseolus vulgaris* L.). *Asian J. Hort*. **5**(1): 117-118.

Kalia, N.R., Lal, M. and Kalia, R. (2001). Genetic divergence in common bean (*Phaseolus vulgaris* L). *Indian J. Agric. Res*. **35**(2): 139-140.

Kamaluddin S.A. (2011). Variability, correlation and path analysis for seed yield and yield related traits in common beans. *Indian J. Hort*. **68**(1): 5660.

Kapila, R.K., and Pawar, K.S. (1997). Genetic parameters and association analysis in rajmash. *Indian J. Pulses Res.* **10**(1): 38-41.

Karasu, A. and Oz, M. (2010). A study on co-efficient analysis and association between agronomical characters in dry beans (*Phaseolus vulgaris* L). *Bulg. J. Agric. Sci*. **16**: 203-211.

Kumar, N. (1997). Collection and evaluation of land races diversity in bean (*Phaseolus vulgaris*) from north western Himalayas. *Prog. Hort.* **29**(3-4): 160-164.

Kumar, P. A., Reddy, R. V. S. K., Pandravada, S. R., Rani, Ch.V.D. and Chaitanya, V. (2014). Phenotypic variability, correlation and path coefficient analysis in pole type French bean (*Phaseolus vulgaris* L). *Plant Arch*. **14**(1): 313-319.

Kumar Swamy, A.G. (1990). Genetic variability studies in French bean (*Phaseolus vulgaris* L). M.Sc. Thesis. Univ. Agric. Sci. Bangalore, India. Pp 1-93.

Kumara, B.M.D., Shambulingappa, K.G., Kulkarni, R.S., Swamy, G.S.K. and Lohithashwa, H.S. (1997). Analysis of genetic variability and character association in Rice bean (*Vigna Umbellata*). *Mysore J. Agric. Sci*. **31**: 23-28.

Kumari, V., Arora, R.N. and Singh, V.P. (2003). Variability and path analysis in grain cowpea. Scientific Publishers (India), Jodhpur. Pp: 59-62.

Kurek, A. J., Carvalho, F. I. F., de Assmann, I. C., Marchioro, V. S. and Cruz, P. J. (2001). Path analysis as an indirect selection criterion for bean grain yield. *(Portuguese) Rev. Brasileira Agrociencia.* **7**(1) 29-32.

Lima, R.B.S., Gonçalves, J.F.C., Pando, S.C., Fernandes V. and Santos, A.L.W. (2008). Primary metabolite mobilization during germination in rosewood (*Aniba rosaedora* Ducke) seeds. *Rev Árvore*. **32**: 19-25.

Lu, W., & Chang, K. C. (1996). Correlation between chemical properties and canning quality attributes of navy beans (*Phaseolus vulgaris* L.). *Cereal Che*. **73** (6): 785-787.

Lush, J.L. (1940). Inter-sire correlation and regression of offspring on damasasa method of estimating heritability characters. *Proc. Amer. Soc. Anim. Prod*. **33**:293–301.

Lush, J.L. (1949). Heritability of quantitative characters in farm animal. Heriditas.**35**: 256-261.

Mahalanobi's, P.C. (1936). On the generalized distances in statistics. *Proc.Natl. Acad. Sci*., India. **2**: 49-55.

Makhdoomi, M.I. and Dar, S.A. (2011). Genetic variability, heritability and genetic advance in dry bean (*Phaseolus vulgaris* L.). *Trends Biosciences*. **4**(1) 44-46.

Mandal, N. and Dana. (1998). Genetic variability and path coefficient analysis in rice bean. *Annual Agric. Res*. **19**(1): 107-109.

Manivannan, N. and Nadajarajan, N. (1996). Character association and component analysis in Green gram. *Madras Agric. J*. **83**(2): 782784.

Mather, K. (1949). Biometrical Genetics: The study of continuous variation. Methuen and Co., Ltd., London.

Mcclean, P.E., Myers, J.R. and Hammond, J.J. (1993). Coefficient of parentage and cluster analysis of North American dry bean cultivars. *Crop Sci*. **33**:190–197.

Mehra, R., Tikle, A.N., Saxena, A., Munjal, A., Rekhakhandia and Singh, M. (2016). Correlation, path-coefficient and genetic diversity in Blackgram (*Viginamungo* (L) Hepper). *Intl. Res. J. Plant Sc*. **7**(1): 001-011.

Mishra, S.N. and Dash, S.N. (1991). Variability for quantitative characters in French bean (*Phaseolus vulgaris* L). *J. South. Indian Hortic.* **39**:285-288.

Mishra, H.N. Killadi, B. and Mishra, R.C. (1996). Character association and path-coefficient analysis in pole type French bean. *Environ. Eco*. **14**(1): 103-106

Mishra, S., Kumar, M. and Sahu, G. S. (2008). Relationships among yield contributing characters in pole type French bean (*Phaseolus vulgaris* L.). *Orissa J. Hortic.* **36**(2) 108-113.

Mittal, V.P. and Singh, P. (2005). Component analysis of yield and other characters in Green gram. *J. Arid Leg*. **2**(2): 408-409.

Moniruzzaman, M., Halim, G.M.A. and Firoz, Z.A. (2009). Performances of French bean as influenced by plant density and nitrogen application. *Bangladesh J. Agric. Res*. **34**(1): 105-111.

Murthy, G.S. and Pavate, M.V. (1962). Studies on quantitative inheritance in Nicotiana tabacum L. varietal classification and selection of multivariate analysis. *Indian J. Genet. Plant Breed*. **22**: 68-69.

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

Nadarajan, N. and Gunasekaran, M. (2005). Quantitative genetics and biometrical techniques in plant breeding. Pp: 50-54.

Nandi, A., Tripathi, P. and Samal, K.M. (1996). Variability genetics in pole French bean (*Phaseolus vulgaris* L.) mutant lines. ACIAR *Food Legume Newsl.* **24**: 7-8.

Nandi, A., Tripathy, P., Lenka, D. and Dhal, A. (1998). Genetic studies in pole French bean mutants: variability and performance. ACIAR *Food Leg. Newsl*. 27, 89.

Nandi, A., Tripathi, P. and Lenka, D. (2000). Genetic divergence in hyacinth bean (*Dolichos lablab*). *Indian J. Agric. Sc*. **70**(7): 450-451.

Narsinghani, V. G. and Saxena, A. K. (1991). Character associationship in French bean *Agron. J.* **48**(2)**:** 274-276.

Neupane, R.K., Shrestha, R., Vaidya, M.L. and Bhattarai, Ek.M. (2003). Agromorphological diversity in Common bean (*Phaseolus vulgaris* L.) landraces of Jumla, Nepal. In: Proceedings of 2nd SAS-N Convention, 30 July - 1 August 2003, Kathmandu (Agricultural Research for Enhancing Livelihood of Nepalese People Kathmandu. Joshi, B.K, Joshi, S.L. and Paudyal, K.P. (Eds.) 2004.

Newell, L.C. and Eberhart, S.A. (1961). Clone and progemy evaluation in the improvement of switch grass (*Panicum virgatum*). *Crop Sci*. **1**: 117-121.

Nienhuis, J. and Singh, S.P. (1986). Combining ability analyses and relationships among yield, yield components and architectural traits in dry bean. *Crop Sci*. **26**:21–27.

Noor, F. Hossain, F. and Ara, U. (2014). Screening of french bean (*Phaseolus vulgaris* L.) genotypes for high yield potential. *Bangladesh J. Sci. Ind. Res*. **49**(4): 227-232.

Oboh, H.A., Muzquiz, M., Burbano, C., Cuadrado, C., Pedrosa, M.M., Ayet, G. and Osagie, A.U. (1998). Antinutritional constituents of six underutilized legumes grown in Nigeria. *J.Chromatogr A*. 828. 307- 312.

Omoigui, L.O., Ishiyaku, M.F., Kamara, A.Y. and Alibi, S.O. (2006). Evaluation of cowpea accessions for the southern Guinea Savannah. *Top. Sci*. **46**:227-232.

Oseni, T.O. Lence, D.D. and Pal, V.R. (1992). Correlation and path coefficient analysis of yield attributes in diverse lines of cowpea (*Vigna unguiculata* L.). *Indian J. Agri.Sci*. **62**: 365-368.

Padi, K.F. and Edhlers, D.F. (2008). Effectiveness of early generation selection in cowpea for grain yield and agronomic characters in semi-arid West Africa. *Crop Sci*. **48**:533-540.

Patil, J.V., Mutker, M.L. and Nimbalkar, V.S. (1993). Variability and character association in French bean. *J. Maharashtra Agril. Univ.* **18**: 76-78.

Pande, G.K., Seth, J.N. and Lal, S.D. (1975). Variability and correlation studies in dwarf French bean in relation to green pod yield. *Punjab Hort. J.* **15**: 126-131.

Pandey, Y.R., Gautam, D.M., Thapa, R.B., Sharma, M.D. and Paudyal, K.P. (2011). Variability of French bean in the western mid hills of Nepal. *Kasetsart J., Natural Sciences*. **45**(5) 780-792.

Prakash, K.S. and Ram, H.H. (1981). Path coefficient analysis of morphological traits and development stages in French bean. *Indian J. Agric. Sci*. **51**: 76-80.

Prakash, J. and Ram, R.B. (2014). Genetic variability, correlation and path analysis for seed yield and yield related traits in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions. *Intl. J. Innovative Sci., Engineeri. Tech*. **1**(6): 41-50.

Prakash, Jay., Ram, R.B. and Meena, M.L. (2015). Genetic variation and characters interrelationship studies for quantitative and qualitative traits in French bean (*Phaseolus vulgaris* L.) under Lucknow conditions. *Legume Res*. **38**(4) 2015:425-433.

Prasad, V.S.R. (1995). Genetic divergence of yield and its components in bush bean. *Indian J. Hort*. **52**: 46-50.

Raffi, S.A. and U.K. Nath. (2004). Variability, heritability, genetic advance and relationships of yield and yield contributing characters in dry bean (*Phaseolus vulgaris* L.*). J. Biological Sci*. **4**: 157-159.

Rai, N. Asati, B.S. Yadav, D.S. and Singh, A.K. (2004). Genetic analysis in French bean (*Phaseolus vulgaris* L.). *Veg. Sci*. **31**(2): 138-141.

Rai, N., Asati, B.S., Singh, A. K. and Yadav, D. S. (2006). Genetic variability, character association and path coefficient study in pole type French bean. *Indian J. Hort.* **63**(2): 188-191.

Rai, N., Asati, B.S. and Singh, A. K. (2009). Genetic divergence in Indian bean. *Legume Res.* **32**(2): 166-172.

Rai, N. Singh, P.K. Verma, A. Yadav, P.K and Choubey, T. (2010). Hierarchical anal ysis forgenetic variability in pole type French bean. *Indian J. Hort.* **67**(special issue): 150-153.

Rangaiah, S., Nehru, S.D. and Mahadevu, P. (1999). Genetic studies in two cross derivatives of French bean (*Phaseolus vulgaris* L.). *Mysore J. Agric. Sci*. **33**:125-129.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrica Research, John Wiley and Sons. New York. Pp: 357-369.

Reddy, D.M., Rao, Y.K., Murty, S.S.N. and Reddy, M.V. (2004). Genetic variability and divergence in Mung bean. *Indian J. Pulses Res*. **17**: 77-79.

Robinson, H. F., Comstock, R. E. and Harvey, P. (1966). Quantitative genetics in relation to breeding on the centennial of mendelism. *Indian J. genet.* **26**:171-177.

Rodiño, A.P., Santalla, M., Montero, I., Casquero, P.A. and de Ron, A.M. (2001). Diversity of common bean (*Phaseolus vulgaris* L.) germplasm from Portugal. *Genet. Resourc. Crop Evolution*. **48**: 409-417.

Rodiño, A.P., Santalla, M., De Ron, A.M. and Singh, S.P. (2003). A core collection of common bean from the Iberian Peninsula. *Euphytica*. **131**: 165-175.

Roy, S.K. (2004). Characterization and yield variation in bush bean (*Phaseolus vulgaris* L.) genotypes. M.S.Thesis. BSMRAU, Gazipur.

Rubatzky, V.E. and M. Yamaguchi. (1997). World vegetables: Principles, production, and nutritive values. *Intl. Thomson Publ*. Florence, KY, USA.

Sabokdast, M. and Khyalparast, F. (2008). A study of relationship between grain yield and yield component in common bean cultivars (*Phaseolus vulgaris* L.). (Persian) *J. Sci. Techno. Agric. Natural Resources.* **11**(42A): 123-134.

Saha, P., Hazra, P. and Maity, T.K. (1990). Genetic variability and correlation studies in french bean (*Phaseolus vulgaris* L.). *Veg. Sci*. **17**(2): 213-216.

Saifullah, M. and Rabbani, M.G. (2009). Evaluation and characterization of okra (*Abelmoschus esculentus* L. Moench.) genotypes. *SAARC J. Agri.* **7**(1): 92-99.

Salunkhe, D. K., Sathe, S. K. and Deshpande, S.S. (1989). French bean. CRC Handbook of World Food Legumes: Nutritional Chemistry, Processing Technology, and Utilization, D. K. Salunkhe and S. S. Kadam, eds. CRC Press: Boca Raton,FL. **2**: 23.

Samal, K.M., Senapati, N., Lenka, D., Nandi, A. and Tripathy, P. (1995). Varietal performance, genetic variability and correlation in rajmash (*Phaseolus vulgaris* L.). *Legume Res*. **18**: 223-227.

Sarafi, A. (1978). A yield component selection experiment involving American and Iranian cultivars of common bean. *Crop Sci*. **18**: 5-7.

Sarangi, S.K. and De, L.C. (2010). Varietal evaluation of French bean (*Phaseolus vulgaris* L.) at mid-hills of Arunachal Pradesh. *Indian J. Hill Farming*. **23**(2): 53-54.

Savitha, B.N. (2008). Characterization of Avare (*Lablab purpureus* L.Sweet) local collections for genetic variability. M.Sc. (Agril.) Thesis. UAS, Dharwad.

Schoonhoven, A.V. and Voysest, O. (1991). Common Bean Research for crop improvements. Red wood press Ltd., melksham, witshine. Pp: 7-42.

Scully, B.T., Vallace, D.H. and Viands, D.R. (1991). Heritability and correlation of biomass, growth rates, harvest index, and phenology to the yield of common beans. *J. Amer. Soc. Hort. Sci*. **116**: 127- 130.

Seth, J.N., Pandey, G.K., Lal, S. D. and Solanki, S.S. (1972). Genetic variability in dwarf French bean (*Phaseolus vulgaris* L.) under rainfed conditions of U. P. hills., *Prog. Hort*. **4**(2): 63-70.

Shah, D., Pant, C. C. and Solanki, S.S. (1999). Studies on agroeconomic traits and genetic parameters in French bean (*Phaseolus vulgaris* L.). *Prog. Hortic*. **31**: 3/4: 194-198.

Sharifi, P. (2014). Correlation and path coefficient analysis of yield and yield component in some of broad bean (*Vicia faba* L.) genotypes. *Genetika*. **46** (3): 905 - 914.

Sharma, R.N., Pandey, B.L. and Chitale, M.W. (1998). Genetic variability and character association for yield components in Rice bean germplasm. *Indian J. Pulses Res*. **11**(20): 127-128.

Sharma, M.K, Smaranika, M. and Rana, N.S. (2009). Genetic divergence in French bean (*Phaseolus vulgaris* L.) pole type cultivars. *Legume Res*. **32**(3): 220-223.

Shettar, B.I., Vijayakumar, S. and Setty, M.V.N. (1975). Path analysis of pod yield components in snap bean (*Phaseolus vulgaris* L). *Maysore J. Agric.Sci*. **9**: 649-651.

Shimelis, E.A. and Rakshit, S.K. (2005). Proximate composition and physico-chemical properties of improved dry bean (*Phaseolus vulgaris* L.) varieties grown in Ethiopia. *Food Sci. and Tech. Int*. **38**: 331-338.

Shinde, S.S. and Dumbre, A.D. (2001). Correlation and path coefficient analysis in French bean. *J. of Maharashtra Agric. Univer.* **26**(1): 48-49.

Siddiq, M., Ravi, R., Harte, J.B. and Dolan, K.D. (2010). Physical and Functional Characteristics of Selected Dry Bean (*Phaseolus vulgaris* L.) *Flours. J. Food Sci. Tech*. **43**: 232-237.

Siddique, J.A. and Gupta, S.N. (1991). Genotypic and phenotypic variability for yield and other traits in cowpea (*Vigna unguiculata* L.). *Int. J. Tropical Agric*. **9**: 55-62.

Singh, R.K. and Caudhary, B.D. (1977). D^2 analysis in: Biometrical Methods in Quantitative Genetic Analysis. *Kalynai Pub*., New Delhi. Pp 304.

Singh, K.N., Santoshi, U.S and Singh, I.B. (1985). Path Coefficient study in pea. *Indian J. Genet*. **45**:499-504.

Singh, S.P., Gepts, P. and Debouck, D.G. (1991). Races of common bean (*Phaseolus vulgaris*, Fabaceae). *Econ. Bot*. **45**:379-396.

Singh, D.N., Nandi, A. and Tripathy, P. (1993). Performance of French bean (*Phaseolus vulgaris* L) cultivars in non-central plateau zone of Orissa. *Indian J. Agric.Sci*. **63**: 658-659.

Singh, D.N., Nandi, A. and Tripathy, P. (1994). Genetic variability and character association in French bean. *Indian J. Agri. Sci*. **64** (2): 114-116.

Singh, R.V. (2000). Response of French bean (*Phaseolus vulgaris* L.) to plant spacing and nitrogen, phosphorus fertilization. *Indian J. Hort*. **57**(4): 338-341.

Singh, A.K., Singh, K.P. and Singh, B.K. (2007). Genetic variability, heritability and genetic advance in French bean (*Phaseolus vulgaris* L.). *Haryana J. Hort. Sci*. **36**(3): 352-353.

Singh, A.K., Tomer, A.K., Tyagi, K. and Singh, P. P. (2007). Stability analysis for yield and its components in French bean (*Phaseolus vulgaris* Lam.). *Legume Res.* **30**(3) 166-172.

Singh, K.P., Jattan, M. and Bhardwaj, M. (2007). Genetic variability in French bean (*Phaseolus vulgaris* L.). *Res. Crops*. **8**: (3) 636-637.

Singh, D. and Mishra, A.K. (2008). Studies on genetic divergence in pea (*Pisum sativum* L.). *Agric. Sci. Digest*. **28**(1): 77-78.

Singh, D.N., Sivakumar, R. and Bhanja, P.K. (2011). Variability and character association in new genotypes of French bean. *Environ. Eco.* **29**(4): 1811-1813.

Sivasubramania, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J*. **60**:1139.

Subhadeep, N. and Korla, B.N. (2004). Path analysis of some quantitative characters in dwarf French bean (*Phaseolus vulgaris* L.) in relation to pod yield Legume Research. **27**(3): 228-230.

Sureja, A.K. and Sharma, R.R. (2001). Genetic divergence in Garden Pea (*Pisum sativum* L. subsp. *hortense* Asch and Graebn). *Veg. Sci*. **28**(1): 63-64.

Tamilselvan, A., and Das, L.D.V. (1994). Correlation in French bean (*Phaseolus vulgaris* L.) for seed yield. *Madras Agric. J*. **81**: 445-446.

Teixeira, A.B., Amaral-Junior, A.T. do., Rodrigues, R., Pereira, T.N.S. and Bressan-Smith, R.E. (2004). Genetic divergence in snap-bean (*Phaseolus vulgaris* L.) evaluated by different methodologies. *Crop Breed. Applied Biotec*. **4**:57-62.

Thaware, B.L., Birari, S.P. and Apte, U.B. (1997). Genetic divergence in forage cowpea. *Legume Res*. **20**(3-4): 236238.

Toker, C. and Cagirgan, M.I. (2004). Use of phenotypic correlations and factor analysis in determining characters for grain yield selection in chickpea (*Cicer arietinum* L.). *Hereditas*. **140**(2):226-228.

Topwal, M., Gaur, G. and Kaintura, P. (2016). Correlation coefficients study on different quantitative characters in French bean (*Phaseolus vulgaris* L.). *J. Plant Sci. Res.* **1**(1): 1-7

Ulukan, H., Mustafa, G. and Siddik, K. (2003). A Path Coefficient Analysis Some Yield and Yield Components in Faba Bean (*Vicia faba* L.) Genotypes. *Pakistan. J. Biol. Sci*. **6**: 1951-1955.

Upadhayay and Mehta, N. (2010). Biometrical studies in Dolichos Bean (Dolichos lablab L.) for Chattisgarh Plains. *Res. J. Agri. Sci*. **1**(4): 441-447.

Vasic, M., Gvozdanovic-Varga, J., Cervenski, J., Jevtic, S. and Lazic, B. (1997). The interdependence of morphological characters in Yugoslavian bean varieties (*Phaseolus vulgaris* L.). *Acta Hort.* **462**: 235-241.

Venkatkrishnakishore, Navale, P.A. and Gandhi, S.D. (2002). Relationship between yield and component characters in Green gram under summer condition. *J. Maharashtra Agic.Univ.* **27**: 303- 304.

Verma, V.K., Jha, A.K., Pandey, A., Kumar, A., Choudhury, P. and Swer, T. (2014). Genetic divergence, path coefficient and cluster analysis of French bean (*Phaseolus vulgaris*) genotypes. *Indian J. Agri. Sci.* **84** (8): 925–30.

Westermann, D. T. and S. E. Crothers. (1977). Plant population effects on the seed yield components of beans. *Crop Sci*. **17**: 493-496.

Wright, S. (1921). Correlation and Causation. *J. Agric. Res*. **20**: 557-585.

Wu, Xiaojun. (2002). Correlation of physico- chemical characteristics in the seed coat and the canning quality in different dark red kidney beans. The Graduate School, University of Wisconsin-Stout.

www.banglapedia.com

www.digitalglobe.com

www.plantsciences.ucdavis.edu/gepts/a1749.pdf

www.whfoods.com

Yadav, N., Yadav, D. S., Patel, R. K. and Rai, R. K. (2001). Variability, correlation and path-coefficient analysis in between seed morphology and seedling growth in French bean. *J. Assam Sci. Society*. **42**(1):40-43.

Yadav, K.S., Yadava, H.S. and Naik, M.L. (2003). Correlation and path analysis in early generations of cowpea. *Indian. J. Pulses Res*. **16**(2): 101-103.

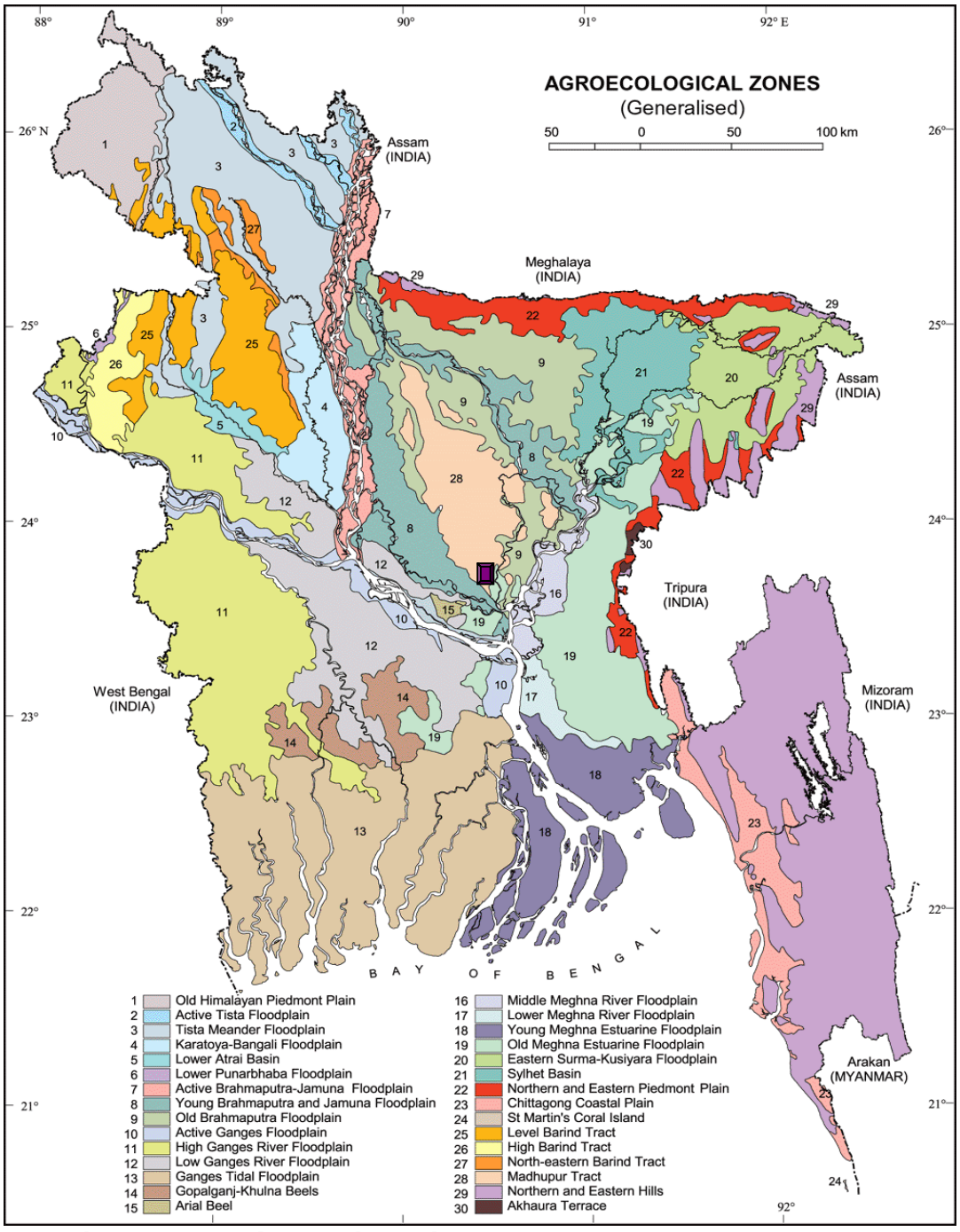
Yoshida, K., Satoh, H., Ishii, N., and Takahashi, U. (1988). Differences in protein content rates in Hokkaido azuki (in Japanese). *Nippon Sakumotsu Gakkai Kiji*. **57**:119.

Zeven, A.C., Waninge, J., Hintum, Th. Van and Singh S.P. (1999). Phenotypic variation in a core collection of common bean (*Phaseolus vulgaris* L.) in the Netherlands. *Euphytica.* **109**: 93-106.

Appendices

APPENDICES

Appendix I. Map showing the experimental site of the study



The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity, Total Rainfall and Sunshine of the experimental site from the period of October, 2016 to March, 2017

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2016	33.8	25.0	81.83	0	5.8
November, 2016	29.3	18.3	72	0	7.9
December, 2016	27.0	17.0	89	0	3.9
January, 2017	26.2	16.1	67	0	5.7
February, 2017	28.9	23.0	45	0	8.7
March, 2017	29.8	20.5	65	0.1	7.3

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargaon, Dhaka - 1212

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
P^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV. Mean performance of various growth parameter and yield components of Kidney bean

Genotypes	LS	FF	50%F	M	FPS	PH	NL	NPP	LA	PL	PdL	PdD	DWP	NSP	1000SW	SY	Y
G1	13.67	34.00	36.00	79.00	38.67	36.59	14.00	21.33	158.84	8.37	11.00	8.13	1.91	4.12	277.54	66.17	1.47
G2	7.33	33.00	36.00	80.00	39.33	33.33	12.67	14.44	161.95	10.77	10.67	7.81	1.84	4.03	370.11	73.37	1.63
G3	7.33	30.00	33.67	79.33	37.67	24.17	15.33	25.67	123.72	6.70	10.30	7.33	2.17	4.60	278.00	101.07	2.25
G4	7.33	32.33	36.00	80.00	39.00	29.67	16.47	27.93	121.09	9.30	11.09	7.03	2.33	4.70	290.24	112.03	2.49
G5	7.67	30.00	34.33	80.00	37.33	30.00	18.33	27.67	169.59	9.00	11.18	8.35	2.50	5.04	283.36	115.07	2.56
G6	7.67	30.00	34.33	78.00	39.33	29.72	21.93	30.68	169.67	12.67	12.38	7.48	2.75	5.50	318.21	120.43	2.68
G7	7.67	33.67	35.33	79.67	39.33	28.50	14.73	15.49	83.80	6.93	10.47	8.12	1.92	3.44	348.97	99.47	2.21
G8	8.00	30.00	33.33	82.33	38.67	29.73	14.00	14.13	147.69	9.80	10.33	8.04	1.79	3.76	335.77	88.80	1.97
G9	12.67	38.67	42.00	89.33	47.00	36.38	13.83	17.67	152.89	12.48	8.00	8.36	1.92	4.03	291.70	72.60	1.61
G10	8.67	35.67	38.67	86.00	42.00	24.43	13.00	14.33	127.85	8.07	8.67	7.76	1.91	4.64	299.86	78.60	1.75
G11	7.00	30.00	33.33	82.33	36.67	30.30	17.00	22.00	106.04	8.90	9.99	7.76	2.05	4.53	338.86	90.15	2.00
G12	13.33	34.33	36.67	78.00	41.33	20.53	14.67	19.17	114.67	7.33	9.99	8.33	1.62	4.19	443.33	81.15	1.80
G13	9.00	30.33	34.33	80.33	38.67	24.64	13.40	16.00	104.08	7.37	9.51	8.40	1.69	3.98	337.05	64.05	1.42
G14	9.33	34.67	37.00	78.67	39.67	26.89	11.93	20.67	106.00	7.37	9.60	7.41	1.43	4.10	244.61	84.00	1.87
G15	7.67	30.00	35.00	82.67	39.00	33.33	16.37	18.67	117.33	7.17	9.63	7.21	1.42	4.17	213.64	58.50	1.30
G16	7.67	34.00	37.33	82.33	39.67	31.79	14.67	19.67	108.10	8.47	10.09	8.92	1.27	4.23	245.77	51.30	1.14
G17	12.00	31.67	33.67	80.67	38.33	29.00	9.17	12.50	94.33	5.87	6.67	7.85	1.11	3.37	277.45	38.55	0.86
G18	11.67	31.00	33.00	85.33	38.33	27.21	7.93	10.67	91.33	5.43	6.53	8.37	1.00	3.23	225.32	35.85	0.80
Min	7.00	30.00	33.00	78.00	36.67	20.53	7.93	10.67	83.80	5.43	6.53	7.03	1.00	3.23	213.64	35.85	0.80
Max	13.67	38.67	42.00	89.33	47.00	36.59	21.93	30.68	169.67	12.67	12.38	8.92	2.75	5.50	443.33	120.43	2.68
Average	9.20	32.41	35.56	81.33	39.44	29.23	14.41	19.37	125.50	8.44	9.78	7.92	1.81	4.20	301.10	79.51	1.77

LS = Days to 5 leaves stage
FF =Days to 1st Flowering
50%F = Days to 50% flowering
M= Days to Maturity
FPS = Days to 1st Pod Setting
PH = Plant Height (cm)
NS = No of Leaves
NPP = No of Pod/Plant
LA = Leaf Area (cm²)
PL = Petiole Length (cm)
PdL= Pod Length (cm)
PdD = Pod Diameter (cm)
DWP = Dry Weight of Pod
NSP = No of Seeds/Pod
1000SW= 1000 Seed Weight
SY = Seed Yield (g/Plant)
Y = Seed Yield (g/Plant)

Appendix V: Maximum, minimum, mean and LSD value with standard error of seventeen parameters of Kidney bean

Parameters	Minimum	Maximum	Mean	CV(%)	SE	$LSD_{0.05}$
Days to 5 leaves stage	7.00	13.67	9.20	8.53	0.642	2.431
Days to 1st Flowering	30.00	38.67	32.41	3.47	0.932	3.526
Days to 50%	33.00	42.00	35.56	3.16	0.928	3.511
Days to Maturity	78.00	89.33	81.33	3.27	2.190	8.271
Days to 1st Pod	36.67	47.00	39.44	3.48	1.130	4.278
Plant Height (cm)	20.53	36.59	29.23	9.55	2.350	8.884
No of Leaves	7.93	21.93	14.41	7.94	0.933	3.529
No of Pod/Plant	10.67	30.68	19.37	10.66	1.700	6.442
Leaf Area (cm^2)	83.80	169.67	125.50	4.14	4.330	16.396
Petiole Length (cm)	5.43	12.67	8.44	4.73	0.337	1.276
Pod Length (cm)	6.53	12.38	9.78	9.05	0.724	2.739
Pod Diameter (cm)	7.03	8.92	7.92	8.47	0.549	2.739
Dry Weight of Pod	1.00	2.75	1.81	5.88	0.087	0.330
No of Seeds/Pod	3.23	5.50	4.20	5.06	0.174	0.657
1000 Seed Weight	213.64	443.33	301.10	20.21	49.210	18.218
Seed Yield (g/Plant)	35.85	120.43	79.51	17.75	11.450	4.325
Yield	0.80	2.68	1.77	17.77	0.255	0.964

Appendix VI: ANOVA table for nutrient components of Kidney bean

Source of Variance	Degrees of freedom	Protein	Moisture	Fat	Fiber	Ash	Carbohydrate
Treatments	17	10.50**	1.41**	0.267**	0.336**	0.386**	11.107**
Error	36	0.0161	0.0048	0.014	0.0013	0.0035	0.7068