GENETIC VARIABILITY OF YIELD AND QUALITY CHARACTERS OF MUNGBEAN (*Vigna radiata* L.)

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GENETIC VARIABILITY OF YIELD AND QUALITY CHARACTERS OF MUNGBEAN (*Vigna radiata* L.)

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CERTIFICATE

This is to certify that thesis entitled, "Genetic variability of yield related traits and quality characters of Mungbean (Vigna radiata L.)" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by Munni Akter, Registration number 12-04774 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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(Prof. Dr. Naheed Zeba)
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ABSTRACT

An experiment was conducted to study the genetic variability analysis based on different yield contributing and quality traits of Mungbean genotypes in Sher-e-Bangla Agricultural University, Dhaka-1207 and Bangladesh Council of Scientific and Industrial Research, Bangladesh during Rabi season (2019). In case of morphological traits, analysis of variance revealed significant differences among all the genotypes for all the characters. Number of pod per plant showed highest range of variation (53.67-16). That means wide range of variation present for this character .High heritability coupled with high genetic advance in percent of means were observed number of cluster per plant, number of pod per plant, pod length, number of seed per pod, thousand seed weight. The significant positive correlation with grain weight per plant was found in number of cluster per plant, number of pod per cluster, pod length, thousand seed weight at genotypic level and phenotypic level, number of pod per plant at phenotypic level. Path co-efficient analysis showed that number of per pod per plant, pod length, number of seed per pod, thousand seed weight had significant positive direct effects on yield. It had also significant positive correlation with yield. The maximum inter cluster distance was observed between the cluster I and V indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population. In case of eleven qualitative traits, the analysis of variances showed significant mean squares for different characters that indicated the presence of sufficient variation among the genotypes for all the characters. High heritability coupled with high genetic advance in percent of means were found for all traits. The significant positive correlation with protein percentage was found in fiber at genotypic and phenotypic level. Path co-efficient analysis showed that potassium %, and phosphorous % had direct positive effect on protein % and fiber had significant positive correlation with matter protein %. The highest inter genotypic distance was observed between G1 and G7. Considering group distance and other agro-morphological and qualitative performance, genotypes G4 and G6 found to be potential for future hybridization program in the response of increase yield and hybridization between G1 and G15 respond to increase nutrient content.

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Some commonly used abbreviations

Full word	Abbreviations	Full word	Abbreviations
Abstract	Abstr	Journal	J.
Advances/Advanced	Adv.	Limited	Ltd.
Agriculture	Agric.	Ministry	Min.
Agricultural	Agril.	Murate of Potash	MP
Bangladesh Bureau of Statistics	BBS	Percentage	%
Biology	Biol.	Phenotypic Coefficient of Variation	PCV
Botany	Bot.	Physiology	Physiol.
Breeding	Breed.	Principle Component Analysis	PCA
Centimeter	Cm		
Coefficient of variance	CV	Proceedings	Proc.
Cross between two dissimilar parents	X	Randomized Complete Block Design	RCBD
Degree Celsius	°C	Research	Res.
Division	Div.	Review	Rev.
Economic	Econ.	Science	Sci.
Environment	Environ.	Society	Soc.
Etcetera	etc.	Statistics	Stat.
Experimental	Expt.	That is	i.e.
Food and Agricultural Organization	FAO	The First Generation of a cross between two dissimilar parents	F_1
Gazette	Gaz.		
General	Gen.	Ton per Hectare	ton/h
Genetics	Genet.	Triple Super Phosphate	TSP
Gram	G	University	Univ.
Horticulture/ Horticultural	Hort.	Variety	Var
		Vegetable	Veg.
Incorporated	Inc.	Videlicet (namely)	viz.
Information	Inf.	Weight	Wt.
International	Intl.	Yield Per Plant	YPP

CHAPTER I

INTRODUCTION

Pulses are the cheapest and most vastly consumed source of protein in the world, having predominantly vegetarian population. On an average, pulses contain almost 20-28% protein, which is 2.5 to 3.0 times higher than that of cereals (Hall *et al*., 2016). Besides protein, it is also rich source of amino acid, vitamins and minerals essential for human nutrition. Thus, increased production and higher consumption of pulses is one of the best solution to overcome the wide spread malnutrition problem in the developing countries. Besides, pulses are also important for sustainable agriculture as they improve physical, chemical and biological properties of soil and function as mini nitrogen factory by fixing atmospheric nitrogen.

Among the various pulse crops grown in our country, mungbean (*Vigna radiata* L.) is the most important. Mungbean, also known as moongor green gram and belongs to the family Fabaceae of the order Leguminales (Chauhan *et al*., 2018). It is a highly self-pollinated crop having somatic chromosome number 2n =2x =22. Mungbean is grown principally for its proteinous seeds that are used as human food. The protein present in mungbean is of highly digestible nature and therefore, it is recommended as a medical diet in case of flatulence. The whole or split seeds of mungbean are eaten after boiled as Dal. Mungbean has established itself as a highly valuable short duration grain legume crop having many desirable characteristics like wider adaptability, low input requirement and ability to improve the soil fertility by fixing atmospheric nitrogen with the help of symbiotic bacteria, *Rhizobium* present in root nodules. Mungbean is the most widely distributed and cultivated in the world. Bangladesh, India, Pakistan, Myanmar, Bhutan, Thailand, Malaysia, Philippines, Afganistan, China, Indonesia and Iran are the major mungbean producing countries. It holds 4th position among all the pulses in production and area coverage in Bangladesh.

The last documented area under this crop in Bangladesh is 102838 acres with production of 39187 M.tons (BBS, 2018). But it is very low. The main reason for low productivity is the lack of high yielding and disease resistant mungbean varieties, adapted to different regions, seasons, cropping system and agronomic conditions. Thus, there are urgent needs of high yielding, disease resistant varieties of mungbean suited to different situation so that this crop can fulfill its potential in combating the malnutrition prevalent in primarily vegetarian population of our country.

Genetic variability is the 1st stem for a successful breeding program for any crop species and a successful survey of genetic variability is important before aiming to high yielding variety development. The correlation co-efficient among yield components usually show a complex chain of interacting relationship. Path co-efficient analysis partitions the components of co-relation co-efficient into direct and indirect effects and visualizes the relationship in more meaningful way. Multivariate statistics help the researcher to summarize data and reduce the number of variables necessary to describe it (Anderson, 2003). The multivariate techniques comprise of cluster analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. To select germplasm in a more systemic and effective way and to develop strategies to incorporate useful diversity in their breeding programs, study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationships among accessions (Lavanya*et al.*, 2008). Multivariate technique also plays an important role in choice of divergent parents for hybridization to exploit maximum heterosis.

Yield is the ultimate target product in Bangladesh aspect. Recently we achieved self- sufficiency in food crops. Now we have to proceed towards quality research on food crops. Approximately one billion people in developing country suffer from malnutrition (FAO, 2015) caused by a lack of food of sufficient dietary quality particularly proteins and minerals.

Thus there is an emergent recognition of mungbeanas a cheap produce for combating food insecurity and malnutrition. Because of mungbean's short growth duration (2-3 months), mungbean is considered to be a suitable crop for rotation with cereal crops in Asia (Tsou *et al.*, 1979). It is now required to screen out the suitable genotype of mungbean of higher yield and better quality.

It is essential to have proper understanding on genetic variability of a biological population. A survey of genetic variability with the help of suitable parameter such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start a breeding program. Genetic variation of various attributes is useful for effective selection. These yield contributing attributes are correlated with pod yield and also among themselves. Path analysis find out the real contribution of these traits to yield and desired genotypes can be traced through diversity analysis.

Keeping this view in mind, for better genotype searching as well as find out a better parent for hybridization, a study was conducted on diverse mungbean genotypes using agro-morphogenic and quality characters with the following objective:

- To assess the magnitude of genetic divergence among the genotypes of mungbean based on their yield and quality traits.
- To measure the association of yield related trait and their contribution towards yield.
- To provide farmers with better and superior genotype of mungbean.

CHAPTER II

REVIEW OF LITERATURE

The requirements for the preservation of wild species, local varieties and traditional genotypes in gene banks have become a vital frame of gene maintenance (Gepts, 2006). The accessions preserved in the gene banks should be well-characterized and evaluated in order to determine the magnitude of genetic diversity, which would allow the identification of redundant accessions and genotypes of interest in breeding programmes (Balestre*et al.*, 2008; Terzopoulos and Bebeli, 2008). Many studies have been done using different genes to examine the genetic diversity of mungbean.

2.1 Origin and Distribution

Mungbean is an annual herbaceous legume belonging to the family papilionaceae, includes the genus *vigna*, and subgenus Ceratotropis distinguished two species *Vigna radiata*, the mungbean, and *Vigna mungo*, the black gram. The origin and progenitor of mungbean is *V. sublobatus*, according to Verdcourt (1970). The primary center of origin of mungbean are the mountainous regions of Southwest-Asia, particularly Indian subcontinent (Blixt, 1970). The genus *Vigna* is originated in tropical region and now has been broadened to include about 170 species: 120 from Africa, 22 from Indo-Pak subcontinent and Southeast Asia and a few from other parts of the world (Ghafoor *et. al.* 2001). The subgenus Ceratotropis is considered to have originated in Asia and is called Asian Vigna. It forms a discrete group of about seventeen species largely confined to Asia and the Pacific.

2.2 Morphology

Mungbean is an annual herbaceous plant. It has a tap root system, stems are slender usually branched, and upright in growth, and leaves are pinnately compound with three to several leaflets. There are large stipules clasping the stem. The inflorescence is raceme arising from the axil of a leaf. The lowest node at which flower initiation occurs is quite constant under a given set of conditions and used for classifying the varieties with respect to flowering and fruiting duration.

2.3 Genetic Variability

Genetic variability is the pre-requisite for any crop improvement programme, since this not only works as a working branch on which selection operates but also provides valuable information regarding selection of diverse parents to be used in ahybridization programme. Plant breeders consider the concept of heritability, a corner stone upon which much of quantitative genetic theory practice and accomplishment is built. The idea of heritability offers an index of the transmissibility to measure the genetic relationship of the characters in the population. Lush (1947) defined heritability in broad sense as well as narrow sense. Broad sense heritability is the properties of total genetic variance to the total phenotypic variance similarly the narrow sense heritability are the ratio of additive genetic variance to the total phenotypic variance. The estimates of genetic advance as percentage of mean provide more reliable information regarding the effectiveness of selection. Thus the estimates of genetic variability, heritability and genetic advance are great significance to plant breeder for developing suitable breeding strategy. Man studies conducted as variability, heritability and genetic advance for different characters in mungbean by different workers.

Mehandi *et al*. (2018) studied 48 mungbean genotypes to study genetic variability, heritability and genetic advance for yield and 13 yield associated traits. The analysis of variance revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability among the 48 genotypes for all the traits studied. The highest genotypic coefficient of

variations was found for characters viz., harvest index, number of effective branches/plant. The heritability highest was observed for seed yield per plant, days to maturity and days to 50% flowering. The higher estimates of heritability indicated that these characters were less affected by the environment and under the control of additive gene effect. High heritability and high genetic advance as percent of may be attributed due to additive gene action. Therefore, direct selection for characters viz., number of effective branches/plant, number of pods/cluster, number of seeds/pod would be effective and therefore, considered to be of prime importance in formulating the selection programme. In both environments high estimates of variation were observed for number of effective branches/plant, seed index, seed yield/plant, biological yield/plant and harvest index, it indicates the existence of enormous inherent variability that remains unaltered by environmental conditions among the genotypes, which is more useful for exploitation in selection and hybridization programme. Consequently, based on the genetic parameter analysis days to 50% flowering, number of effective branches/plant, seed index, seed yield/plant, biological yield/plant and harvest index should be given significant precedence while formulating a selection strategy for effective improvement of mungbean varieties. Similarly, Ahmed *et al.* (2016) evaluated different mungbean varieties/ lines for their quality characteristics like proximate composition, phosphorus contents and yield. Grain samples of two local varieties (AZRI-Mung 2006 and NM-2006) and four promising lines (M-6, No. 07007, No. 98004 and No. 97001) were collected and analyzed for dry matter, nitrogen free (NFE) moisture, crude protein, crude fat, ash, crude fiber, phosphorus and using standard testing methods. Results revealed that maximum grain yield (986 t/ha) was recorded in Line No. 98004 and minimum (801 t/ha) in NM-2006. However dry matter (95.19%), ash (4.00%), crude fiber (3.66%), crude protein (25.61%) and phosphorus contents (0.36%) were higher in AZRI-Mung-2006 as compared to other varieties/ lines.

A research was performed on genotypic and phenotypic variation, heritability and genetic advance that expressed as percentage of mean for yield and yield contributing traits were studied in 14 genotypes of mungbean (*Vigna radiata* L.). Genotypic and phenotypic variances were high for number of pods per plant (18.60 and 19.50) and days to maturity (16.39 and 17.69). Heritability was high for 100-seed weight (0.99) and lowest for seed yield per plant (0.42). High heritability with high genetic advance as percentage of mean for number of pods per plant showed the additive gene effect for these characters. Analysis of variance for parameters showed the significant variations for all variables under consideration. Genotype 8010 produced maximum number of pods per cluster (3.72) and number of pods per plant (27.33). Maximum plant height (41.23) was recorded for genotype 8003 while genotype 98002 took maximum days to flowering (49.66) and days to maturity (86.66). Similarly, maximum 100-seed weight (5.64) and seed yield per plant (13.76) were recorded in genotypes 8004 and 8002, respectively. Existing variation may helpful for selection and further hybridization breeding program in future (Ahmed *et al*., 2014). Again, Li *et al.* (2010) studied sixteen mungbean varieties for their proximate composition and protein isolates' properties. A wide range of variation was observed: crude protein content ranged 24.26–28.50%, crude fiber 3.21–4.18%, crude fat 0.57–1.86%, ash content 3.64–4.24%, moisture 7.49–8.45% and carbohydrates 54.25–58.69%, respectively. The content of protein, ash, fat and moisture in isolated proteins ranged from 69.22% to 74.85%, 2.19% to 3.04%, 0.36% to 0.64% and 8.20% to 9.28%, respectively. The functional properties of isolated proteins analysed including water absorption capacity, oil absorption capacity, foaming capacity, foam stability, emulsifying activity and protein solubility, which ranged from 1.03 g,1 to 2.78 g, 1.00 mL to 3.38 mL, 33.00% to 67.50%, 56.00% to 20.00%, 1.77 mL to 3.30 mL and 28.7% to 65.52%, respectively. Properties of mungbean protein isolates except oil absorption capacity were similar to most of legumes' but lower than soybean's.

A wide range of phenotypic and genotypic coefficient of variation (PCV and GCV) were observed for number of seeds per plant, followed by seed yield per plant, number of pods and number of branches per plant by Kumar *et al.* (2010). High heritability was observed for number of pods per plant, followed by seeds per plant, days to flowering, number of branches per plant, days to poding and days to maturity, selection on the basis of phenotypes is expected to be effective for the traits. Abrahim *et al.* (2007) evaluated genetic variability and heritability analyses for yield and yield components which were conducted for 646 accessions of green gram grown in Coimbatore, Tamil Nadu, India, during the Rabi and Kharif of 2002-04. The estimates of phenotypic (PCV) and genetic (GCV) coefficients of variation were higher for single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height, and length of branch, indicating greater scope of selection for these traits. Dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values, indicating the highly significant effect of environmental factors. The number of days to initial flowering, number of days to 50% flowering, number of days to initial maturity, number of days to full maturity, 100-seed weight, seed length, seed breadth, length of pod, and protein content were less affected by environmental factors, as the difference between the estimates of PCV and GCV was low. The estimates of heritability in the core collection indicated that the number of days to full maturity, number of days to initial maturity, number of days to initial flowering, number of days to 50% flowering, seed length, seed breadth, plant height, length of branch, 100-seed weight, and length of pod were highly heritable. High genetic advance as a percentage of mean was recorded for the number of clusters per branch, length of branch, single plant yield and number of pods per plant, number of clusters per plant, plant height and number of branches per plant, suggesting the possibility of selection for these traits in the core collection. High genetic advance coupled with high heritability and GCV was observed for length of branch, number of branches per plant, number of clusters per branch, number

of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for this traits.

Makeen *et al.* (2007) studied twenty diverse mungbean genotypes which were evaluated in Uttar Pradesh, India, to estimate the genetic variation, heritability, genetic advance for 10 quantitative characters. The genotypes differed significantly for all characters studied. Maximum heritability values were recorded in seed protein content, plant height and test weight. High heritability coupled with high genetic advance was observed in pods per plant, plant height and test weight, indicating the importance of additive gene effect for the expression of these characters. Again, Rao *et al.* (2006) studied sixty genotypes of mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India for 13 characters to assess genetic variability, heritability and genetic advance. Total dry matter, plant height, number of pods per plant and yield per plant exhibited high variability and heritability coupled with genetic advance, indicating the influence of additive gene action.

Significant differences for yield and yield attributing traits was observed by Kapoor *et al.* (2005). Number of primary branches, pod length, plant height, pods per plant, seeds per plant, 100 seed weight and seed yield per plant, pods per plant exhibiting high phenotypic coefficient of variability, heritability and genetic advance. Sirohi*et al.* (2006) observed significant variability for clusters per plant, productive branches per plant, productive pods per plant, biological yield and seed yield. High estimates of heritability and genetic advance were observed for 100 seed weight, while moderate heritability and high genetic advance were observed for clusters per plant and productive pods per plant.

Parameswarappa (2005) observed a wide range of genotypic and phenotypic variability. The association of high heritability with high genetic advance was observed in pods per plant, indicating the presence of additive gene effects and high genetic gain from phenotypic selection. High heritability with low genetic gain was observed for test weight and yield per plant. The correlation

co-efficient at the genotypic level were generally higher than the corresponding phenotypic level. Path coefficient analysis indicated that pods per plant had the highest positive direct effect followed by test weight. The positive direct effect of plant height (0.024) and number of branches (0.120) were highly substantiated by positive indirect effects of pods per plant, which ultimately resulted in significant positive correlation of these two characters with yield per plant.

In a study performed by Reddy *et al*. (2003), thirty-six genotypes of mungbean for genetic variability of seed yield and its contributing characters in summer 2000 at Tirupati, Andbra Pradesh, India. High magnitude of variability was observed for pods per plant and grain yield per plant, while moderate variability was recorded for pods per cluster, clusters per plant, plant height and days to 50% flowering suggesting the possibility of their improvement by selection. High heritability coupled with high genetic advance was observed for pods per plant, grain yield per plant, pods per cluster, clusters per plant, plant height and days to 50% flowering, while high heritability and moderate genetic advance was recorded for seeds per pod, 100- seed weight and days to maturity suggesting that these traits were controlled by additive gene action. In another study, Khairnar*et al.* (2003) evaluated twenty-two mungbean genotypes for genetic variability in the kharif season of 1997, in Rahuri, Maharashtra, India. A wide range of variability was observed for plant height, clusters per plant, pods per plant, grain yield per plant and 100 grain weight. The estimates of genotypic as well phenotypic coefficients of variation were highest for pods per plant followed by 100-grain weight. High heritability coupled with high genetic advance was observed for clusters per plant, pods per plant, grain yield and 100- grain weight indicating that these characters can be improved by selection. Das *et al.* (1998) reported that plant height, branches per plant pods per plant, pod length and yield per plant had high genotypic coefficient of variation suggesting the possibility of improvement of mungbean by selection breeding. High heritability associated with high genetic advance over mean was observed for plant height, branches

per plant, pod per plant and pod length. It indicated that these traits were mostly controlled by additive gene action. Seeds per pod and yield per plant recorded low heritability and high genetic advance.

Loganathan *et al.* (2001) reported high phenotypic coefficient of variability indicated the favourable effect of environment for number of clusters per plant, seed yield per plant and high genotypic co-efficient of variability suggested substantial amount of genetic variability for number of pods per plant and seed yield per plant . High genetic advance additive gene action and phenotypic selection were effective for number of pods per plant, seed yield per plant and number of seeds per pod. Kumar *et al.* (2001) observed analysis of variance indicated the existence of significant differences among the genotype for the entire 13 trait studied. Plant height exhibited maximum range of variation, while proline content exhibited maximum range of variation. The maximum genotypic and phenotypic co-efficient of variation were observed for seed yield per plant. High heritability correlated with high genetic advance as percentage of mean were recorded for 100 -seed weight, plant height, primary branches per plant, secondary branches per plant, proline content and seed yield per plant.

High estimates of coefficient of genetic variation, heritability and genetic advance for plant height, clusters per plant and biological yield in mungbean was reported by Vikas*et al.* (1998) noted. They also observed moderate to high genetic variance, heritability and genetic advance for plant height, clusters per plant, pods per plant, days to maturity and biological yield. Sharma (1999) observed high heritability and high genetic advance for days to flowering, pods per plant, seed per pod, 100-seed weight and seed yield in mungbean. Venkateswarlu (2001) observed most of the characters showed high heritability. The seed yield expressed high genetic advance coupled with high heritability and GCV indicating the predominance of additive gene effects for this trait.

Pundir *et al.* (1992) found high estimates of heritability for yield and its components studied by evaluating 351 germplasm collections. The estimates of genetic advance were also high for seed yield, pods per plant and 100-seed weight. Hamid *et al.* (1996) observed high heritability coupled with high genetic advance for plant height, seed size and pods per plant in 24 genotypes of mungbean. Byregowda *et al.* (1997) reported high heritability along with genetic advance for seed yield and pods per plant in mungbean which was attributed to additive gene action. Miah and Bhadra (1989) noted high values of expected genetic advance for number of pods per plant and seeds per pod among the eight yield components in seven varieties of mungbean and their 21 F2 hybrids and 21 reciprocals. Sarma and Talukdar (1991) observed high heritability and genetic advance for primary branches, pods per cluster and cluster per plant in induced micro-mutants of mungbean. Parida (1982) observed high heritability estimates for seed weight, pods per plant and seeds per pod, it was lowest for yield per plant in green gram. Yield had the highest genetic advance in F 2 generation. Natrajan*et al.* (1988) recorded highest heritability for 100 seed weight followed by days to flowering, plant height and pod length while seed yield showed the highest genetic advance as percent of mean followed by height, 100-seed weight and pods per plant. Similar result was observed by Singh and Malhotra (1970) where he observed high heritability for seed weight in green gram which was also accompanied with high genetic advance, indicating that heritability could be due to additive gene action. High genetic advance also observed for pod number, branch number and seed yield. Sawarkar (1978) observed high heritability accompanied with high expected genetic advance for clusters per plant, grains per plant, number of pods per plant indicated that it was due to additive gene effects.

2.4 Correlation and Path Co-Efficient Analysis

The basic concept of correlation was developed by Golton (1889). Later on Fisher (1918) and Wright (1921) elaborated and discussed its importance in plant breeding. The degree of correlation between two observable characters

based on phenotypic value of the traits is known as simple correlation or total correlation or phenotypic correlation. It includes both genotypic and environmental effects and therefore differs under, different environmental condition. Environmental correlation is a measure of environmental influence. On the covariance between the two characters in question Johnson *et al.* (1955) pointed out that genotypic correlation coefficient provide a measure of association between characters at genotypic level and give an indication of the characters they may be useful as the indicators of the more important as under consideration. The basic concept of path coefficient analysis was formulated by Sewall Wright (1921). Path coefficient analysis provides an effective means of untangling the direct and indirect causes of association and permits the critical examination specific forces acting to produces given correlation and measure the relative importance of casual factors. Correlation between two characters is the result of direct effect of a characters as well as its indirect effect via other characters on the dependent characters like yield. Li (1956) emphasized the use of this technique in genetic and plant breeding studies later. Dewey and Lu (1959) applied it for the first time in plant breeding using wheat grass (*Agropyron crystatum*) as test genes the cause (various yield components) and effect (yield relationship) had been worked out by various workers in mungbean using path coefficient analysis.

In association analysis of Marappa *et al.* (2010), he revealed that yield is significantly and positively correlated with all the characters except seeds per pod at both genotypic and phenotypic level, path analysis revealed that pods per plant had maximum direct effect on seed yield at both phenotypic and genotypic level. The days to 50% flowering, primary branches per plant, clusters per plant, pod per plant, pod length and test weight recorded maximum positive indirect effect on yield via pods per plant. Singh *et al.* (2009) positive association at phenotypic and genotypic level was recorded between pods per cluster and seeds per pod; pods per plant and harvest index. Path analysis using phenotypic and genotypic co-relation identified biological yield per plant, cluster per plant and seeds per pod and were most important

direct and indirect yield components across three environments. Bais*et al.* (2007) observed that yield is significantly and positively correlated with pods/plant, pods per cluster, number of nodes per plant and nodal dry weight, path analysis showed that pods per plant, 100 seed weight and dry weight had significant direct positive effect on grain yield. The pods per cluster had indirect positive effect via pods per plant on grain yield. Thus the present study revealed that pods per plant, 100 seed weight and dry weight were the important components of grain yield in summer mungbean which may be exploited for the improvement of grain yield.

Sirohi *et al.* (2007) observed the maximum and positive genotypic correlation coefficient (0.86) was between pod length and seed yield per plant, whereas, maximum and positive phenotypic correlation co-efficient (0.496) was observed between days to 50% flowering with days to maturity. In general magnitudes of genotypic correlation coefficients were higher than there corresponding phenotypic correlation co-efficient. Path coefficient analysis revealed that at phenotypic level, harvest index showed maximum (0.46) direct and positive contribution towards seed yield.

Verma and Garg (2007) observed the genotypic correlations were higher than the phenotypic correlation. Seed yield per plant showed positive association with biological yield and harvest index while it was negatively associated with days to 50% flowering. The path analysis revealed the seed yield per plant was influenced directly by biological yield and harvest index. It was indirectly influenced by days to 50% flowering and plant height via biological yield and harvest index. It is considered for improving the seed yield of mungbean. Similarly, Makeen *et al.* (2007) studied twenty diverse mungbean genotypes which were evaluated in Uttar Pradesh, India to estimate correlation coefficient for 10 quantitative characters. Higher genotypic and phenotypic coefficients of variation were observed for seed yield and number of pods per plant. Character association indicated that pods per plant and plant height had significant positive correlation with seed yield. Sirohi and Kumar (2006),

studied correlation analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*Vigna radiata*) grown in Berthin, Himachal Pradesh, India, during the spring of 1999. The genotypic correlation was dominant to the phenotypic correlation. The number of clusters per plant and number of productive pods per plant exhibited significant and positive correlation with seed yield per plant.

Rao *et al.* in 2006 studied sixty genotypes of mungbean (*Vigna radiata*) which were evaluated during 2000 in Guntur, Andhra Pradesh, India.Total dry matter and number of pods per plant had direct positive effect on seed yield while plant height had negative effect. Dhuppe*et al.* (2005) studies on co-relation and path analysis which were carried outin 35 genotypes (1 parental lines and 24 hybrids) of mungbean, grown in Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Path analysis revealed that the number of seeds per plant and 100-seed weight were the major yield contributing characters. The performance of Jal-781 x AKM9504 and Jal-781 K-H x AKM-9242 were found.

Dhuppe *et al.* (2005) studies on correlation which were carried out in 35 genotypes (11 parental lines and 24 hybrids) of mungbean, grown in Parbhani, Maharashtra, India, in 1998. Data were recorded for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per plant, 100-seed weight and yield per plant. Grain yield per plant showed positive and significant correlation with days to maturity, number of secondary branches per plant, number of pods per plant and 100seed weight at genotypic level, whereas secondary branches per plant and100-seed weight were correlated with grain yield at phenotypic level. 1781 K-H x AKM-9242 were found. Similarly Pandey *et al.* (2002) studied yield correlations and

performance of green gram cultivars MT 552 PS 16, ML 371, LM 1510, PDM 11, Pusa Baishakhi 1. PDM 84- 139, PDM 54, ML 374 and ML 574 in rice-wheat cropping system in a field experiment conducted in Meerut, Uttar Pradesh, India during the kharif season of 1998 and summer of 1999. Grain yield had significant positive association with number of seeds per pod and test weight. A 300% cropping intensity can be achieved using the compatible cultivars of rice (Pant Dhan 12 or 10), wheat (UP 233 8/PBW 343) and green gram (PS 16).

Rajan *et al.* (2000) were studied the correlation in 7 parents and F2 population of their 21 crosses in green gram for 13 characters. Seed yield had significant positive genotypic correlation with number of secondary roots at maturity, dry weight of plants at maturity, plant height, pods per plant, seeds per pod and thousand grain weight and harvest index. Number of pods, pod per plant and harvest index showed high positive correlation on grain yield and also with each other. Again, Islam *et al.* (1999) studied on genetic correlation on 9 yield components in 53 genotypes studied in Joydebpur during 1993.Yield per plant was significantly and positively, correlated with plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and 1000-seed weight. Sharma (1999) studied on correlation coefficients is derived from data on 9 yield-related traits in 15 mungbean crosses and their six parents grown at Raipur during 1995-96. Seed yield was significantly correlated with branches/plant, seeds/plant, pods/plant, pod clusters/plant, seeds/plant and 1000 seed weight. In an evaluation, Niazi*et al.* (1999) genotypic correlation and path-coefficient analysis for 8 agronomic characters affecting seed yield which was accomplished in 15 elite genotypes of mungbean. All the correlation coefficients were significant, whilst number of filled pods per plant, plant height, number of columns and seed per pod and number of clusters per plant revealed a strong positive association with seed yield per plant. Pods per plant emerged as a reliable component that can serve as a selection criterion in breeding high yielding cultivars of mungbean. Makeen *et al.* (2007) examined twenty diverse mungbean genotypes and

found maximum direct effect on seed yield was observed in pods per plant, test weight andplant height. Sirohi and Kumar (2006) also studied path-coefficient analysis for yield and yield components which were conducted for 19 diverse genotypes of mungbean (*Vigna radiata*) grown in Berthin, Himachal Pradesh, India, during the spring of 1999. All the traits except plant height and number of productive branches per plant had higher magnitude of indirect effects than the direct effects on seed yield per plant. The number of productive branches per plant had a direct significant contribution to seed yield per plant. Vikas *et al.* (1999) studied correlation coefficient and direct and indirect relationship of component characters with seed yield in mungbean over environments and reported that genotypic correlations were higher than their corresponding phenotypic correlation. Seed yield per plant showed positive association with number of cluster per plant, umber of pods per plant, number of seeds per pod, 100 -seed weight and harvest index. The path analysis revealed that seed yield per plant was influenced directly by biological yield and harvest index in most of the environments. Reddy *et al.* (2005) observed that the number of seeds per plant was significantly and positively correlated with plant height and number of clusters per plant at both genotypic and phenotypic level. The seed yield /plant was significantly and positively associated with the number of seeds per pod, test weight, days to maturity and days to 50% flowering at the genotypic level and with number of pods per plant at the phenotypic level. Path analysis indicated that plant height, days to 50% flowing and test weight had the highest direct effect on seed yield.Kalpande*et. al.* (1997) reported significant positive association of seed yield with primary branches and clusters per plant on the basis of evaluation of 24 mungbean lines for 12 yield components in all the three environment viz. Kharif, late kharifand Rabi. Path analysis revealed that primary branches and secondary branches per plant had direct positive effect on seed yield through days to 50% flowering, secondary branches per plant, clusters per plant, pods per cluster and seeds per pod were important in almost all the three environments. Yaqoob *et al.* (1997) reported that seed

yield had a positive genotypic association with days to 50% flowering, number of branches, number of pods per plant, number of clusters, 100 seed weight, dry matter yield and harvest index. Path coefficient analysis revealed positive direct effects of days to 50% flowering, days to maturity, number of branches, 100-seed weight, dry-matter yield and harvest index on seed yield. In a similar study, Hamid *et al*. (1996) observed significantly positive correlation of seed yield with pods per plant, pod length and seeds per pod along with negative association with seed size. Sharma and Talukdar (1996) studied correlation and path analysis for yield components in 34 M7 generations of green gram micro-mutant lines and their 2 base genotypes. They found that seed yield per plant was positively correlated with plant height, number of primary branches, pods per cluster, days to maturity, seeds per pod and 100-seed weight. Plant height and pods per cluster had maximum direct effect on seed yield per plant. Sharma and Gupta (1994) carried out correlation and path analysis in which seed yield was found to be positively correlated with biological yield per plant, harvest index, clusters per plant, pods per plant, plant height and 100-seed weight in mungbean. Path analysis showed biological yield per plant had positive direct effect on seed yield followed by harvest index, pods per plant, days to maturity, days to flowering, clusters per plant, 100 -seed weight and pod length. Considerable negative direct effects on seed yield per plant were exerted by seeds per pod, plant height and protein content in 32 lines of Mungbean x Mungbean crosses. Kumar *et al.* (1995) found that seed yield was significantly and positively correlated with pods per plant and 100 seed weight in mungbran (*Vigna radiata*). Hamid *et al.* (1996) observed significantly positive correlation of seed yield with pods per plant, pod length and seeds per pod along with negative association with seed size. Significant positive correlation was also found in the study of Pundir*et al.* (1992) for seed yield with number of branches, clusters and pods per plant, pod length, seeds per pod and 100-seed weight. The significant and positive correlation between branches per plant clusters per plant and pods per plant and 100-seed weight were also observed.

In path analysis, pods per plant and 100-seed weight emerged as characters making marked positive direct and indirect effects on seed yield. Holker and Raut (1992) observed significant positive correlation between seed yield and 100 seed weight, pods per plant and pod length. Patil and Deshmukh (1988) noted significant positive association of seed yield with 100 seed weight, seeds per pod and pods per plant. Path analysis indicated days to flowering and 100 seed weight were the most important positive direct contributors towards seed yield while days to maturity and seeds per pod showed negative direct effects on seed yield. Singh (1985) studied inter relationship of yield and its components in F3 progenies of a cross (T-44 X K-851). They observed that seed yield per plant was significantly and positive by associated with pods per plant, primary branches per plant, clusters per plant, pod length, seeds per pod and 100- seed weight in mungbean. Path analysis revealed pods per plant was the most important yield contributing characters. Khan and Ahamed (1989) identified branch number per plant, pods number per plant and seeds per pod were the major contributors of seed yield on the basis of correlation and path co-efficient analysis. Satyan *et al.* (1989) noted that seed yield was positively and significantly correlated with plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length and days to maturity in (*Vigna radiate* (L.) Wilczek).Chaudhary (1985) observed highest positive association of seed yield with number of seeds per pod, followed by branches per plant and clusters per plant in mungbean. The negative estimates of correlation of seed yield with plant height and 100 seed weight were recorded. Strong positive co-relation between cluster per plant and pods per plant; branches per plant and clusters per plant was observed. Path analysis identified seeds per pod and clusters per plant are most important yield influencing traits. Nafade (1988) reported that plant height, number of cluster per plant, number of pods per plant, number of seed per pod and shelling percentage showed significant and positive correlation with seed yield at genotypic level whereas, path analysis revealed that number of pods per plant,

plant height, number of seeds per pod and shelling percentage were the major yield contributing characters.

CHAPTER III

MATERIALS AND METHODS

This chapter covers the detailed methodology used in the execution of the experiment. The experiments were then divided into two parts viz. **Experiment 1:** Evaluation of mungbean genotypes based onagro-morphogenic traits, and **Experiment 2:** Evaluation of mungbean genotypes based on quality analysis. The different steps of the experiments are described here chronologically in section 3.1 and in 3.2 respectively.

3.1 Experiment 1:Evaluation of mungbean genotypes based on agro-morphogenic traits

It encompasses a brief description of the experimental site, planting materials, climate and soil, seedbed preparation, layout and design of the experiment, land preparation, manuring and fertilizing, intercultural operations, harvesting, data collection procedure, statistical procedure etc., which are presented as follows:

3.1.1 Experimental site

The experiment was conducted in the experimental field of Sher-e-Bangla Agricultural University, Dhakaduring the period from March 2019 to June 2019. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meters from the sea level in Agro-ecological zone of "MadhupurTract" (AEZ-28) (Anonymous,1999). The experimental site is shown in the map of AEZ of Bangladesh in (Appendix I).

3.1.2 Planting materials

The materials were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh Agricultural Development Corporation, (BADC) the name and origin of these genotypes are presented in Table 1 and seeds are shown in Plate 1.

Table1. List of twenty-three mungbean genotypes used in the study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Source of collection
1	G1	BARI Mug 1	BARI
2	G2	BARI Mug 2	
3	G3	BARI Mug 3	
4	G4	BARI Mug 4	
5	G5	BARI Mug 5	
6	G6	BARI Mug 6	
7	G7	BARI Mug 7	
8	G8	BARI Mug 8	BADC
9	G9	BINA 5	
10	G10	BINA 8	
11	G11	PPD 28	BARI
12	G12	PPD 29	
13	G13	PPD 30	
14	G14	PPD 31	
15	G15	PPD 32	
16	G16	PPD 33	
17	G17	PPD 35	
18	G18	PPD 36	
19	G19	PPD 37	
20	G20	PPD 38	
21	G21	PPD 39	
22	G22	PPD 40	
23	G23	PPD 41	

BARI=Bangladesh Agricultural Research Institute

BADC= Bangladesh Agricultural Development Corporation

Plate 1. Seeds of twenty-three mungbean genotypes used in the experiment.

3.1.3 Soil

The soil belongs to "The Modhupur Tract", AEZ-28 that comprises of silty clay in texture at the top, olive-graycolored clay loam with common fine to medium distinct dark yellowish brown mottles. The pH was in 5.63 and 0.82% organic carbon content (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were collected from the Bangladesh Meteorological Department, Agargaon, Dhaka(Appendix III).

3.1.4 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The field size was 20 m × 20 m. Line to line distance was 30 cm. The whole field was divided into three unit plot. In each plot 23 genotypes were planted in three replications.

3.1.5 Land preparation

The experimental plots were ploughed and brought into a fine tilth and the recommended dose of fertilizers and farmyardmanure (FYM) was applied. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done in March 2019. Land preparation is shown in Plate 2A.

3.1.6 Manure and fertilizers application

Total cow dung, zinc sulphate, boric acid and Triple Super Phosphate (TSP) were applied in the field during final land preparation. Half Urea and half Muriate of Potash (MOP) were applied in the plot after three weeks of seedling. Remaining Urea and Muriate of Potash (MOP) were applied after five weeks of transplanting. Doses of manure and fertilizers used in the study are presented in Table 2. Picture of fertilizer application is shown in Plate 2B.

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

Sl. No.	Fertilizers/ Manures	Dose	
		Applied in the plot	**Quantity/ha**
1.	Urea	2.08 kg	52 kg
2.	TSP	1.66 kg	41.5 kg
3.	MOP	3.8 kg	95 kg
4.	Cow dung	Applied earlier	3 ton
5.	Zinc Sulphate	330 gm	8.25 kg
6.	Boric Acid	350 gm	8.75 kg

3.1.7 Seed sowing

Seeds of the 23 genotypes were sown directly in line on 17thMarch, 2019. Seed sowing is presented in Plate 2C and seed germination is shown in Plate 2D.

3.1.8 Intercultural operations

When the seedlings were well established, first weeding was done uniformly in all the plots. Second weeding was done after 20 days of the first one. During early stages of growth tagging (Plate 3A), draining (Plate 3B) and pruning was done by removing some of the lateral branches to allow the plants to get more sunlight and to reduce the self-shading and incidence of increased insect infestation. First thinning was done 20 days after sowing (DAS). 2nd thinning was done 15 days after the first and 3rd and 4th were done 15 days interval for proper growth and development of the seedlings.

3.1.9 Harvesting and processing

Different genotypes matured at different times. The harvesting was completed on 16 June 2019. Pods were harvested when fruits were matured turning into

Plate 2. Process of land preparation to seed sowing A. Field preparation, B. Fertilizer application, C. Seed sowing, D. Seed germination.

Plate 3. Intercultural operation to data collection process. A. Tagging, B. Making drain for irrigation, C. Harvesting, D. Data collection.

brown in color. The pods per plant were allowed to ripe properly and then seeds were collected. Harvesting is shown in Plate 3C.

3.1.10 Data recording

Data collection is shown in Plate 3D. Ten plants in each replication of each genotype were selected randomly and were tagged. These tagged plants were used for recording observations for the following characters.

3.1.10.1 Days to 50% flowering

The number of days was counted from the date of sowing to days to 50% flowering.

3.1.10.2 Days to maturity

The number of days was counted from the date of sowing to first harvesting.

3.1.10.3 Plant height at vegetative Stage (cm)

The plant height was measured before flowering started from ground level to tip of the plant and mean was calculated.

3.1.10.4 Plant height at maturity (cm)

The average plant height at the matured stage was measured from ground level to tip of the plant.

3.1.10.5 Number of branches per plantat maturity

Number of branch of each plant was counted.

3.1.10.6 Number of Leaf per plantat maturity

Average number of leaves in each genotype from each plant was counted.

3.1.10.7Stem length (cm)

Average length of stem was measured.

3.1.10.8 Root length (cm)

Average length of the root was measured.

3.1.10.9 Number of cluster per plant

The number of clusters per plant was recorded at the time of harvesting.

3.1.10.10 Number of pod per cluster

Three clusters in each plant were taken at random and the number of pod in each cluster was counted. Then the average number of pod per cluster was calculated.

3.1.10.11 Number of pod per Plant

The number of pod per plant was recorded.

3.1.10.12 Pod Length (cm)

Average length of the pod was measured.

3.1.10.13 Number of seed per Pod

The total number of seeds from the five pods of individual genotype was counted and the average number of seeds per pod was calculated.

3.1.10.14 Grain weight per Plant (g)

The total seed from the five plant of individual genotype was weighted and the average weight of seeds per plant was calculated.

3.1.10.15 Thousand seed weight (g)

Weight of thousand seeds from each of the genotype which are randomly selected was recorded and expressed in grams.

3.1.10.16 Number of secondary root per plant

Number of secondary root of the each plant was counted.

3.1.10.17 Nodule number

Number of nodule in the root of each plant was counted.

3.2 Experiment 2:Evaluation of mungbean genotypes based on quality trait analysis

It comprises a brief description of quality traits.The experiment was conducted in the Bangladesh Council of Scientific and Indrustrial Research, during the period from July 2019 to September 2019.The quality traits included chlorophyll content, percentage of moisture, protein, ash, fat, carbohydrate and different minerals, data collection procedure, statistical procedure etc. are presented as follows:

3.2.1 Chlorophyll content

Leaf chlorophyll content was measured with SPAD-502 plus Portable Chlorophyll meter. The chlorophyll content was counted from four different portion of the leaf from five leaves of same genotype and then averaged for analysis. Process is shown in Plate 4A.

3.2.2 Moisture percentage

In Plate 4(B-D) moisture percentage determination is shown. 0.8 g of sample in three replications was oven-dried at 105°C until weight remained constant (AOAC, 2000). Percentage moisture was calculated as:

$$\text{Moisture\%} = \frac{(\text{Fresh weight} - \text{Dry matter}) \times 100}{\text{Fresh weight}}$$

3.2.3 Percentage of Ash

3 g of sample was introduced into the porcelain crucible. The crucible and sample were carefully ignited over hot plate and heated until the sample was thoroughly charred. Then, it was placed in the muffle furnace at 600°C for 24 hours until residue was free from carbon. The crucible and ash were then cooled in the desiccators and weighed. The weighing, heating in the furnace and cooling were repeated until the constant weight was obtained. Process is shown in Plate 5. The ash content of sample was calculated as follows:

$$\textbf{\% of Ash} = \frac{(\text{After ignition weight} - \text{After dry weight}) \times 100}{\text{Sample weight}}$$

3.2.4 Percentage of Protein

Protein percentage was estimated in three steps-

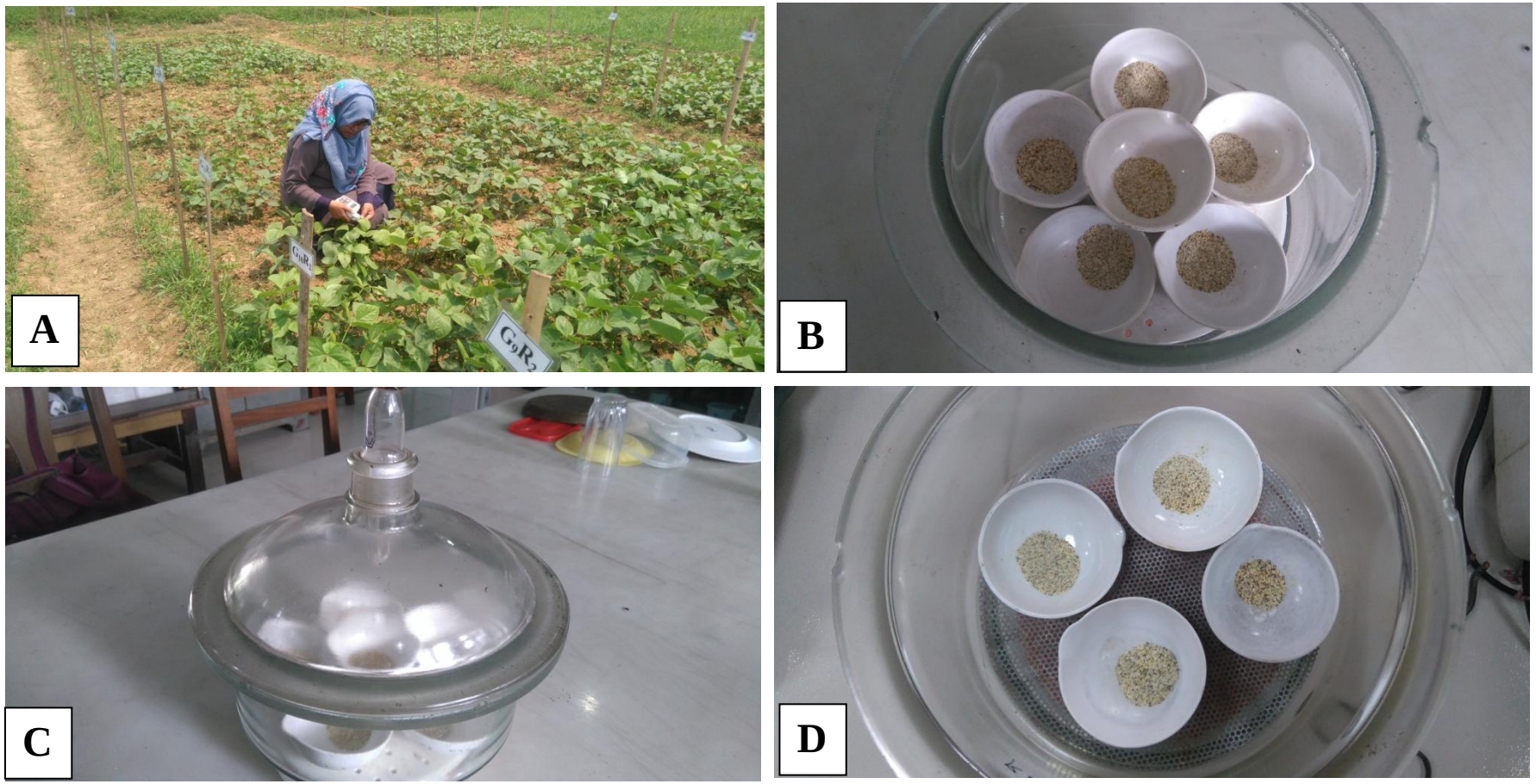

Plate 4. Determination of chlorophyll content and moisture percentage. A. Measurement of chlorophyll content, B. Sample in the basin in desiccator before dry, C, D. Sample in the basin in desiccator after dry.

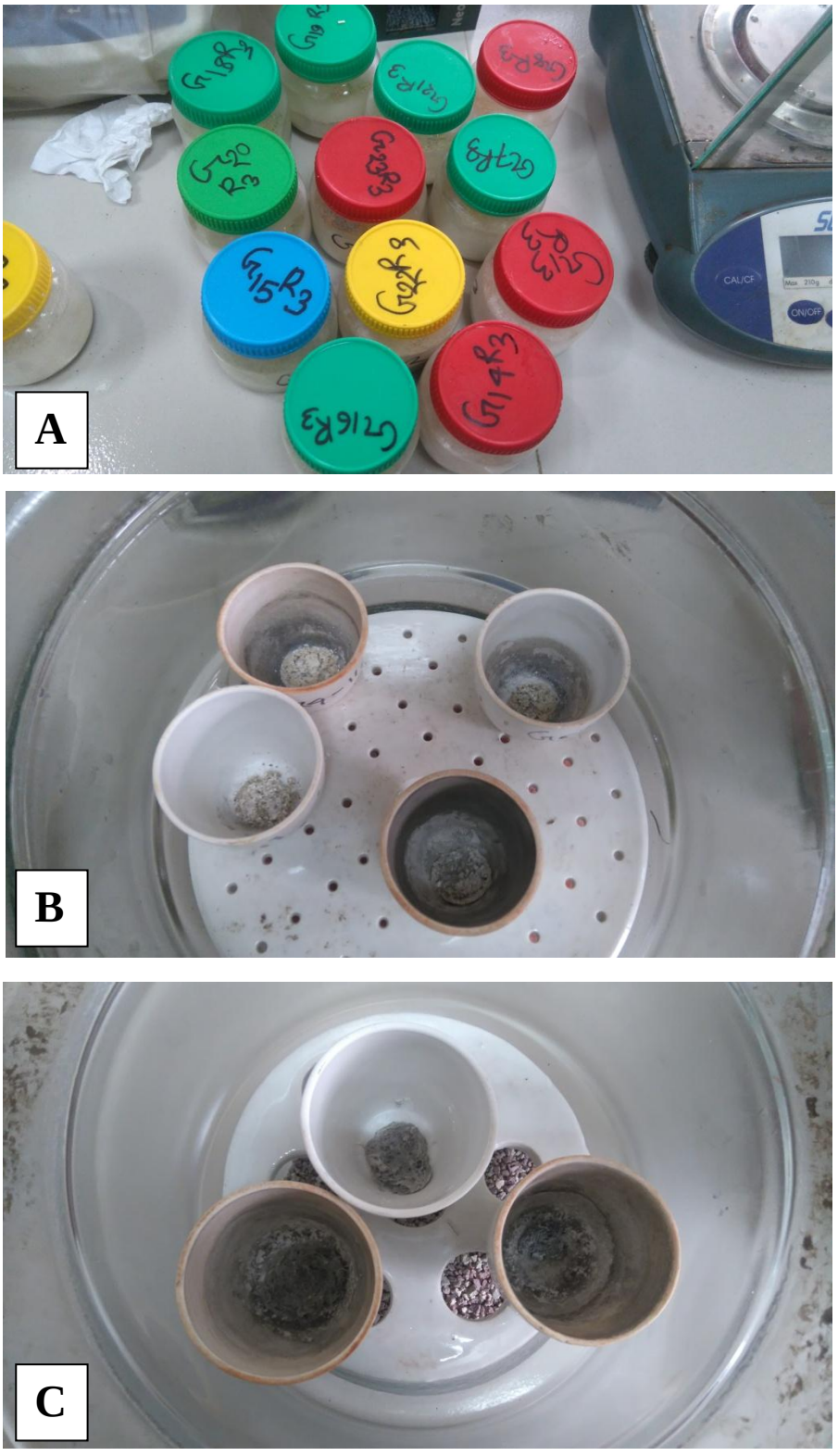

Plate 5. Determination of Ash percentage A. Sample as powdered form for analysis, B. Sample in crucible after dry, C. Sample in crucible after ignition.

3.2.4.1Protein digestion

98 g solid Sodium sulphate and 2 g powdered Copper sulphate were mixed properly in a mortar. 2 g of this mixture was kept into digestion tube. 20 mL concentrated H_2SO_4 and 0.6 g powder of mungbean grain was mixed in the digestion tube. This tube was kept in digestion chamber at 420^oC temperature for 1 hour. Then the solution was taken in 100 mL volumetric flask and volume it with distilled water. Digestion process is shown in Plate 6.

3.2.4.2 Protein distillation

10 mL Boric acid solution was taken in a conical flask. 2 drop methyl red indicator and 2 drop methyl blue indicator was put into the flask. The conical flask was kept inside the right portion of the distillation machine. 10mL sample solution was taken from the 100 mL volumetric flask into the distillation tube and kept in the left side in the machine and the machine was started. After 5 minutes the color turned from light purple into sky blue. Distillation process is shown in Plate 7.

3.2.4.3 Titration

0.02 normalHCl was taken in burette and titrated with the solution of the conical flask. Concentration of HCl was recorded at the point when the sky blue color of the conical flask changed into the previous light purple color. Titration process is shown in Plate 8. The protein calculation was as follows:

$$\% \text{ of Protein} = \frac{\text{NormallityofHCl} \times (\text{Titrati onreading} - \text{Blankreading}) \times 14 \times 6.25}{\text{Weightofsample}}$$

3.2.5 Percentage of Fat

8 g of the sample was taken inside the thimble and a piece of cotton was placed at the open end of the thimble. The thimble containing the sample was kept inside Soxhlet apparatus fixed with 500 mL round bottom flask containing 250 mL petroleum ether (B.P 105°C). The extraction flask was heated on the heating mantle for 24 hours at the boiling point of petroleum ether. After the extraction

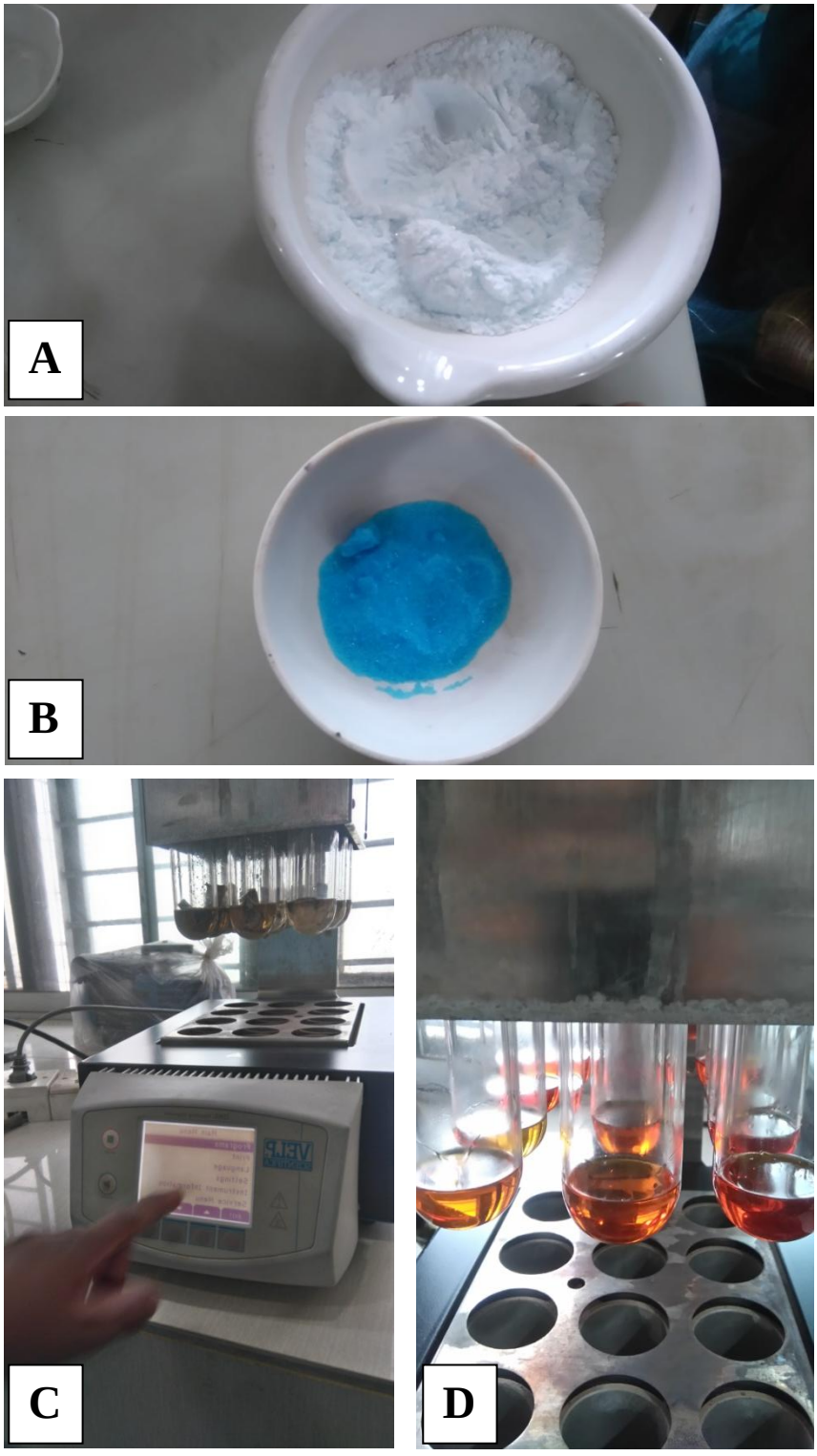

Plate 6. Protein digestion. A. Sodium sulphate used in digestion, B. Copper sulphate used in digestion, C+D sample in digestion chamber.

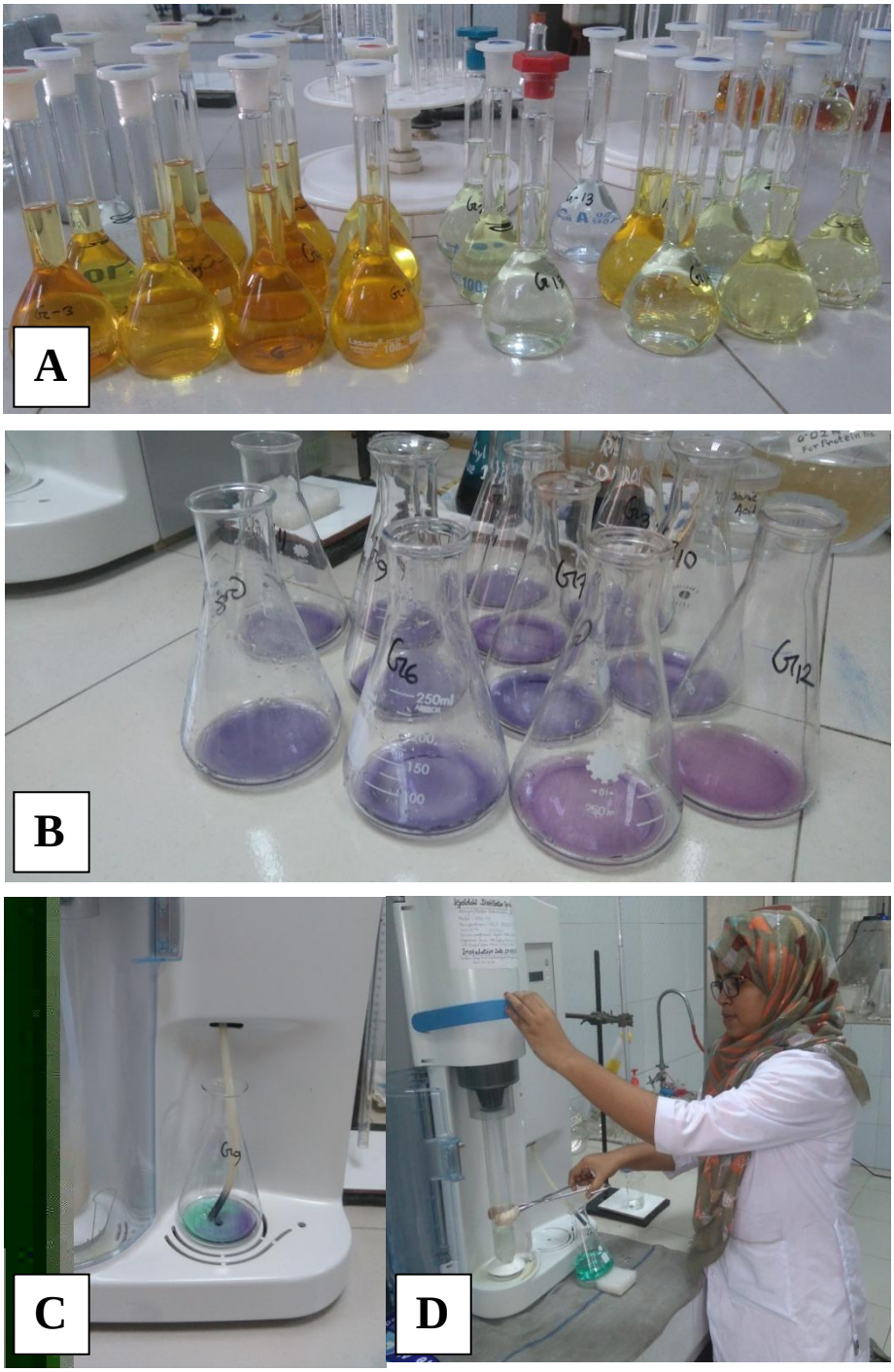

Plate 7. Protein distillation. A. Digested sample in volumetric flask, B. Indicator with boric acid in conical flask, C. Distillation machine, D. Placement of distillation tube with sample in distillation machine.

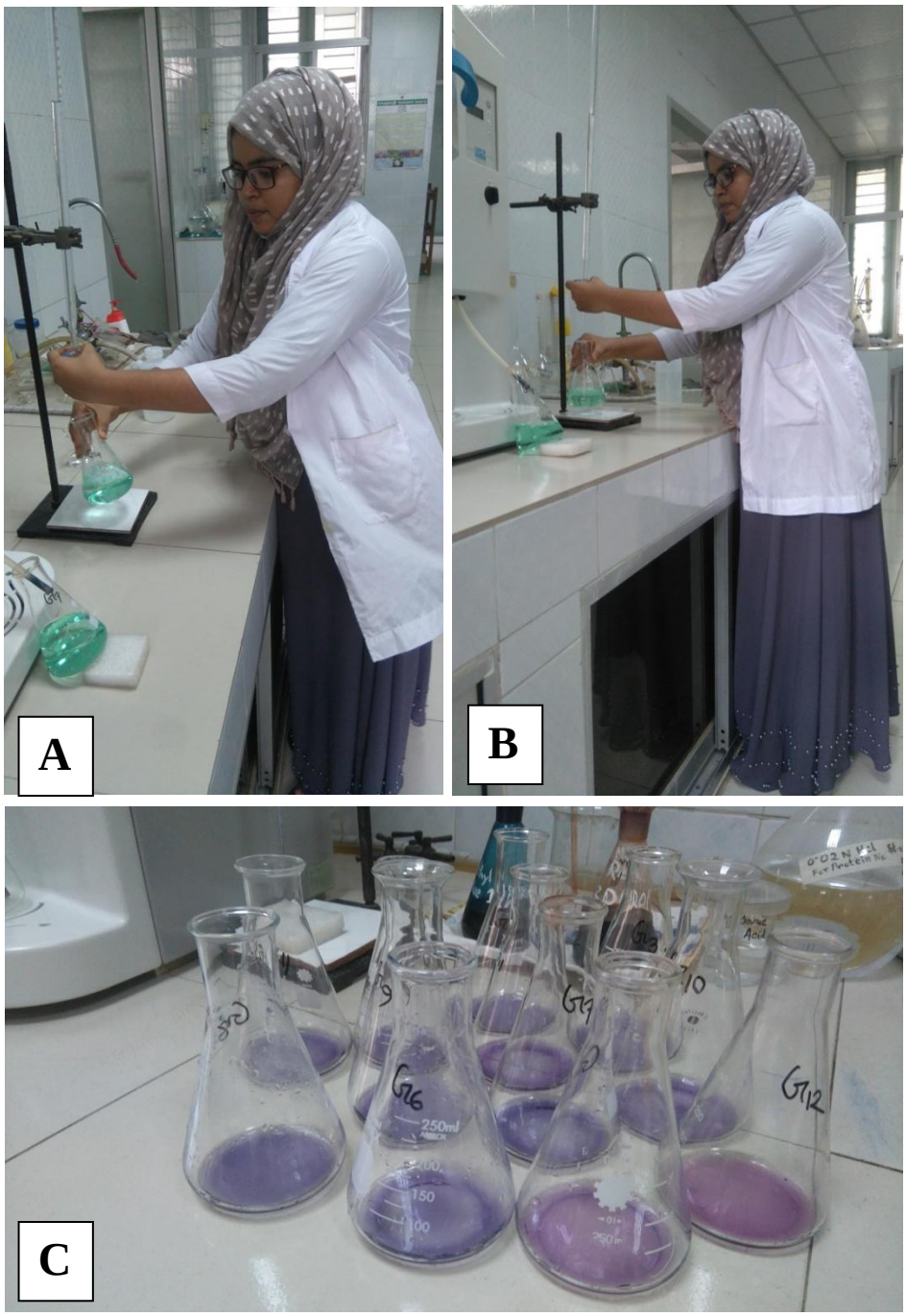

Plate 8. Titration for protein determination. A, B. Titration, C. Color change of the solution after titration .

was completed, the ether dissolving oil was transferred into the beaker. Then, the ether was removed by evaporation. Process is shown in plate 9A. Fat content was calculated as follows:

$$\textbf{\% of fat=} \frac{(\text{After dry weight} - \text{Empty flask weight})}{\text{Sample weight} \times 100}$$

3.2.6 Percentage of Fiber

After fat extraction from the thimble 5 g of the remaining sample was taken into a flat round bottom flask of 1L with boiling chips. 200 mL of normal 0.255 N sulphuric acid was added into it and heat it continuously for 30 minutes. The flask was connected with condenser that digests the sample at boiling temperature 30 minutes. The mixture then filtrated through muslin cloth and the residue is washed with hot water until it free from acid.The material was then transferred to the same beaker and 200 mL of boiling 0.313 N (1.25 percent w/v) NaOH was added. After boiling for 30 minutes the mixture was filtered to a crucible, dried overnight at 80-100°C and weighed. The crucible was kept at in a muffle furnace at 600 °C for 20 minutes. Then it was cooled in desiccators and weighed again. The difference in residue weights and ash represents the weight of crude fiber. Process is shown in plate 9B. Fiber content was calculated as follows:

$$\textbf{\% of fiber=} \frac{(\text{After dry weight} - \text{After ignition weight})}{\text{Sample weight} \times 100}$$

3.2.7 Percentage of Carbohydrate

The carbohydrate content of a food can be determined by calculating the percent remaining after all the other components have been measured: % carbohydrates = (100 - %moisture - %protein - %lipid- ash%-fiber% - % mineral).

3.2.8 Minerals (Iron, Magnesium, Potassium, Phosphorus)

Dry weight of mungbean were identified: general content of phosphorus,

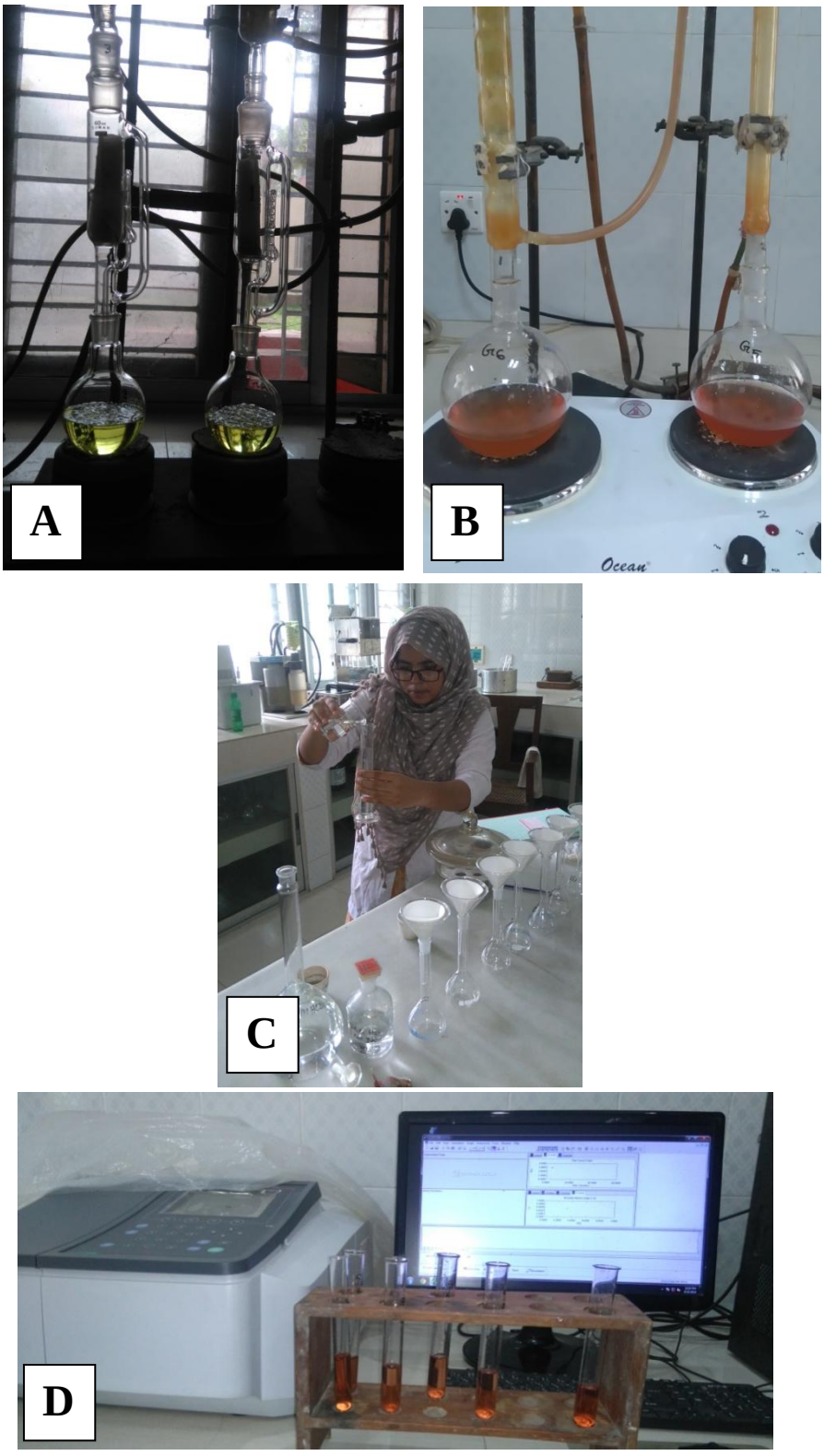

Plate 9. Determination of fat, fiber and iron percentage. A. Fat% determination, B. Fiber% determination, C. Making iron solution, D. Iron% determination by UV-ray machine. and reading was noted from computer.

potassium, calcium, magnesium and sodium in a stock solution, which was obtained after the "dry" mineralization of mungbean in a nm; K –766.490nm; Mg –285.213 nm. Operating parameters of the camera were as follows: RF –1300 W, flow rate of cooling argon –15 L min^{-1}, muffle furnace at 450°C. In such a prepared stock solution, the concentration of examined macronutrients was determined using ICP-AES method on an emission spectrometer with the inductively coupled plasma (argon) Optima 3200 RL, produced by the Perkin Elmer Company. For this purpose, the following wavelengths were used: for Fe –450 nm (plate 9.C, D); P – 680.914auxiliary argon –0.5 L min^{-1}, nebulizated argon – 0.8 L $min^{-1}$and the speed of sample loading –1.5 L min^{-1}.

3.3 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. 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 coefficient 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 Canical Vector Analysis (CVA).

3.3.1 Estimation of genotypic and phenotypic variances

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

Genotypic variance, $\sigma^2_g = \frac{GMS - EMS}{r}$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

Phenotypic variance, $\sigma^2_{ph} = \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

Environmental variance ($\sigma^2 e$) = EMS

Where,

EMS = Mean square error

3.3.2 Estimation of genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation was calculated by the formula suggested by Burton (1952).

Genotypic coefficient of variation, GCV % = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic coefficient of variation was calculated from the following formula.

Phenotypic coefficient variation, PCV = $\frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.3.3 Estimation of heritability

Broad-sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.3.4 Estimation of genetic advance

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

Genetic advance, $GA = K. h^2. \sigma_p$

Or Genetic advance, $GA = K. \frac{\sigma^2_g}{\sigma^2_{ph}} . \sigma_{ph}$

Where,

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

σ_{ph}= Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.3.5 Estimation of genetic advance mean's percentage

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

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

3.3.6 Estimation of simple correlation coefficient:

Simple correlation coefficient (r) was estimated with the following formula (Clarke, 1980; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.3.7 Estimation of genotypic and phenotypic correlation coefficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combinations the formula suggested by Miller *et al.* (1958) and Johnson *et al.* (1955) were adopted. The genotypic covariance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The covariance components were used to compute the genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation, $r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx} . \sigma^2_{gy})}}$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

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

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.3.8 Estimation of path co-efficient

Path co-efficient analysis was carried out according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

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

$r_{yx1} = P_{yxl} + P_{yx2} r_{xlx2} + P_{yx3} r_{x1x3}$

$r_{yx2} = P_{yxl} r_{x1x2} + P_{yx2} + P_{YX3} r_{x2x3}$

$r_{yx3} = P_{yxl} r_{x1x3} + P_{yx2} r_{x2x3} + P_{yx3}$

Where, r´s denotes simple correlation co-efficient and P´s denote path co-efficient (Unknown). P´s in the above equation may be conveniently solved by arranging them in matrix from.

Total correlation, say between x_1 and y is thus partitioned follows:

Pyx1= The direct effect of x1 via x_2 on y.

$P_{yx2} r_{x1x2}$= The indirect effect of x1 via x_2 on y.

$P_{yx3} r_{x1x3}$= The indirect effect of x1 via x_3 on y.

3.3.9 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents 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 programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canical Vector analysis (CVA), which quantify the differences among several quantitative traits, are an efficient method of evaluating genetic diversity. These are as follows:

3.3.10 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. The contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.3.11 Principal Coordinate analysis (PCO)

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

3.3.12 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.

3.3.13 Canical Vector analysis (CVA)

Canical vector analysis (CVA) finds a linear combination of original variability 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 the ratio of among groups were measured to the within-group variations. The canical 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.

3.3.14 Calculation of D^2 values

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

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

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.

3.3.15 Computation of average intra-cluster distances

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

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.

3.3.16 Computation of average inter-cluster distances

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

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

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in clusters i and j.

n_i= Number of populations in cluster i.

n_j= Number of populations in cluster j.

3.3.17 Selection of genotypes for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by a largest statistical distance (D^2) express the maximum divergence among the genotypes included in these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985).

According to them the following points should be considered while selecting genotypes for hybridization programme:

1. Choice of the cluster from which genotypes are selected for use as a parent (s)
2. Selection of particular genotype(s) from the selected cluster(s)
3. The relative contribution of the characters to the total divergence
4. Other important characters of the genotypes performance

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to perform the variability analysis of different genotypes of mungbean using yield contributing and quality traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment. The pods were harvested when they began the color change from green to brown. Pictorial differences of the plant, pod, seeds and root of the genotypes are presented in Plate (10-15), respectively. The data pertaining to 27 characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.1 Experiment 1:Evaluation of mungbeangenotypes based on agro morphogenictraits

This part of the chapter will discuss the results and their interpretation in order for evaluation of mungbean genotypes based on theseagromorphogenic traits.

4.1.1 Agromorphogenic traits

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the sixteen characters studied (Table 3). The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore, there is a lot of scope for selection of the genotypes based on these traits.

4.1.2 Genetic variability, heritability and genetic advance

The mean values for each character of all the genotypes are shown in (Table 4). Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of seventeen characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g),

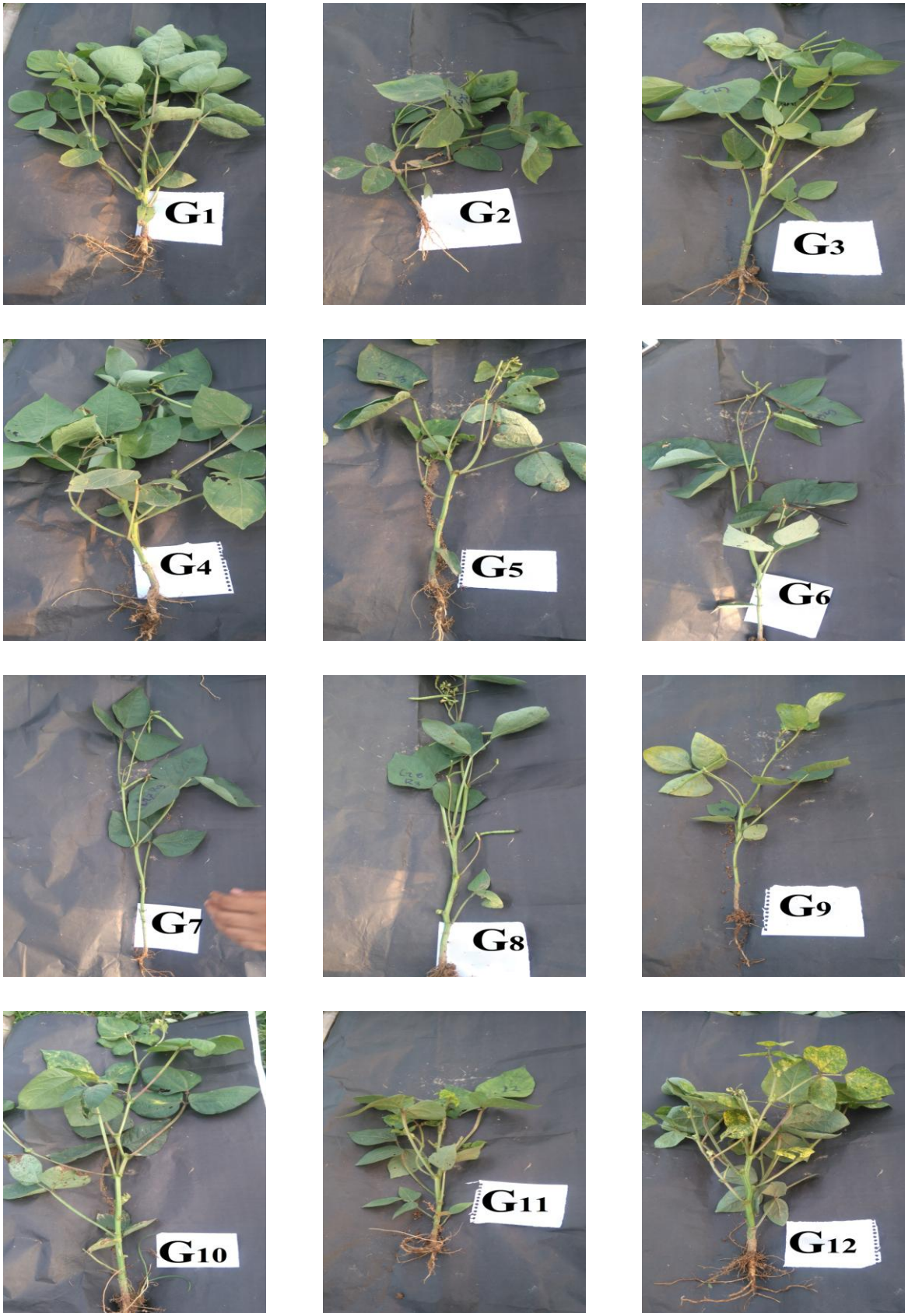

Plate 10. Plants of first twelve mungbean genotypes.

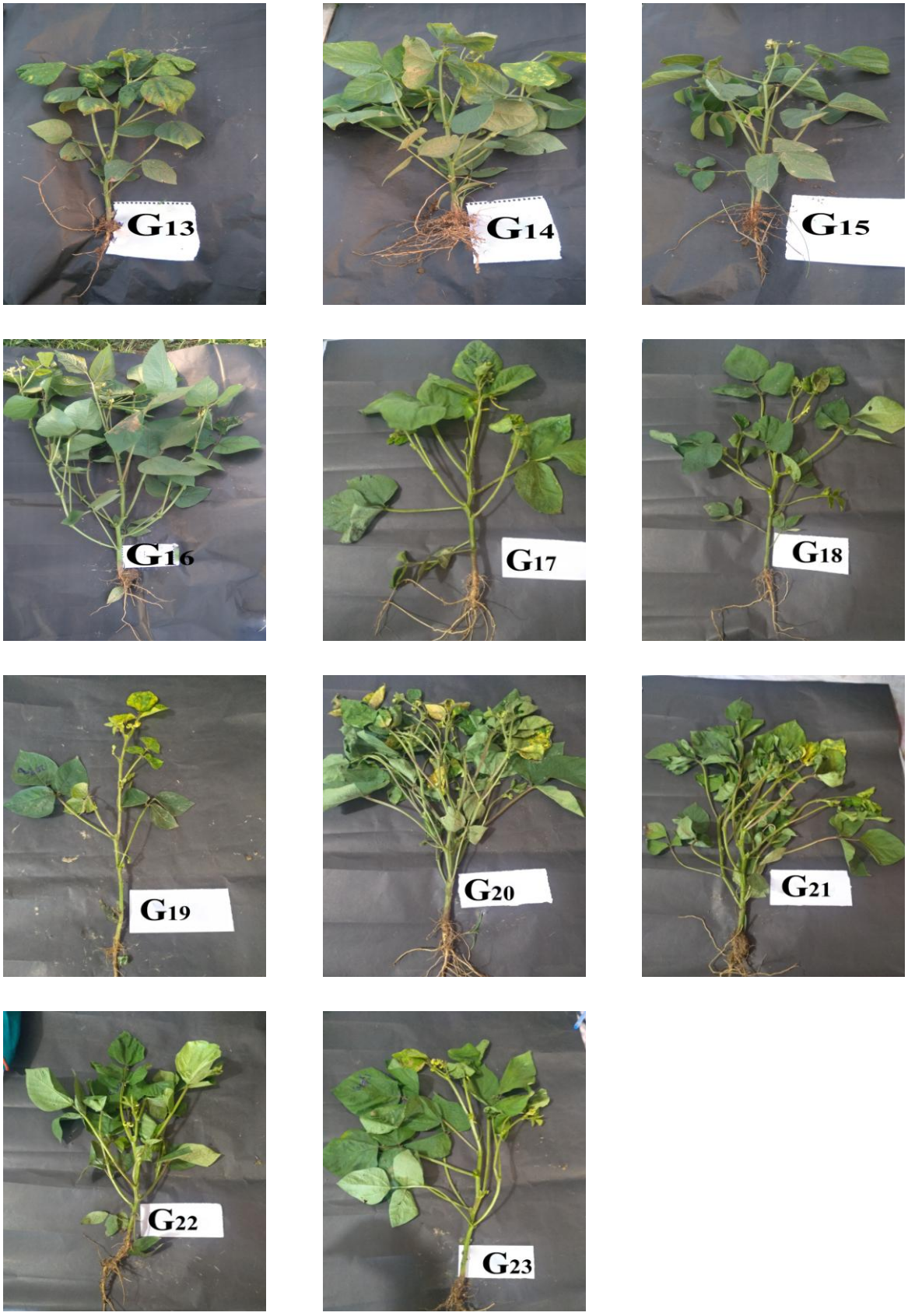

Plate 11. Plants of next eleven mungbean genotypes.

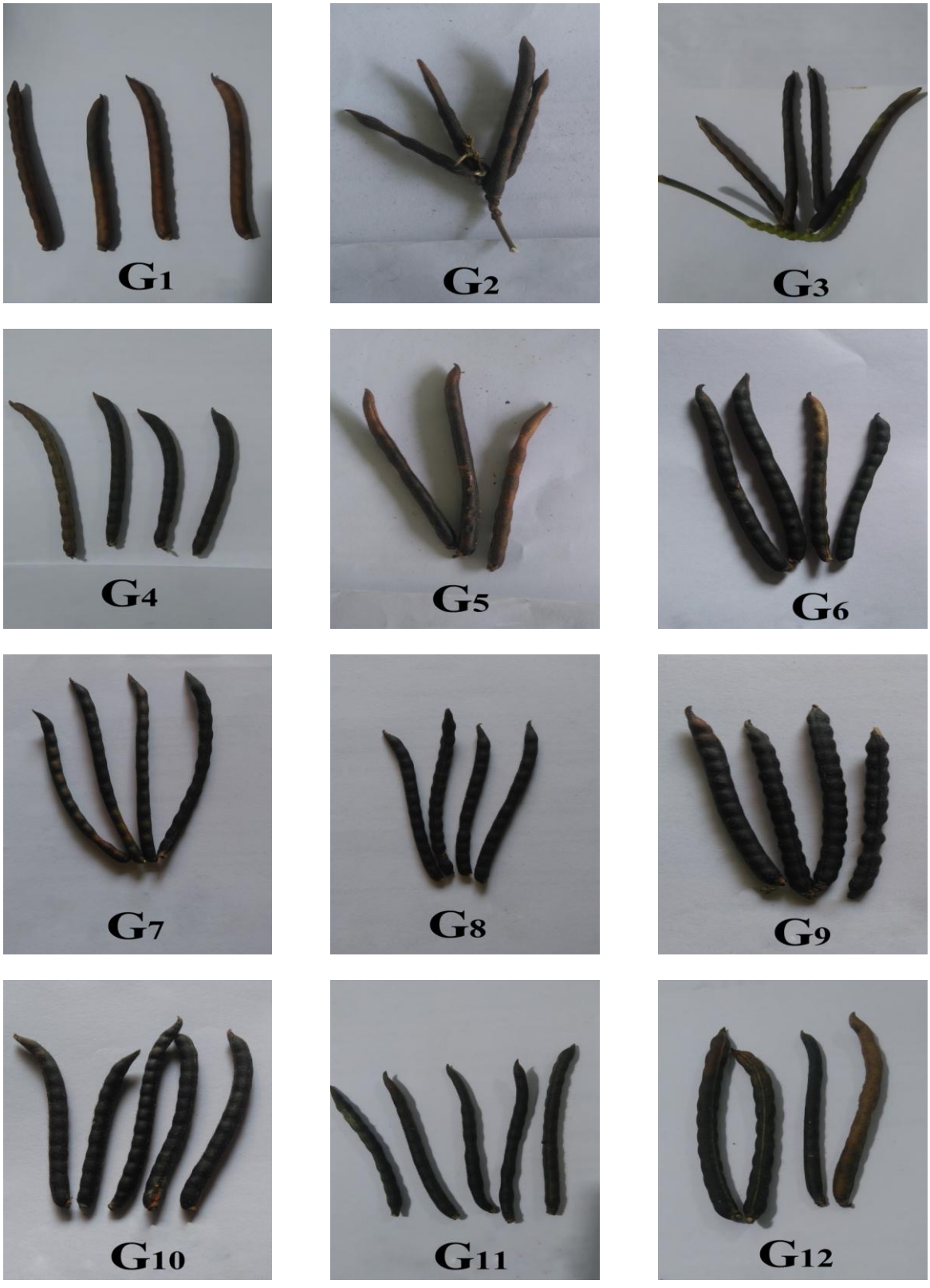

Plate 12. Pods of first twelve mungbean genotypes.

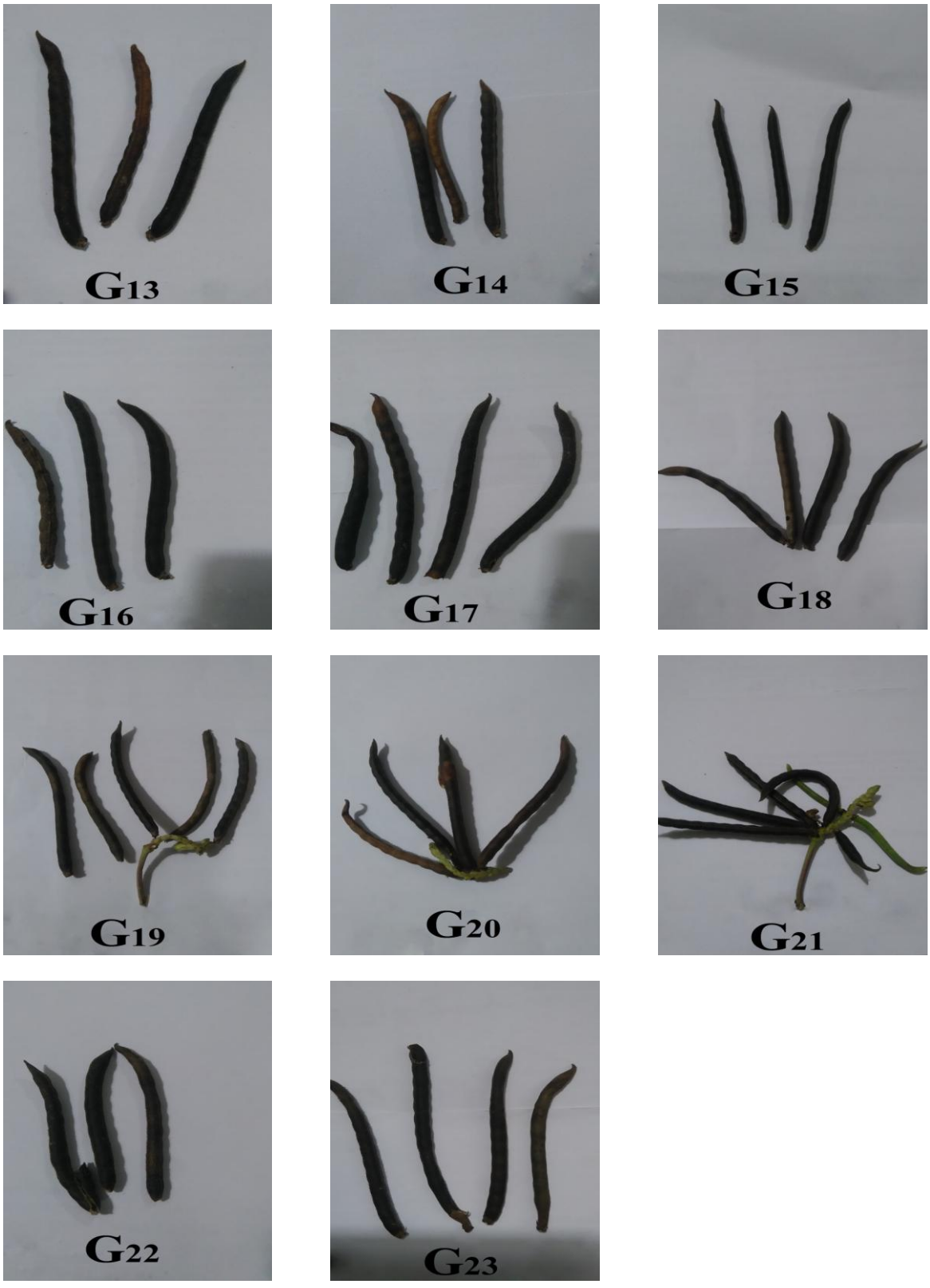

Plate 13. Pods of next eleven mungbean genotypes

Plate 14. Root of 23 mugbean genotypes

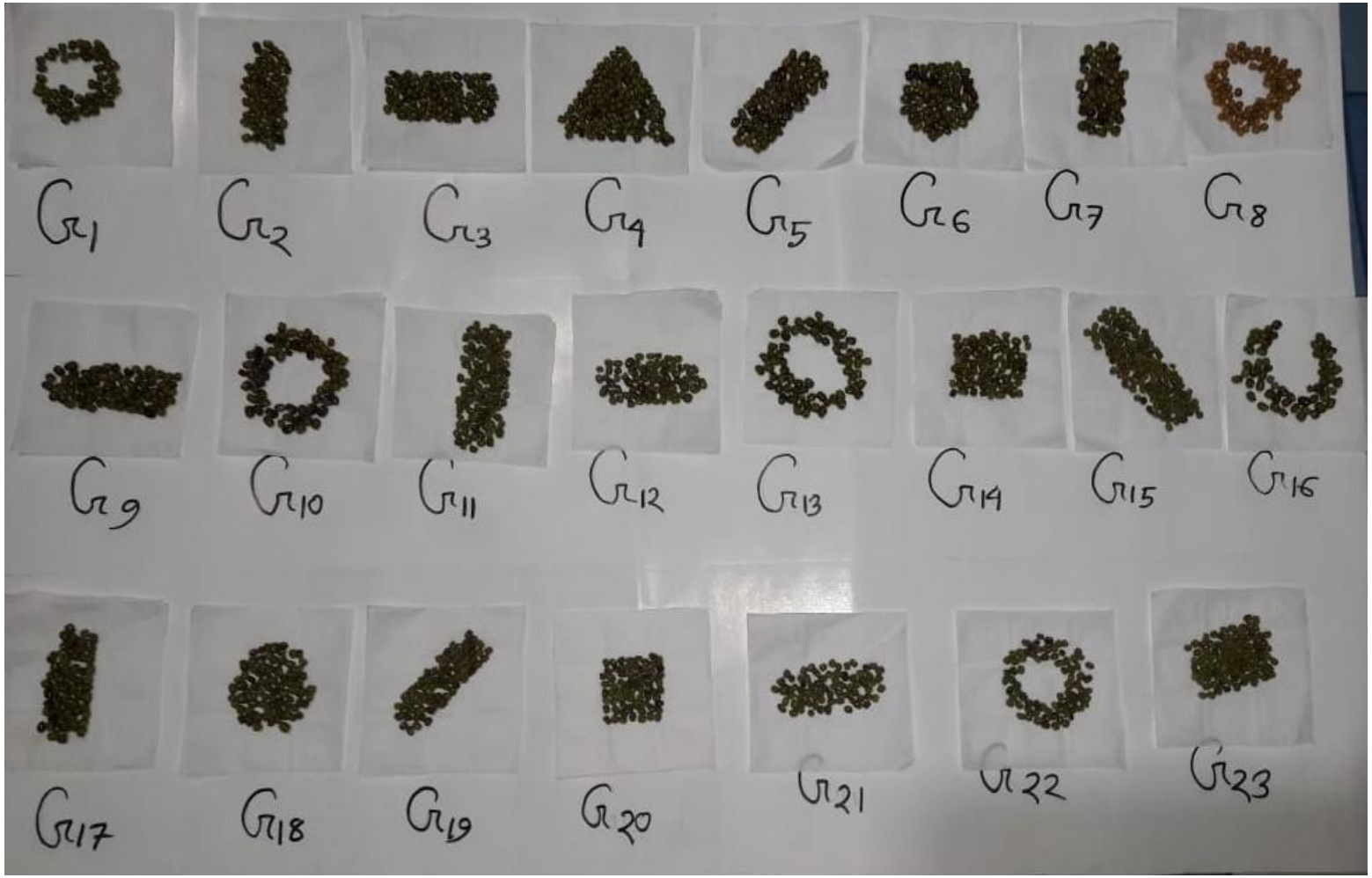

Plate 15. Seeds of twenty-three mungbean genotypes.

Table 3. Analysis of variance for sixteen characters in mungbean genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 22	Error (r-1)(g-1) = 44
DFF	1.45	57.81**	3.45
DM	0.10	41.47**	0.87
PHVG(cm)	66.09	61.74**	6.17
PHM	286.19	77.63**	12.77
NBM	1.20	1.91**	0.41
NLM	1.86	33.96**	2.84
SL	17.96	105.74**	22.86
RL	7.94	6.72**	3.02
NN	66.09	61.74**	6.17
NCPP	5.97	244.50**	18.35
NPPC	1.10	11.45**	0.63
NPPP	2.30	1.24**	0.26
PL	20.193	236.495**	7.166
NSPP	2.29	3.92**	0.33
1000SW	1.45	57.81**	3.45
GWPP	0.873	6.427**	0.594

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule,NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight,GWPP- Grain weight per plant.

** Denote Significant at 1% level of probability, ^{NS}-non-significant

Table 4. Mean analysis of growth, yield and yield contributing parameters

Gen	DFF	DM	PHVG	PHM	NBM	NLM	SL	RL	NN	NCPP	NPPC	NPPP	PL	NSPP	1000 SW	GWPP
G1	44.00	60.67	22.61	50.70	3.03	16.33	35.44	16.78	47.00	4.00	4.00	16.00	7.46	9.48	35.55	4.99
G2	41.33	58.67	27.96	45.35	4.73	18.47	43.31	15.82	43.00	4.77	5.07	24.03	10.20	12.26	30.50	7.80
G3	38.00	57.67	33.43	52.69	4.60	10.34	35.36	14.47	45.00	4.03	5.82	23.37	6.66	9.55	29.67	6.29
G4	42.67	64.67	32.32	61.85	4.43	11.87	46.89	17.61	31.33	12.83	5.67	53.77	7.53	6.50	36.13	9.20
G5	36.33	54.67	37.05	54.03	3.20	9.80	43.43	16.31	35.00	7.20	5.80	35.92	10.18	10.50	50.83	15.01
G6	38.67	60.67	35.12	54.20	2.50	12.33	33.57	11.97	36.67	6.77	5.60	32.33	9.23	8.72	57.50	15.85
G7	35.33	55.67	35.57	63.93	2.87	7.20	41.51	14.11	27.33	3.03	5.92	19.90	8.23	9.73	51.47	10.42
G8	35.00	60.00	36.20	55.93	3.07	7.40	26.74	13.91	42.67	5.67	6.95	35.81	7.49	10.18	31.50	11.40
G9	33.00	56.00	37.42	63.07	3.00	9.80	26.04	14.55	32.67	4.20	6.13	22.09	8.57	8.19	60.00	9.85
G10	39.67	59.00	35.42	61.80	3.60	8.53	30.75	14.18	24.33	4.03	6.27	25.13	8.89	9.36	50.00	11.74
G11	42.67	61.67	33.53	56.40	4.20	10.87	36.12	15.17	37.67	4.70	5.87	27.57	7.38	9.87	26.00	7.01
G12	42.00	60.67	33.05	56.13	4.07	7.60	30.33	12.27	18.00	4.47	6.73	30.38	8.11	10.64	29.33	9.44
G13	35.67	56.67	31.56	55.20	2.47	7.27	34.33	15.46	25.00	4.53	5.93	26.77	9.35	9.06	45.33	10.93
G14	39.33	60.67	28.96	52.60	2.33	7.47	31.91	15.53	29.00	4.33	6.07	26.28	9.71	12.00	38.33	12.36

Table4. (Cont'd)

Gen	DFF	DM	PHVG	PHM	NBM	NLM	SL	RL	NN	NCPP	NPPC	NPPP	PL	NSPP	1000 SW	GWPP
G15	41.67	55.00	26.93	49.53	2.33	7.13	26.71	14.76	56.67	5.07	6.87	35.44	7.36	12.92	25.33	11.26
G16	36.00	54.33	32.21	52.73	2.17	7.70	30.11	14.86	22.00	6.33	5.43	34.31	9.61	8.66	41.33	10.88
G17	44.33	63.00	28.10	47.87	2.93	7.47	29.29	16.75	42.33	6.73	6.13	40.89	8.80	9.22	39.67	15.43
G18	32.33	57.33	25.37	50.93	2.27	8.73	26.78	13.12	43.00	6.33	6.87	49.05	6.96	10.61	25.50	13.25
G19	42.33	63.00	27.65	51.27	2.27	8.87	27.48	13.26	39.33	4.23	6.10	25.71	6.78	10.28	23.50	6.01
G20	47.00	62.67	28.79	54.40	2.53	8.60	32.88	13.41	36.33	5.03	6.07	32.02	7.95	11.10	23.17	8.45
G21	45.33	63.67	28.20	55.20	3.33	16.60	31.96	13.35	37.33	3.98	6.20	24.70	6.84	11.97	23.87	6.98
G22	42.33	65.33	23.78	48.67	3.47	14.27	31.45	13.46	41.33	5.10	5.94	30.37	6.97	10.58	21.33	6.82
G23	48.33	68.00	23.46	46.59	2.73	7.83	26.97	12.86	37.33	5.43	6.67	35.85	7.18	11.35	22.50	9.37
Min	32.33	54.33	22.61	45.35	2.17	7.13	26.04	11.97	18.00	3.03	4.00	16.00	6.66	6.50	21.33	4.99
Max	48.33	68.00	37.42	63.93	4.73	18.47	46.89	17.61	56.67	12.83	6.95	53.77	10.20	12.92	60.00	15.85
Mean	40.15	59.99	30.64	53.96	3.14	10.11	33.02	14.52	36.10	5.34	6.00	30.77	8.15	10.12	35.58	10.03
LSD	3.06	1.54	4.09	5.88	1.05	2.77	7.87	2.86	7.05	1.30	0.84	4.41	0.94	1.27	3.25	1.10

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in (Table 5). The data were analyzed and possible interpretations are given here based on established scales. According to Deshmukh*et al.* (1986) PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Wide difference between PCV and GCV for the traits implies their susceptibility to environmental fluctuation, whereas narrow difference suggested their relative resistance to environmental variation. Heritability is the percentage of phenotypic variance that is attributed to genetic variance. Heritability of a trait is considered as vary high or high at values 80% or more and moderate when it ranged from 40-80% and when it is less than 40%, it is low (Singh, 2009). The estimates of heritability alone fail to indicate the response to selection (Johnson *et al*., 1955). Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance and the genetic advance at percentage of mean. Deshmukh*et al.* (1986) classified genetic advance as percentage of mean as low (<10%), moderate (10-20%) and high (>20%).

4.1.2.1 Days to 50% flowering

Highly significant variation was observed among all the genotypes (57.81**) studied for this character (Table 3). The mean value of days to 50% flowering was observed significantly the lowest in G18 (32.33 days) (Table 4). The highest days taken to 50% flowering was found in G23 (48.33 days). The genotypic and phenotypic variance of days to 50% flowering was observed 18.12 and 21.56, respectively (Table 5) and values of genotypic coefficient of variation and phenotypic coefficient of variation were 10.60% and 11.57% respectively which indicated that the genotypes have relatively less variation (Table 5) Days to 50% Flowering showed high heritability (84.01%) with low genetic advance (8.04) and genetic advance in the percentage of the mean (20.02%).

Table 5: Estimation of genetic parameters in sixteen characters of twenty-three genotypes in mungbean

Parameters	Mean	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	Genetic Advance (5%)	Genetic Advance (% of mean)	CV (%)
DFF	40.15	21.57	18.12	3.45	11.57	10.60	0.97	84.01	8.04	20.02	4.63
DM	59.99	14.41	13.53	0.87	6.33	6.13	0.19	93.93	7.34	12.24	1.56
PHVG(cm)	30.64	24.69	18.53	6.17	16.22	14.05	2.17	75.03	7.68	25.07	8.10
PHM	53.96	34.39	21.62	12.77	10.87	8.62	2.25	62.88	7.60	14.08	6.62
NBM	3.14	0.91	0.50	0.41	30.40	22.56	7.85	55.05	1.08	34.48	20.38
NLM	10.11	13.21	10.37	2.84	35.96	31.86	4.10	78.52	5.88	58.16	16.67
SL	33.02	50.49	27.63	22.86	21.52	15.92	5.60	54.73	8.01	24.26	14.48
RL	14.52	4.26	1.23	3.02	14.21	7.65	6.56	28.95	1.23	8.48	11.98
NN	36.10	93.73	75.38	18.35	26.82	24.05	2.77	80.42	16.04	44.43	11.87
NCPP	5.34	4.23	3.61	0.63	38.53	35.57	2.96	85.23	3.61	67.65	14.81
NPPC	6.00	0.59	0.33	0.26	12.76	9.55	3.21	55.96	0.88	14.71	8.47
NPPP	30.768	83.61	76.44	7.17	29.72	28.42	1.30	91.43	17.22	55.97	8.70
PL	8.1491	1.53	1.20	0.33	15.17	13.43	1.73	78.46	2.00	24.51	7.04
NSPP	10.118	2.54	1.94	0.59	15.75	13.78	1.97	76.59	2.51	24.84	7.62
1000SW	35.58	145.73	141.82	3.91	33.93	33.47	0.46	97.32	24.20	68.02	5.56
GWPP	10.032	9.61	9.16	0.45	30.90	30.18	0.73	95.34	6.09	60.70	6.67

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

σ^2p: Phenotypic variance, PCV: Phenotypic coefficient of variation, GA (5%): Genetic advance, σ^2g: Genotypic variance, GCV: Genotypic coefficient of variation, GAM: Genetic advance (% of mean),σ^2e: Environmental variance, ECV: Environmental coefficient of variation, CV (%) = coefficient of variation

4.1.2.2 Days to Maturity

Highly significant variation was observed among all the genotypes (41.47**) studied for this character (Table 3). The mean value of days to maturity was observed significantly the lowest in G16 (54.33 days) (Table 4). The highest number of days taken to maturity was found in G23 (68.00 days). The genotypic and phenotypic variance of days to maturity was observed 13.53 and 14.41 respectively and values of genotypic coefficient of variation and phenotypic coefficient of variation were 6.13% and 6.33% respectively which indicated that this trait has less environmental influence and selection would be effective (Table 5). Days to Maturity showed high heritability (93.93%) with low genetic advance (7.34) and genetic advance in the percentage of the mean (12.24%) which indicates this character controlled by additive gene and there is a wide scope for crop improvement through selection of this trait.

4.1.2.3 Plant Height at Vegetative Stage (cm)

Highly significant variation was observed among all the genotypes (61.74**) studied for this character (Table 3). The mean value of plant height at vegetative stage was observed significantly the lowest in G1 (22.61 cm) (Table 4). The highest value taken to plant height at vegetative stage) was found in G9 (37.42 cm). The genotypic and phenotypic variance of plant height at vegetative stage was observed 18.53 and 34.39, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 14.05% and 16.22% respectively which indicated that the genotypes have relatively less variation (Table 5) plant height at vegetative stage showed moderate heritability (75.03%) with low genetic advance (7.68) and genetic advance in the percentage of the mean (25.07%).

4.1.2.4 Plant height at maturity(cm)

Highly significant variation was observed among all the genotypes (77.63**) studied for this character (Table 3). The mean value of plant height at maturity was observed significantly the lowest in G2 (45.35) (Table 4). The highest value taken to plant height at maturity was found in G7 (63.93). The genotypic and phenotypic variance of plant height at maturity was observed 21.62 and 34.39, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 8.62% and 10.87% respectively which indicated that the genotypes have relatively less variation (Table 5). Plant height at maturity showed moderate heritability (62.88%) with low genetic advance (7.60) and genetic advance in the percentage of the mean (14.08%).

4.1.2.5 Number of branches at maturity

Highly significant variation was observed among all the genotypes (1.91**) studied for this character (Table 3). The mean value of number of branch was observed significantly the lowest in G16 (2.17) (Table 4). The highest value taken to number of branch was found in G2 (4.73). The genotypic and phenotypic variance of number of branch was observed 0.50 and 0.91 and values of genotypic coefficient of variation and phenotypic coefficient of variation were 22.56% and 30.40% respectively which indicated that the genotypes have relatively less variation (Table 5). Number of branch showed moderate heritability (55.05%) with low genetic advance (1.08) and genetic advance in the percentage of the mean (34.48%).

4.1.2.6 Number of leaf per plant at maturity

Highly significant variation was observed among all the genotypes (33.96**)studied for this character (Table 3). The mean value of number of leaf

was observed significantly the lowest in G15 (7.13) (Table 4). The highest value taken to number of leaf was found in G2 (18.47). The genotypic and phenotypic variance of number of leaf was observed 10.37 and 13.21, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic co-efficient of variation and phenotypic co-efficient of variation were 31.86% and 35.96% respectively which indicated that the genotypes have relatively less variation (Table 5) number of leaf showed moderate heritability (78.52%) with low genetic advance (5.88) and genetic advance in the percentage of the mean (58.16%).

4.1.2.7 Stem length(cm)

Highly significant variation was observed among all the genotypes (105.74**) studied for this character (Table 3). The mean value of Stem length was observed significantly the lowest in G9 (26.04) (Table 4). The highest value taken to Stem length was found in G4 (46.89). The genotypic and phenotypic variance of Stem length was observed 27.63 and 50.49, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 15.52% and 21.52% respectively which indicated that the genotypes have relatively less variation (Table 5). Stem length showed moderate heritability (54.73%) with low genetic advance (8.01) and genetic advance in the percentage of the mean (24.26%).

4.1.2.8 Root length(cm)

Highly significant variation was observed among all the genotypes (6.72**)studied for this character (Table 3). The mean value of root length was observed significantly the lowest in G6 (11.97) (Table 4). The highest value taken to root length was found in G4 (17.61). The genotypic and phenotypic variance of root length was observed 1.23 and 4.26, respectively with high

differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 7.65% and 14.21% respectively which indicated that the genotypes have relatively less variation (Table 5). Root length showed moderate heritability (28.95%) with low genetic advance (1.23) and genetic advance in the percentage of the mean (8.48%).

4.1.2.9Nodule number

Highly significant variation was observed among all the genotypes (244.50**) studied for this character (Table 3). The mean value of nodule number was observed significantly the lowest in G12 (18) (Table 4). The highest value taken to nodule number was found in G15 (56.67). The genotypic and phenotypic variance of nodule number was observed 75.38 and 93.73, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 24.05% and 26.82% respectively which indicated that the genotypes have relatively less variation (Table 5). Nodule number showed high heritability (80.42%) with moderate genetic advance (16.04) and genetic advance in the percentage of the mean (44.43%) this trait was controlled by additive gene and selection would be effective.

4.1.2.10Number of cluster per plant

Highly significant variation was observed among all the genotypes (11.45**) studied for this character (Table 3). The mean value of number of cluster per plant was observed significantly the lowest in G7 (3.03) (Table 4). The highest value taken to number of cluster per plant was found in G4 (12.83). The genotypic and phenotypic variance of number of cluster per plant was observed 3.61 and 4.23 and values of genotypic coefficient of variation and phenotypic

coefficient of variation were 35.57% and 38.53% respectively which indicated that the genotypes have relatively less variation (Table 5). Number of cluster per plant showed moderate heritability (85.23) with low genetic advance (3.61) and genetic advance in the percentage of the mean (67.65%).

4.1.2.11Number of pod per cluster

Highly significant variation was observed among all the genotypes (1.24**) studied for this character (Table 3). The mean value of number of pod per cluster was observed significantly the lowest in G1 (4) (Table 4). The highest value taken to number of pod per cluster was found in G8 (6.95). The genotypic and phenotypic variance of number of pod per cluster was observed 0.33 and 0.59 and values of genotypic coefficient of variation and phenotypic coefficient of variation were 9.55% and 12.76% respectively which indicated that the genotypes have relatively less variation (Table 5). Number of pod per cluster showed low heritability (55.96%) with low genetic advance (0.88) and genetic advance in the percentage of the mean (14.71%).

4.1.2.12Number of pod per plant

Highly significant variation was observed among all the genotypes (236.495**) studied for this character (Table 3). The mean value of number of pods per plant was observed significantly the lowest in G1 (16) (Table 4). The highest value taken to number of pod per plant was found in G4 (53.77). The genotypic and phenotypic variance of number of pod per plant was observed 76.44 and 83.61, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 28.42% and 29.72% respectively which indicated that the genotypes have relatively less variation (Table 5). Number of pod per plant showed high heritability (91.43%) with moderate genetic advance (17.22) and genetic advance

in the percentage of the mean (55.97%) this controlled by additive gene so selection would be effective based upon thistrait.

4.1.2.13Pod length(cm)

Highly significant variation was observed among all the genotypes (3.92**) studied for this character (Table 3). The mean value of pod length was observed significantly the lowest in G3 (6.66) (Table 4). The highest value taken to pod length was found in G2 (10.20). The genotypic and phenotypic variance of pod length was observed 1.30 and 1.53 and values of genotypic coefficient of variation and phenotypic coefficient of variation were 13.43% and 15.17%, respectively which indicated that the genotypes have relatively less variation (Table 5). Pod length showed moderate heritability (78.46%) with low genetic advance (2.0) and genetic advance in the percentage of the mean (24.51%).

4.1.2.14Number of seed per pod

Highly significant variation was observed among all the genotypes (6.427**) studied for this character (Table 3). The mean value of number of seeds per pod was observed significantly the lowest in G4 (6.50) (Table 4). The highest value taken to number of seeds per pod was found in G15 (12.92). The genotypic and phenotypic variance of number of seed per pod was observed 1.94 and 2.54, respectively with and values of genotypic coefficient of variation and phenotypic coefficient of variation were 13.78% and 15.75%, respectively which indicated that the genotypes have relatively less variation (Table 5). Number of seeds per pod showed moderate heritability (76.59%) with low genetic advance (2.51) and genetic advance in the percentage of the mean (24.84%).

4.1.2.15 Thousand seed weight (g)

Highly significant variation was observed among all the genotypes (429.37**) studied for this character (Table 3). The mean value of thousand seed weight was observed significantly the lowest in G22 (21.33) (Table 4). The highest value

taken to thousand seed weight was found in G9 (60). The genotypic and phenotypic variance of thousand seed weight was observed 141.82 and 145.43and values of genotypic coefficient of variation and phenotypic coefficient of variation were 33.47% and 33.93% respectively which indicated that the trait has less environmental variation (Table 5). Thousand seed weight showed high heritability (97.32%) with high genetic advance (24.20) and genetic advance in the percentage of the mean (68.03%).

4.1.2.16Grain weight per plant (g)

Highly significant variation was observed among all the genotypes (27.941**) studied for this character (Table 3). The mean value of grain weight per plant was observed significantly the lowest in G1 (4.99) (Table 4). The highest value taken to grain weight per plant was found in G6 (15.85). The genotypic and phenotypic variance of grain weight per plant was observed 9.16 and 9.61 and values of genotypic coefficient of variation and phenotypic coefficient of variation were 30.18% and 30.90% respectively which indicated that the trait has relatively less environmental variation (Table 5) so selection based upon their phenotypic expression would be effective. Grain weight per plant showed high heritability (95.34%) with moderate genetic advance (6.09) and genetic advance in the percentage of the mean (60.70%) this trait controlled by additive gene and that indicate selection would be effective for better crop improvement.

4.1.3 Correlation Co-efficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. Singh and Chaudhary, (1985) suggested that simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components. As we know yield is a complex product being influence by several inter-dependable quantitative characters. If the understanding of other contributing components influences the yield directly or indirectly is not clear,

selection may not be effective. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. While phenotypic correlation coefficient was higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. The depicted of genotypic and phenotypic correlation co-efficient among yield and yield contributing characters of mungbean are shown in (Table 6).

4.1.3.1 Days to 50% Flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (G=0.813, P=0.700), number of leaf at maturity (G=0.321, P=0.246) and number of seed per pod (G=0.330, P=0.255). It was also observed that highly significant but negative correlation with plant height at vegetative stage (G=-0.604, P=-0.509), plant height at maturity (G=-0.477, P= -0.278), pod length (G=-0.329, P=-0.238) and thousand seed weight (G=-0.555, P=-0.501), grain weight per plant (G=-0.421, P=-0.372). Non-significant and positive correlation with number of branches at maturity (G=0.184, P=0.179), Stem length (G=0.036, P=0.014), root length (G=0.017), nodule number (G=0.211, P=0.215), number of cluster per plant (G=0.042, P=0.043), and non-significant but negative correlation number of pod per cluster (G=-0.153, P=-0.113), number of pod per plan (G=-0.014, P=-0.010).

4.1.3.2 Days to Maturity

Days to maturity showed a highly significant and positive correlation with number of leaf at maturity(G=0.268, P=0.246). It also observed a highly significant but negative correlation with plant height at vegetative stage (G=-0.536, P=-0.427), plant height at maturity (G=-0.286), pod length (G=-0.474, P=-

0.398) and thousand seed weight (G=-0.477, P=-0.466), grain weight per plant (G=-0.328, P=-0.318). Non-significant and positive correlation with number ofbranches at maturity (G=0.188, P=0.155), nodule number (G=0.115, P=0.089), number of cluster per plant (G=0.187, P=0.170), number of pod per cluster (G=0.072, P=0.046), number of pod per plant (G=0.188, P=0.171), number of seed per pod (G=0.328, P= 0.057).And non-significant but negative correlation Stem length (G=-0.095, P=-0.069).

4.1.3.3 Plant height at vegetative stage (cm)

Plant height at vegetative stage showed highly significant and positive correlation with plant height at maturity (G=0.828, P=0.617), pod length (G=0.428, P=0.332),thousand seed weight (G=0.658, P=0.548),grain weight per plant (G=0.379, P=0.343), and It also observed a highly significant but negative correlation with number of leaf at maturity (G=-0.382), nodule number (G=-0.526, P=-0.391), number of seed per pod (G=-0.501, P=-0.373),and Non-significant and positive correlation with number of pod per cluster (G=0.098, P=0.150),and non-significant but negative correlation with root length (G=-0.051),number of cluster per plant (G=-0.096).

4.1.3.4 Plant height at maturity(cm)

Plant height at maturity showed highly significant and positive correlation with thousand seed weight (G=0.575, P=0.548). It also observed a highly significant but negative correlation with number of leaf at maturity (G=-0.267), nodule number (G=-0.624, P=-0.452). Non-significant and positive correlation with number of pod per cluster (G=0.078, P=0.010),pod length (G=0.058, P=0.036),Stem length (G=0.213, P=0.229),and non-significant but negative correlation with number of pod per plant (G=-0.120, P=-0.077).

Table 6. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of mungbean

Characters	DFF	DM	PHVG	PHM	NBM	NLM	SL	RL	NN	NCPP	NPPC	NPPP	PL	NSPP	1000SW	GWPP
DFF	1															
DM	0.813**	1														
PHVG	-0.604**	-0.536**	1													
PHM	-0.477**	-0.286*	0.828**	1												
NBM	0.184^{NS}	0.188^{NS}	0.251*	0.114^{NS}	1											
NLM	0.321**	0.268*	-0.382**	-0.267*	0.574**	1										
SL	0.036^{NS}	-0.095^{NS}	0.245*	0.213^{NS}	0.712**	0.443**	1									
RL	0.017^{NS}	-0.240*	-0.051^{NS}	-0.056^{NS}	0.499**	0.134^{NS}	0.697**	1								
NN	0.211^{NS}	0.115^{NS}	-0.526**	-0.624**	0.011^{NS}	0.367**	-0.134^{NS}	0.137^{NS}	1							
NCPP	0.042^{NS}	0.187^{NS}	-0.096^{NS}	-0.123^{NS}	0.029^{NS}	-0.078^{NS}	0.259*	0.440**	0.045^{NS}	1						
NPPC	-0.153^{NS}	0.072^{NS}	0.098^{NS}	0.078^{NS}	-0.240*	-0.694**	-0.631**	-0.706**	-0.043^{NS}	0.134^{NS}	1					
NPPP	-0.014^{NS}	0.188^{NS}	-0.091^{NS}	-0.120^{NS}	-0.087^{NS}	-0.300*	-0.005^{NS}	0.105^{NS}	0.069^{NS}	0.944**	0.450**	1				
PL	-0.329**	-0.474**	0.428**	0.058^{NS}	-0.085^{NS}	-0.076^{NS}	0.393**	0.427**	-0.509**	0.057^{NS}	-0.296*	-0.072^{NS}	1			
NSPP	0.330**	0.039^{NS}	-0.501**	-0.618**	-0.160^{NS}	0.098^{NS}	-0.283*	-0.365**	0.410**	-0.383**	0.351**	-0.198^{NS}	-0.114^{NS}	1		
1000SW	-0.555**	-0.477**	0.658**	0.575**	-0.264*	-0.238*	0.089^{NS}	0.133^{NS}	-0.427**	-0.223^{NS}	-0.203^{NS}	-0.272*	0.623**	-0.476**	1	
GWPP	-0.421**	-0.328**	0.379**	0.063NS	-0.449**	-0.501**	-0.104^{NS}	0.027^{NS}	-0.182^{NS}	0.374**	0.362**	0.471**	0.592**	-0.134NS	0.569**	1

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

Table 7. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of mungbean

Characters	DFF	DM	PHVG	PHM	NBM	NLM	SL	RL	NN	NCPP	NPPC	NPPP	PL	NSPP	1000SW	GWPP
DFF	1															
DM	0.700**	1														
PHVG	-0.509**	-0.427**	1													
PHM	-0.278*	-0.228^{NS}	0.617**	1												
NBM	0.179^{NS}	0.155^{NS}	0.150^{NS}	0.145^{NS}	1											
NLM	0.246*	0.240*	-0.184^{NS}	-0.196^{NS}	0.374**	1										
SL	0.014^{NS}	-0.069^{NS}	0.231^{NS}	0.229^{NS}	0.374**	0.380**	1									
RL	-0.025^{NS}	-0.107^{NS}	0.068^{NS}	0.079^{NS}	0.071^{NS}	0.196^{NS}	0.432**	1								
NN	0.215^{NS}	0.089^{NS}	-0.391**	-0.452**	-0.021^{NS}	0.247*	-0.153^{NS}	0.096^{NS}	1							
NCPP	0.043^{NS}	0.170^{NS}	-0.083^{NS}	-0.068^{NS}	0.025^{NS}	-0.049^{NS}	0.223^{NS}	0.278*	0.031^{NS}	1						
NPPC	-0.113^{NS}	0.046^{NS}	0.150^{NS}	0.010^{NS}	-0.133^{NS}	-0.491**	-0.415**	-0.315**	0.025^{NS}	-0.001^{NS}	1					
NPPP	-0.010^{NS}	0.171^{NS}	-0.039^{NS}	-0.077^{NS}	-0.066^{NS}	-0.226^{NS}	0.015^{NS}	0.121^{NS}	0.084^{NS}	0.905**	0.403**	1				
PL	-0.238*	-0.398**	0.332**	0.036^{NS}	-0.055^{NS}	-0.049^{NS}	0.251*	0.241*	-0.359**	-0.004^{NS}	-0.256*	-0.115^{NS}	1			
NSPP	0.255*	0.057^{NS}	-0.373**	-0.471**	-0.105^{NS}	0.076^{NS}	-0.191^{NS}	-0.246*	0.325**	-0.362**	0.236^{NS}	-0.223^{NS}	0.009^{NS}	1		
1000SW	-0.501**	-0.466**	0.548**	0.454**	-0.182^{NS}	-0.221^{NS}	0.058^{NS}	0.041^{NS}	-0.395**	-0.224^{NS}	-0.167^{NS}	-0.274*	0.551**	-0.435**	1	
GWPP	-0.372**	-0.318**	0.343**	0.070^{NS}	-0.330**	-0.422**	-0.055^{NS}	0.001^{NS}	-0.145^{NS}	0.355**	0.312**	0.468**	0.516**	-0.073^{NS}	0.542**	1

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

4.1.3.5 Number of branches per plant at maturity

Number of branches showed highly significant and positive correlation with number of leaf at maturity (G=0.574, P=0.374), Stem length (G=0.712, P=0.374). It also observed a highly significant but negative correlation with number of pods per cluster (G=-0.240), thousand seed weight (G=-0.264) and grain weight per plant (G=-0.449, P=-0.330).Non-significant and positive correlation with nodule number (G=0.011) and non-significant but negative correlation with number of pod per plant (G=-0.087, P=-0.066), pod length (G=-0.085, P=-0.055),number of seed per pod (G=-0.160, P=-0.105).

4.1.3.6 Number of Leaf per plant at maturity

Number of leaf showed highly significant and positive correlation with Stem length (G=0.443, P=0.380), nodule number (G=0.367)It also observed a highly significant but negative correlation with number of pod per cluster (G=-0.694), grain weight per plant (G=-0.501, P=-0.422), thousand seed weight (G=-0.238) and Non-significant and positive correlation with root length (G=0.011), Number of clusters per plant (G=0.032), and number of seed per pod (G=0.098) and non-significant but negative correlation with number of cluster per plant (G=-0.078, P=-0.049),number of pod per plant (G=-0.076, P=-0.049).

4.1.3.7 Stem length(cm)

Stem length showed highly significant and positive correlation with Root length (G=0.697, P=0.432), pod length (G=0.393, P=0.251),nodule number (G=0.259). It also observed a highly significant but negative correlation with number of pods per cluster (G=-0.631, P=-0.415). Non-significant and positive correlation with thousand seed weight (G=0.089, P=0.058)and non-significant but negative correlation with number of pod per plant (G=-0.005).

4.1.3.8 Root length(cm)

Root length showed highly significant and positive correlation with number of cluster per plant (G=0.440, P=0.278), pod length (G=0.427, P=0.241). It also observed a highly significant but negative correlation with number of pods per cluster (G=-0.706, P=-0.315). Non-significant and positive correlation with nodule number (G=0.137, P=0.096), number of pod per plant (G= 0.105, P=0.121), thousand seed weight (G=0.133, P=0.401),grain weight per plant (G=0.027, P=0.001).

4.1.3.9 Nodule number

Nodule numbers showed positive significant correlation with number of seed per pod (G=0.410, P=0.325),and significant negative correlation with pod length (G=-0.509, P=-0.559), thousand seed weight (G=-0.427, P=-0.395), Non-significant positive correlation with number of cluster per plant (G=0.045, P=0.031), number of pod per plant (G=0.069, P=0.084). Non-significant negative correlation with grain weight per plant (G=-0.182, P=0.145).

4.1.3.10 Number of cluster per plant

Number of clusters per plant showed a highly significant and positive correlation with number of pods per plant (G=0.944, P=0.905), grain weight per plant (G=0.374, P=0.355)It also observed a highly significant but negative correlation with number of seed per pod (G=-0.383, P=-0.362) Non-significant and positive correlation with pod length (G=0.057) and non-significant but negative correlation thousand seed weight (G=-0.223, P=-0.224).

4.1.3.11 Number of pod per cluster

Number of pod per cluster showed highly significant and positive correlation with number of pod per plant (G=0.450, P=0.403), number of seed per pod (G=0.351), Grain weight per plant (G=0.362, P=0.312). It also observed a highly significant but negative correlation with pod length (G=-0.296, P=-0.256) and

non-significant but negative correlation withthousand seed weight (G=-0.203, P=-0.167).

4.1.3.12 Number of pod per plant

Number of pods per plant showed a highly significant and positive correlation with Grain weight per plant (G=0.471, P=0.468)significant negative correlation with thousand seed weight (G=-0.272, P=-0.274)and non-significant but negative correlationwith pod length (G=-0.072, P=-0.115), number of seed per pod (G=-0.198, P=-0.223).

4.1.3.13 Pod length

Pod length showed highly significant and positive correlation with thousand seed weight (G=0.623, P=0.551),Grain weight per plant (G=0.592, P=0.516).

4.1.3.14 Number of seed per pod

Number of seeds per pod showed a highly significant and negative correlation with thousand seed weight (G=-0.476, P=-0.435),Non-significant but negative correlation grain weight per plant (G=-0.134, P=-0.073).

4.1.3.15 Thousand seed weight (g)

Thousand seed weight showed a highly significant and positive correlation with grain weight per plant (G=0.559, P=0.542).

4.1.4 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Dewayand Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of

one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

The direct and indirect effects of yield contributing characters on yield were worked out by using path analysis. Path coefficient analysis was showed direct and indirect effects of different characters on yield of mungbean in (Table 7).

4.1.4.1 Days to 50% flowering

Path coefficient analysis revealed that days to 50% flowering had a significant positivedirect effect (0.062) on grain weight per plant. Days to 50% flowering had positive indirect effect on plant height at plant height at maturity (0.163), number of branches at maturity (0.036), number of pod per cluster (0.072)andnumber of seed per pod (0.092) while negative indirect effect on days to maturity (-0.035), plant height at vegetative stage (-0.76),number of leaf at maturity (-0.058), stem length (0.003),root length (-0.002), nodule number (-0.0005), number of cluster per plant (-0.053), number of pod per plant (0.029), pod length (0.048), thousand seed weight (-0.543). It showed a significant negative genotypic correlation (-0.421) with grain weight per plant.

4.1.4.2 Days to maturity

Path coefficient analysis revealed that days to maturity had a significant negative direct effect (-0.043) on grain weight per plant. Days to maturity had positive indirect effect on days to 50% flowering (0.050), plant height at maturity (0.098), number of branch at maturity (0.036), stem length (0.007), root length (0.028), number of pod per plant (0.403) and number of seed per pod (0.011)while negative indirect effect on plant height at vegetative stage (-0.067), number of leaf at maturity (-0.048), nodule number (-0.003), number of cluster per plant (-0.233), number of pod per cluster (-0.034), pod length (0.069) and

thousand seed weight (-0.466).It showed a significant negative genotypic correlation (-0.328) with grain weight per plant.

4.1.4.3 Plant height at vegetative stage (cm)

Path coefficient analysis revealed that plant height at vegetative stage had a positive direct effect (0.125) on Grain weight per plant. plant height at vegetative stage had positive indirect effect on days to maturity (0.125), number of branches (0.048) , number of leaf at maturity (0.069), root length (0.006), nodule number (0.001), number of cluster per plant (0.120), pod length (0.062), thousand seed weight (0.643) and while negative indirect effect on days to 50% flowering (-0.37), plant height at maturity (-0.283), stem length (-0.18), number of pod per cluster (-0.046), number of pod per plant (-0.194), number of seed per pod (-0.140). It showed a highly significant positive genotypic correlation (0.379) with Grain weight per plant.

4.1.4.4 Plant height at maturity (cm)

Path coefficient analysis revealed that plant height at maturity had a negative direct effect (-0.342) on Grain weight per plant. Plant height at maturity had positive indirect effect on days to maturity (0.012), plant height at vegetative stage (0.104), number of branches at maturity (0.022) , number of leaf at maturity (0.048), root length (0.006), nodule number (0.001), number of cluster per plant (0.153), pod length (0.008), thousand seed weight (0.562), and while negative indirect effect on days to 50% flowering (-0.029), stem length (-0.016), number of pod per cluster (-0.037),number of pod per plant (-0.258) and number of seed per pod (-0.173). It showed a non significant negative genotypic correlation (0.063) with grain weight per plant.

Table 8. Path coefficient analysis showing direct and indirect effects of different characters on yield of mungbean

Direct Effects	DFF	DM	PHVG	PHM	NBM	NLM	SL	RL	NN	NCPP	NPPC	NPPP	PL	NSPP	1000SW	Genotypic correlation with GWPP
DFF	**0.062**	-0.035	-0.076	0.163	0.036	-0.058	-0.003	-0.002	-0.0005	-0.053	0.072	-0.029	-0.048	0.092	-0.543	-0.421**
DM	0.050	**-0.043**	-0.067	0.098	0.036	-0.048	0.007	0.028	-0.0003	-0.233	-0.034	0.403	-0.069	0.011	-0.466	-0.328**
PHVG	-0.037	0.023	**0.125**	-0.283	0.048	0.069	-0.018	0.006	0.001	0.120	-0.046	-0.194	0.062	-0.140	0.643	0.379**
PHM	-0.029	0.012	0.104	**-0.342**	0.022	0.048	-0.016	0.006	0.001	0.153	-0.037	-0.258	0.008	-0.173	0.562	0.063^{NS}
NBM	0.011	-0.008	0.031	-0.039	**0.193**	-0.104	-0.052	-0.058	-0.00002	-0.037	0.113	-0.187	-0.012	-0.045	-0.258	-0.449**
NLM	0.020	-0.012	-0.048	0.091	0.111	**-0.181**	-0.032	-0.015	-0.001	0.098	0.327	-0.644	-0.011	0.028	-0.232	-0.501**
SL	0.002	0.004	0.031	-0.073	0.138	-0.080	**-0.073**	-0.081	0.0003	-0.323	0.298	-0.011	0.057	-0.079	0.087	-0.104^{NS}
RL	0.001	0.010	-0.006	0.019	0.096	-0.024	-0.051	**-0.116**	-0.0003	-0.549	0.333	0.224	0.062	-0.102	0.130	0.027^{NS}
NN	0.013	-0.005	-0.066	0.214	0.002	-0.066	0.010	-0.016	**-0.002**	-0.056	0.020	0.147	-0.074	0.115	-0.417	-0.182^{NS}
NCPP	0.003	-0.008	-0.012	0.042	0.006	0.014	-0.019	-0.051	-0.0001	**-1.247**	-0.063	2.028	0.008	-0.107	-0.218	0.374**
NPPC	-0.009	-0.003	0.012	-0.027	-0.046	0.125	0.046	0.082	0.0001	-0.168	**-0.472**	0.965	-0.043	0.098	-0.199	0.362**
NPPP	-0.001	-0.008	-0.011	0.041	-0.017	0.054	0.000	-0.012	-0.0002	-1.178	-0.212	**2.147**	-0.010	-0.055	-0.266	0.471**
PL	-0.020	0.021	0.054	-0.020	-0.016	0.014	-0.029	-0.049	0.001	-0.071	0.140	-0.154	**0.145**	-0.032	0.609	0.592**
NSPP	0.020	-0.002	-0.063	0.211	-0.031	-0.018	0.021	0.042	-0.001	0.478	-0.166	-0.425	-0.016	**0.280**	-0.465	-0.134^{NS}
1000SW	-0.034	0.021	0.083	-0.197	-0.051	0.043	-0.006	-0.015	0.001	0.279	0.096	-0.584	0.090	-0.133	**0.978**	0.569**

Residual effect: 0.001

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

4.1.4.5 Number of branches per plant at maturity

Path co-efficient analysis revealed that Number of Branches at maturity had a positive direct effect (0.193) on Grain weight per plant. Number of Branches at maturity had positive indirect effect on days to days to 50% flowering (0.011), plant height at vegetative stage (0.031), number of pod per cluster (0.113), while negative indirect effect on days to maturity (-0.008), plant height at maturity (-0.039), number of leaf at maturity (-0.104), Stem length (-0.052), root length (-0.058), nodule number (-0.00002), number of cluster per plant (-0.037), number of pod per plant (-0.187),pod length (-0.012) and number of seed per pod (-0.045),thousand seed weight (-0.258). It showed at negative significantgenotypic correlation (-0.449) with Grain weight per plant.

4.1.4.6Number of leaf per plant at maturity

Path coefficient analysis revealed that Number of leaf at maturity had a negative direct effect (-0.181) on Grain weight per plant. Number of leaf at maturity had positive indirect effect on days to days to 50% flowering (0.020), plant height at maturity (0.091), Number of Branches at maturity (0.111) , number of cluster per plant (0.098),number of pod per cluster (0.327),number of seed per pod (0.028) and while negative indirect effect on days to maturity (-0.012), plant height at vegetative stage (-0.048) , Stem length (-0.032), root length (-0.015), nodule number (-0.001), number of pod per plant (-0.644),pod length (-0.011) thousand seed weight (-0.232) and It showed a highly negative significant genotypic correlation (-0.501) with grain weight per plant.

4.1.4.7 Stem length(cm)

Path coefficient analysis revealed that Stem length had negative direct effect (-0.073) on Grain weight per plant. Stem length had positive indirect effect on days to days to 50% flowering (0.002), days to maturity (0.004), plant height at vegetative stage (0.031),Number of branches at maturity (0.138), nodule number

(0.0003),number of pod per cluster (0.298),pod length (0.057)thousand seed weight (0.087)and while negative indirect effect on plant height at maturity (-0.073), Number of leaf at maturity (-0.080), root length (-0.081), number of cluster per plant (-0.323), number of pod per plant (-0.011) , number of seed per pod (-0.079),It showed non-significant negative genotypic correlation (-0.104) with Grain weight per plant.

4.1.4.8 Root length(cm)

Path coefficient analysis revealed that root length had a negative direct effect (-0.116) on Grain weight per plant. Root length had positive indirect effect on days to 50% flowering (0.001), days to maturity (0.010), plant height at maturity (0.019),Number of branches at maturity (0.096), number of pod per cluster (0.333),number of pod per plant (0.224),pod length (0.062), and thousand seed weight (0.130) while negative indirect effect on plant height at vegetative stage (-0.006), Number of leaf at maturity (-0.024), Stem length (-0.051),nodule number (-0.0003)number of cluster per plant (-0.549),number of seed per pod (-0.102). It showed a non-significant positive genotypic correlation (0.027) with Grain weight per plant.

4.1.4.9 Nodule number

Path coefficient analysis revealed that nodule number had a negative direct effect (-0.002) on Grain weight per plant. Nodule number had positive indirect effect on days to 50% flowering (0.013), plant height at maturity (0.214),Number of Branches at maturity (0.002),Stem length (0.010),number of pod per cluster (0.020),number of pod per plant (0.147),number of seed per pod (0.115)while having a negative indirect effect on days to maturity (-0.005), plant height at vegetative stage (-0.066), Number of leaf at maturity (-0.066), root length (-0.016), number of cluster per plant (-0.056), pod length (-0.074), thousand seed weight (-0.417) and It showed a non-significant negative genotypic correlation (-0.182) with Grain weight per plant.

4.1.4.10 Number of cluster per plant

Path coefficient analysis revealed that number of clusters per plant had a negative direct effect (-1.247) on Grain weight per plant. Number of cluster per plant had a positive indirect effect on days to days to 50% flowering (0.003), plant height at maturity (0.042),Number of Branches at maturity (0.006),Number of leaf at maturity (0.014),number of pod per plant (2.028)pod length (0.008),while negative indirect effect on days to maturity (-0.008), plant height at vegetative stage (-0.012), Stem length (-0.019), root length (-0.051), and nodule number (-0.0001), number of pod per cluster (-0.063), number of seed per pod (-0.0107), thousand seed weight (-0.218). It showed a significant positive genotypic correlation (0.374) with Grain weight per plant.

4.1.4.11 Number of pod per cluster

Path coefficient analysis revealed that number of pods per cluster had a negative direct effect (-0.472) on Grain weight per plant. Number of pod per cluster had positive indirect effects on plant height at vegetative stage (0.012), Number of leaf at maturity (0.125), Stem length (0.046),root length (0.082),nodule number (0.0001),number of pod per plant (0.965),number of seed per pod (0.098)and while negative indirect effect on days to 50% flowering (-0.009), days to maturity (-0.003), plant height at maturity (-0.027), Number of Branches at maturity (-0.046) number of cluster per plant (-0.168), pod length (-0.043), and thousand seed weight (-0.199). It showed a highly significant positive genotypic correlation (0.362) with Grain weight per plant.

4.1.4.12 Number of pods per plant

Path coefficient analysis revealed that number of pods per plant had a positive direct effect (2.147) on Grain weight per plant. Number of pod per plant had a positive indirect effect on days to plant height at maturity (0.041), Number of leaf at maturity (0.054),and while having a negative indirect effect on days to 50% flowering (-0.001),days to maturity (-0.008),plant height at vegetative stage (-

0.011),Number of Branches at maturity (-0.017),root length (-0.012),nodule number (-0.0002), number of cluster per plant (-1.178),number of pod per cluster (-0.212), pod length (-0.010),number of seed per pod (-0.055),thousand seed weight (-0.266),and it showed a significant positive genotypic correlation (0.471) with Grain weight per plant.

4.1.4.13 Pod length (cm)

Path coefficient analysis revealed that pod length had positive direct effect (0.145) on Grain weight per plant. Pod length had a positive indirect effect on days to maturity (0.021), plant height at vegetative stage (0.054),Number of leaf at maturity (0.014),nodule number (0.001),number of pod per cluster (0.140),thousand seed weight (0.609),and while negative indirect effect on days to 50% flowering (-0.020), plant height at maturity (-0.020), Number of Branches at maturity (-0.016), stem length (-0.029),root length (-0.049), number of cluster per plant (-0.071), number of pod per plant (-0.154),number of seed per pod (-0.032)It showed significant positive genotypic correlation (0.592) with Grain weight per plant.

4.1.4.14 Number of seed per pod

Path coefficient analysis revealed that number of seeds per pod had a positive direct effect (0.280) on Grain weight per plant. Number of seed per pod had positive indirect effect on days to days to 50% flowering (0.020), plant height at maturity (0.211), Stem length (0.021),root length (0.042), number of cluster per plant (0.478),and while negative indirect effect on days to maturity (-0.002),plant height at vegetative stage (-0.063),Number of Branches at maturity (-0.031) Number of leaf at maturity (-0.018), nodule number (-0.001)number of pod per cluster (-0.166), number of pod per plant (-0.425),pod length (-0.016)thousand seed weight (-0.465), It showed non-significant negative genotypic correlation (-0.134) with Grain weight per plant.

4.1.4.15 Thousand seed weight(gm)

Path coefficient analysis revealed that thousand seed weight had a positive direct effect (0.978) on Grain weight per plant. Thousand seed weight had positive indirect effects on days to maturity (0.021), plant height at vegetative stage (0.083),Number of leaf at maturity (0.043),nodule number (0.001),number of cluster per plant (0.279)number of pod per cluster (0.096),pod length (0.090),
and while negative indirect effect on days to 50% flowering (-0.034), plant height at maturity (-0.197), Number of Branches at maturity (-0.051), Stem length (-0.006), root length (-0.15), number of pod per plant (-0.584), number of seed per pod (-0.133).It showed significant positive genotypic correlation (0.569) with Grain weight per plant.

4.1.5 Multivariate analysis for agromorphogenic characters

To study the genetic divergence pattern, Multivariate analysis techniques *viz*. Cluster Analysis (CA) and Principal Component Analysis (PCA) were used. The success of the hybridization followed by selection depends largely on the selection of parents showing high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). A large amount of genetic diversity has been reported in mungbean (Sinha *et al.* 1996; Francisco and Maeda, 1989) which indicates potential for genetic improvement of the crop. The genetic variability present among the different genotypes of a species may arise either due to geographical separation or due to genetic barriers to crossability. One of the potent techniques of assessing genetic divergence is D^2 statistic proposed by Mahalanobis in 1936. This technique measures the forces of differentiation at two levels viz., intra cluster and inter cluster that helps selection of genetically divergent parents for exploitation in hybridization programmes. While selecting parents on the basis of D^2 statistic, three important points should be considered *viz*., i) the relative contribution of each character to the total genetic divergence, ii) the choice of clusters with the maximum statistical distance and iii) the selection of one or a

few genotypes from such clusters. Evaluation of germplasm collection has the highest priority among germplasm functions. Germplasm enhancement embraces those activities required to aggregate useful genes and gene combinations into usable phenotypes (Sen and De, 2017).Study of genetic diversity in genetic resources is a critical factor for breeders to better understand the evolutionary and genetic relationship among accessions, to select germplasm in a more systemic and effective way and to develop the strategies to incorporate useful diversity in their breeding programmes (Lavanya*et al*., 2008). The genetic divergence analysis also play important role to select the diverse parent for future hybridization programme. The crosses between the parents with more genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981).

4.1.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with 23 genotypes of mungbean which gives Eigen values of principal component axes of coordination of genotypes with the first axes 27.96% of the total variation among the genotypes. First five Eigen values for five principal component axes of genotypes accounted for 80.75% variation showed in Table 10. Fromfigure 1,thescatter diagram revealed that there were five apparent clusters and the genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

4.1.5.2 Canonical variate analysis

Inter-cluster distances was compute by Canonical Variate Analysis (CVA). The intra and inter-cluster distance (D^2) values were shown in Table 10. When inter-cluster distances were higher than the intra- cluster distances, it's indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters I and II (29.53), followed by between clusters I and IV (28.76).

In contrast, the lowest inter-cluster distance was observed between cluster I and III (17.71). However, the maximum inter-cluster distance indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population. On the other hand, the maximum intra-cluster distance was found in cluster V (0.789), which contained of 9 genotypes, while the minimum distance was found in cluster III (0.7) that comprises 4 genotypes. Inter and intra cluster distanceswere showed in Table 9.

4.1.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as attained by principal coordinate analysis (PCO) for all possible combinations between the couple of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G1 and G7 (Table 11).The lowestdistance was observed between the G7 and G10. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 23 genotypes of mungbean studied.

4.1.5.4 Non-hierarchical clustering

From covariance matrix the computations gave non-hierarchical clustering among 23 genotypes of mungbeanand grouped them into five clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by principal component analysis (PCA). So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 12. The cluster V had (G1, G2, G3, G11, G19, G20, G21, G22, G23) maximum number of genotypes (9) followed by cluster II (G6, G7, G9, G10), cluster III (G8, G15, G17, G18) and cluster IV (G5, G12, G13, G14, G16) which had 4, 4 and 5 genotypes respectively.

Table 9. Eigen values and yield percent contribution of sixteenagro-morphogeniccharacters in twenty-three genotypes of mungbean

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	4.473	27.96	27.96
II	3.093	19.33	47.29
III	2.505	15.66	62.95
IV	1.731	10.82	73.77
V	1.116	6.98	80.75
VI	0.987	6.17	86.92
VII	0.636	3.97	90.89
VIII	0.523	3.27	94.16
IX	0.358	2.24	96.4
X	0.222	1.38	97.78
XI	0.173	1.08	98.86
XII	0.111	0.69	99.55
XIII	0.038	0.24	99.79
XIV	0.028	0.17	99.96
XV	0.005	0.03	99.99
XVI	0	0	100

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

Table 10. Intra (Bold) and inter cluster distances (D^2) for 23 genotypes of mungbean

	I	II	III	IV	V
I	**0**				
II	29.53	**0.702**			
III	17.71	18.48	**0.7**		
IV	28.76	16.63	4.79	**0.732**	
V	24.69	20.52	7.17	11.71	**0.789**

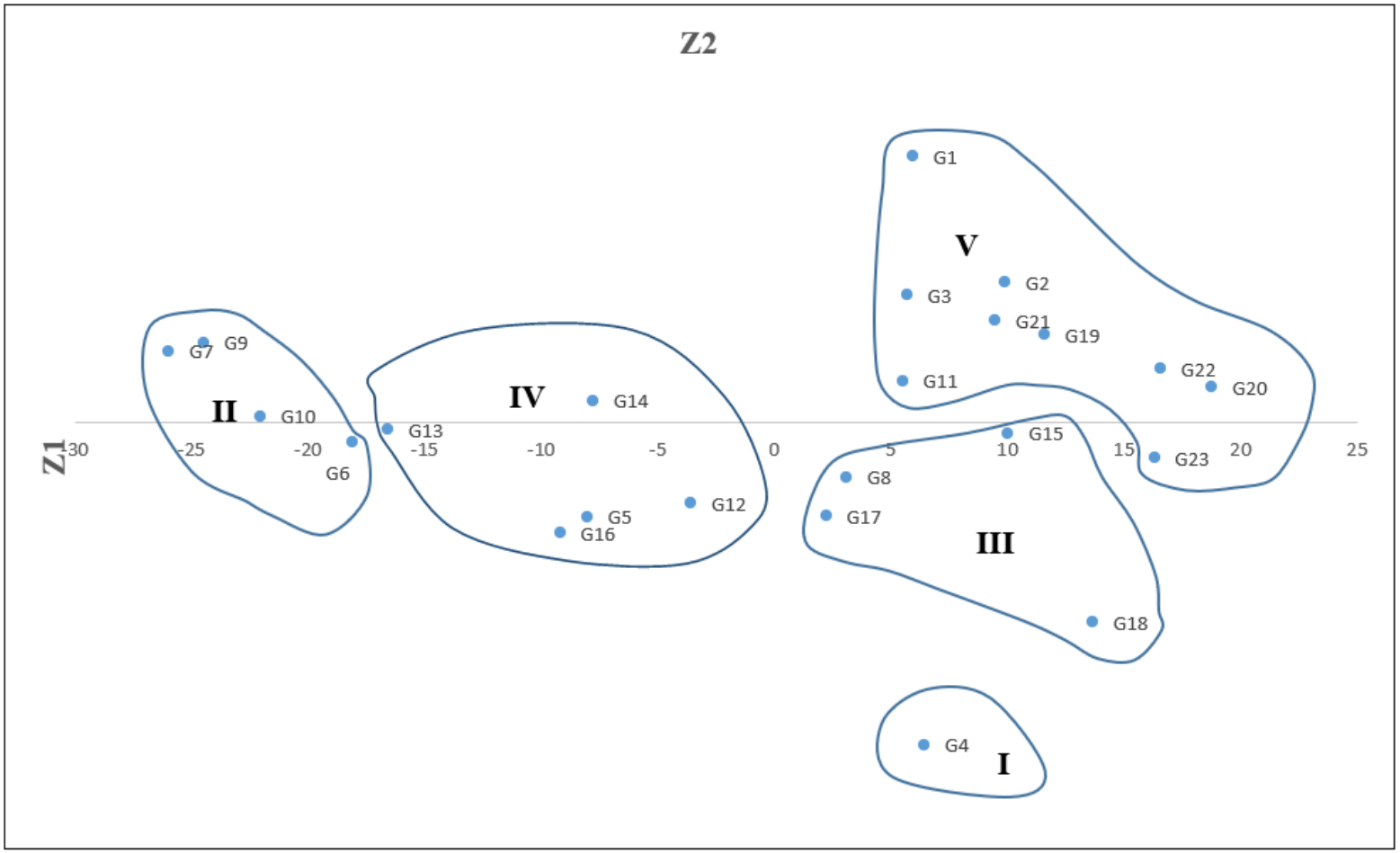

Figure 1. Scatter diagram of 23 mungbean genotypes based on their principal component scores super imposed with clustering based on morphological traits.

Table 11. Ten highest and ten lowest inter genotypic distance of 23 mungbean genotypes

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G1	G7	1.752	G3	G11	0.356
G1	G4	1.739	G13	G14	0.389
G1	G6	1.677	G20	G23	0.406
G4	G7	1.657	G10	G13	0.431
G1	G10	1.612	G21	G22	0.431
G1	G16	1.600	G13	G16	0.485
G1	G5	1.592	G9	G10	0.506
G4	G9	1.574	G19	G20	0.511
G1	G17	1.550	G7	G10	0.515
G7	G18	1.529	G7	G13	0.521

Table 12. Distribution of twenty-three genotypes in different clusters

Cluster no.	Genotypes	No. of genotypes
I	**G4**	**1**
II	**G6, G7, G9, G10**	**4**
III	**G8, G15, G17, G18**	**4**
IV	**G5, G12, G13, G14, G16**	**5**
V	**G1, G2, G3, G11, G19, G20, G21, G22, G23**	**9**
	Total	**23**

4.1.5.5 Cluster mean analysis

The cluster means of 16 different characters (Table 13) were compared and indicated considerable differences between clusters for all the characters studied. The maximum days to 50% flowering were noticed in cluster v (43.48), whereas the minimum maximum days to 50% flowering were noticed in cluster IV (37.87). The maximum days to maturity were observed in cluster I (64.67), whereas the minimum days to maturity in cluster IV (57.4). The maximum plant height at vegetative stagewere noticed in cluster II (35.88), whereas the minimum plant height at vegetative stage were noticed in cluster III (29.15). The maximum number of branches at maturitywas noticed in cluster I (4.43), whereas the minimum number of branches at maturitywere noticed in cluster II (2.99). The maximum number of leaf at maturity were noticed in cluster V (12.46), whereas the minimum number of leaf at maturity were noticed in cluster III (7.68). The maximum stem lengthwas noticed in cluster I (46.89) and the minimum (27.38) in cluster III. Cluster I showed the highest root length (17,61) and cluster II showed the lowest (13.7). The highest nodule number was noticed in cluster III (46.17), whereas the minimum nodule number noticed in cluster IV (25.8). The maximum number of cluster per plant were noticed in cluster I (12.83), whereas the minimum number of cluster per plant were noticed in cluster III(4.18). The maximum (6.76) and the minimum (5.67) number of pod per cluster were observed in cluster III and I, respectively. The maximum number of pod per plant was observed in cluster I (53.77), whereas the minimum number of pod per plant was observed in cluster II (24.86). The maximum (9.39) and the minimum (7.49)pod lengthwere noticed in cluster IV and V, respectively. The maximum number of seed per pod was observed in cluster III (10.73), whereas the minimum number of seed per pod was observed in cluster I (6.5). The maximum thousand seed weight found in cluster II and the minimum thousand seed weight found in cluster V.

Table 13. Cluster mean for sixteen yield and yield related characters in twenty-three genotypes of Mungbean

Characters	I	II	III	IV	V
DFF	42.67	36.67	38.33	37.87	43.48
DM	64.67	57.83	58.83	57.4	62.37
PHVG	32.32	35.88	29.15	32.57	27.71
PHM	61.85	60.75	51.07	54.14	51.25
NBM	4.43	2.99	2.65	2.85	3.43
NLM	11.87	9.47	7.68	7.97	12.46
SL	46.89	32.97	27.38	34.02	33.44
RL	17.61	13.7	14.63	14.89	14.29
NN	31.33	30.25	46.17	25.8	40.48
NCPP	12.83	4.18	5.99	5.17	4.62
NPPC	5.67	5.9	6.76	5.99	5.71
NPPP	53.77	24.86	40.3	30.73	26.62
PL	7.53	8.77	7.65	9.39	7.49
NSPP	6.5	9	10.73	10.17	10.71
1000SW	36.13	53.28	30.7	37.7	25.55
GWPP	9.2	11.96	12.83	11.72	7.08

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

The maximum grain weight per plant found in cluster III (12.83) and the minimum grain weight per plant found in cluster V (7.08).

4.1.5.6 Contribution of characters towards divergence of the genotypes

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis (Jagadev*et al.* 1991). Among the agro-morphogenic traits, high contribution towards total divergence will indicate the possibility of selection of parent(s) for hybridization to manipulate the targeted trait(s) for mungbean improvement. The genotypes of different cluster could be hybridized for the development of desirable genotypes.The characters contribution towards the divergence obtained from principle component analysis is presented in Table 14. The character, which gave highest absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Same as, the characters, which gave highest absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. The same character is given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation. In vector 1 (Z_1), the important characters responsible for genetic divergence in the axis of differentiation were plant height at maturity (1.004), number of branches at maturity (2.632), nodule number (0.228), number of cluster per plant (13.68), number of pod per cluster (8.288), pod length (1.979), thousand seed weight (0.068), grain weight per plant (2.03) In vector 2 (Z_2), the second axis of differentiation plant height at maturity (1.143), number of branches at maturity (2.645), nodule number (0.649), number of cluster per plant (21.268), number of pod per cluster (12.01), pod length (2.221), thousand seed weight (0.64) were important because all thesecharacters had positive signs.

Table14. Relative contributions of sixteen agromorphogenic characters of twenty -three genotypes to the total divergence

Characters	Vector 1	Vector 2
DFF	-0.18	0.044
DM	-0.428	0.453
PHVG	-1.009	-0.785
PHM	1.004	1.143
NBM	2.632	2.645
NLM	-0.448	-0.501
SL	-0.22	0.174
RL	-3.064	-3.465
NN	0.228	0.649
NCPP	13.68	21.268
NPPC	8.288	12.01
NPPP	-2.73	-2.86
PL	1.979	2.221
NSPP	-0.568	0.97
1000SW	0.068	0.64
GWPP	2.03	-1.756

DFF- Days to 50% flowering, DM- Days to maturity, PHVG(cm)- Plant height at vegetative stage, PHM- Plant height at maturity, NBM- Number of branch at maturity, NLM-Number of leaf at maturity, SL- Stem length, RL- Root length, NN- Number of nodule, NCPP- Number of cluster per plant, NPPC- Number of pod per cluster, NPPP- Number of pod per plant, PL- Pod length, NSPP- Number of seed per pod, 1000SW- Thousand seed weight, GWPP- Grain weight per plant.

On the other hand, days to 50% flowering (-0.18), days to maturity (-0.428), plant height at vegetative stage (-1.009), number of leaf at maturity (-0.448), stem length (-0.22), root length (-3.064), possessed the negative sign in the first axis of differentiation, plant height at vegetative stage (-0.785), number of leaf at maturity (-0.501), root length (-0.465) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence.

4.1.5.7 Selection of genotypes as parent for hybridization program

Identification and selection of genetically diverse parents is an urgent step for hybridization program. Three factors (selection of specific variety from a cluster, choice of particular cluster and relative contribution of the character to the total divergence) should be considered for selecting parents for a breeding program. So, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G4 for the maximum number of seed per pod, number of pod per plant, grain weight per plant from cluster I, G6, G9, G10for the minimum days to 50% flowering, maximum number of pod per cluster, number of seed per pod,thousand seed weight, grain weight per plant from cluster II. Therefore considering group distance and other agronomic performance G4 and G6, G9, G10 of mungbean genotypes may be suggested for future hybridization program.

4.2 Experiment 2:Evaluation of mungbean genotypes based on quality traits

This part of the chapter will discuss the results and their interpretation in order for evaluation of mungbean genotypes based on their quality traits.

4.2.1Quality traits

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the quality characters studied (Table 15).

Therefore, there is a lot of scope for selection of the genotypes based on their traits. The mean of all the 11 characters is presented in (Table 16). The extent of variation among the genotypes in respect of seventeen characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in (Table 16).

4.2.2 Genetic variability, heritability and genetic advance

4.2.2.1 Moisture percentage

Significant differences were observed among the genotypes for moisture % which ranged from 5.07 (G23) to 8.88 (G9) with mean value 7.13(Table 16). The σ^2p and σ^2g was observed 0.955 and 0.842 respectively (Table 17). The PCV (13.714) and GCV (12.772) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of mungbean. The heritability estimates for thistrait was high (88.088) with low genetic advance (1.774) over low genetic advance in percent of mean (24.886) (Table 17) revealed that this trait was governed by additive gene and selection would be effective.

Table 15. Analysis of variance for eleven quality characters in twenty-three mungbean genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 22**	**Error (r-1)(g-1) = 44**
Moisture %	0.275	2.639**	0.114
Ash %	0.035	0.274**	0.012
Fat %	0.005	0.083**	0.003
Fibre %	0.073	1.283**	0.079
CHO %	1.335	15.621**	0.380
Iron (mg/100gm)	0.024	3.583**	0.217
K %	0.0007	0.043**	0.0001
P %	0.0003	0.021**	0.0002
Mg %	0.006	0.164**	0.003
CC	0.294	34.819**	0.651
Protein%	0.507	7.744**	0.185

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

** Denote Significant at 1% level of probability, ^{NS}-non-significant

Table 16. Mean analysis of eleven quality parameters in twenty-three genotypes of mungbean

Gen	Moisture %	Ash %	Fat %	Fibre %	CHO %	Iron (mg/100gm)	K %	P %	Mg %	CC	Protien%
G1	5.98	4.03	0.77	4.43	61.72	8.04	0.77	0.50	0.78	42.88	23.05
G2	7.22	3.96	0.66	3.49	61.66	6.65	0.54	0.41	0.44	46.23	22.65
G3	6.35	4.24	0.82	4.62	60.01	5.13	0.81	0.45	0.80	40.66	24.62
G4	7.97	4.48	0.75	4.45	59.12	7.39	0.64	0.40	0.97	37.14	23.24
G5	7.08	4.23	0.66	4.85	58.39	6.77	0.53	0.43	0.48	38.13	24.80
G6	7.82	4.35	0.51	4.19	59.09	5.22	0.57	0.47	0.41	40.38	24.04
G7	7.80	4.56	0.63	4.62	56.53	4.00	0.71	0.43	0.87	42.15	26.20
G8	6.57	4.28	0.72	4.03	59.19	5.28	0.56	0.46	0.39	44.12	25.22
G9	8.88	4.42	0.78	4.16	56.10	4.72	0.61	0.48	0.71	41.30	25.67
G10	7.68	4.12	0.71	5.13	58.24	5.73	0.51	0.35	0.43	44.71	24.00
G11	6.23	4.38	0.72	5.08	58.56	5.08	0.65	0.43	0.65	47.35	25.03
G12	7.22	4.13	0.88	4.58	57.18	5.60	0.56	0.31	0.38	44.64	26.03
G13	7.68	3.53	0.66	4.04	63.07	6.81	0.51	0.36	0.61	48.11	21.02
G14	7.79	4.62	0.85	4.18	59.88	4.95	0.44	0.75	0.41	42.90	22.67

Table 16. (Cont'd)

Gen	Moisture %	Ash %	Fat %	Fibre %	CHO %	Iron (mg/100gm)	K %	P %	Mg %	CC	Protien%
G15	8.84	4.05	0.93	5.51	52.92	5.69	0.62	0.37	1.13	45.90	27.75
G16	7.39	4.01	0.53	4.34	58.60	3.51	0.52	0.40	0.65	41.05	25.13
G17	7.97	4.20	0.66	5.54	54.28	5.85	0.49	0.42	0.48	43.28	27.35
G18	6.46	4.46	0.50	6.32	57.18	5.01	0.76	0.35	1.10	43.43	25.09
G19	6.72	4.12	0.99	5.19	56.75	4.73	0.71	0.41	0.92	47.90	26.24
G20	6.68	5.09	0.87	5.59	58.05	4.62	0.93	0.44	0.86	41.48	23.93
G21	6.65	4.08	0.80	4.22	57.54	4.12	0.55	0.47	0.45	43.43	26.70
G22	5.88	4.54	0.82	4.81	58.71	5.34	0.60	0.38	0.61	48.93	25.23
G23	5.07	4.15	1.25	5.26	59.89	4.91	0.53	0.42	0.54	50.65	24.38
Min	5.07	3.53	0.50	3.49	52.92	3.51	0.44	0.31	0.38	37.14	21.02
Max	8.88	5.09	1.25	6.32	63.07	8.04	0.93	0.75	1.13	50.65	27.75
Mean	7.13	4.26	0.76	4.72	58.38	5.44	0.61	0.43	0.66	43.77	24.78
LSD	0.56	0.18	0.10	0.46	1.01	0.77	0.02	0.02	0.09	1.33	0.71

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

Table 17: Estimation of genetic parameters in eleven quality characters of twenty-three genotypes in mungbean

Parameters	Mean	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	Genetic Advance (5%)	Genetic Advance (% of mean)	CV (%)
Moisture %	7.127	0.955	0.842	0.114	13.714	12.872	0.843	88.088	1.774	24.886	4.730
Ash %	4.262	0.100	0.087	0.012	7.403	6.936	0.467	87.783	0.570	13.387	2.590
Fat %	0.760	0.030	0.026	0.003	22.716	21.404	1.312	88.779	0.316	41.545	7.600
Fibre %	4.723	0.480	0.401	0.079	14.668	13.411	1.257	83.600	1.193	25.261	5.940
CHO %	58.376	5.461	5.080	0.380	4.003	3.861	0.142	93.034	4.478	7.672	1.060
Iron (mg/100gm)	5.441	1.339	1.122	0.217	21.266	19.468	1.798	83.809	1.998	36.715	8.560
K %	0.614	0.015	0.014	0.000	19.615	19.520	0.095	99.035	0.246	40.018	1.910
P %	0.429	0.007	0.007	0.000	19.669	19.447	0.222	97.755	0.170	39.609	2.950
Mg %	0.655	0.057	0.054	0.003	36.322	35.440	0.883	95.197	0.467	71.231	7.960
CC	43.772	12.040	11.389	0.651	7.927	7.710	0.217	94.595	6.762	15.447	1.840
Protein%	24.783	2.705	2.520	0.185	6.636	6.405	0.231	93.146	3.156	12.734	1.740

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

σ^2p: Phenotypic variance, PCV: Phenotypic coefficient of variation, GA (5%): Genetic advance, σ^2g: Genotypic variance, GCV: Genotypic coefficient of variation, GAM: Genetic advance (% of mean),σ^2e: Environmental variance, ECV: Environmental coefficient of variation, CV (%) = coefficient of variation

4.2.2.2 Ash

The analysis of variance revealed significant differences among the genotypes with respect to ash content (Table 15). The genotypic and phenotypic variance was observed 0.087 and 0.100, respectively for ash content with environmental influence. The phenotypic co-efficient of variation (7.403) was higher than the genotypic co-efficient of variation (6.936), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (87.783) estimates for this trait was high, genetic advance (0.570) was a very low and genetic advance in percent of the mean (13.387) was found high, revealed that this trait was governed by the additive gene and selection would be effective.

4.2.2.3 Fat percentage

The σ^2p and σ^2g was observed 0.030 and 0.026 respectively (Table 17). The PCV (22.716) and GCV (21.404) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of mungbean. The heritability estimates for thistrait was high (88.779) with low genetic advance (0.316) over low genetic advance in percent of mean (41.545) (Table 17) revealed that this trait was governed by additive gene and selection would be effective.

4.2.2.4 Fiber

Significant differences were observed among the genotypes for fibercontent which ranged from 3.49 (G2) to 6.32 (G18) with mean value 4.72 (Table 16). The σ2p and σ2g was observed 0.480 and 0.401 respectively (Table 17). The PCV (14.668) and GCV (13.411) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (83.600) with low genetic advance (1.193) over high genetic advance in percent

of mean (25.261) (Table 17) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.2.5 Carbohydrate

Significant differences were observed among the genotypes for Carbohydrate % content which ranged from 52.92 (G15) to 63.07 (G13) with mean value 58.38 (Table 16). The σ^2p and σ^2g was observed 5.461 and 5.080 respectively (Table 17). The PCV (4.003) and GCV (3.461) were same, indicating no environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (93.034) with low genetic advance (4.478) over low genetic advance in percent of mean (7.672) (Table 17) revealed that this trait was governed by environmental influence and selection would be ineffective.

4.2.2.6 Iron (mg/100gm)

The analysis of variance revealed significant differences among the genotypes with respect to iron content (Table 15). The genotypic and phenotypic variance was observed 1.122 and 1.339, respectively for iron content with environmental influence. The phenotypic co-efficient of variation (21.266) was higher than the genotypic co-efficient of variation (19.464), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (83.809) estimates for this trait was high, genetic advance (1.998) was a very low and genetic advance in percent of the mean (36.715) was found high, revealed that this trait was governed by the additive gene and selection would be effective.

4.2.2.7 Potassium

The studied genotypes showed significant difference in case of potassium content (Table 15). Maximum was found 0.93 in (G20) and the minimum was recorded 0.44 in (G14) with mean value 0.61 (Table 16). The σ^2g and σ^2p was observed

0.014 and 0.015 respectively (Table 17). GCV (19.520) and PCV (19.615) were also close to each other (Table 17) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (99.035) with low genetic advance (0.246) over high genetic advance in percent of mean (40.018), revealed that this trait was governed by additive gene and selection is effective for potassium content.

4.2.2.8Phosphorous

The studied genotypes showed significant difference in case of phosphorous content (Table 16). Maximum was found 0.75 in (G14) and the minimum was recorded 0.31 in (G12) with mean value 0.43 (Table 16). The σ^2g and σ^2p was observed 0.007 and 0.007 respectively (Table 17). GCV (19.447) and PCV (19.669) were also close to each other (Table 17) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (97.755) with low genetic advance (0.170) over high genetic advance in percent of mean (39.609), revealed that this trait was governed by additive gene and selection is effective for phosphorous content.

4.2.2.9 Magnesium

Significant differences were observed among the genotypes for magnesium which ranged from 0.38 (G12) to 1.13 (G15) with mean value 0.66 (Table 16). The σ^2p and σ^2g was observed 0.057 and 0.054 respectively (Table 17). The PCV (36.322) and GCV (35.440) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high

(95.197) with low genetic advance (0.467) over high genetic advance in percent of mean (71.231) (Table 17) revealed that this trait was governed by additive gene and selection is effective.

4.2.2.10 Chlorophyll content

The studied genotypes showed significant difference in case of Chlorophyll content (Table 16). Maximum was found 50.65 in (G23) and the minimum was recorded 37.14 in (G4) with mean value 43.77 (Table 16). The σ^2g and σ^2p was observed 11.389 and 12.040 respectively (Table 17). GCV (7.710) and PCV (7.927) were also close to each other (Table 17) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (94.595) with low genetic advance (6.762) over high genetic advance in percent of mean (15.447), revealed that this trait was governed by additive gene and selection is effective for phosphorous content.

4.2.2.11 Protein

The studied genotypes showed significant difference in case of protein % content (Table 16). Maximum was found 27.75 in (G17) and the minimum was recorded 21.02 in (G13) with mean value 24.78(Table 16). The σ^2g (2.520) was lower than σ^2p (2.705). GCV (6.405) and PCV (6.636) were also close to each other (Table 17) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (93.146) with low genetic advance (3.156) over high genetic advance in percent of mean (12.734), revealed that this trait was governed by additive gene and selection is effective for protein content.

4.2.3 Correlation Co-efficient

The genotypic and phenotypic correlation co-efficient among yield and yield contributing characters of mungbean are shown in Table 18 and Table 19.

4.2.3.1 Moisture

Moisture had non-significant positive correlation with protein (G= 0.150, P=0.122), iron (G=0.045), phosphorus (G=0.062, P=0.060) and magnesium (G=0.095, P=0.089) at both genotypic and phenotypic level (Table 18 and Table 19). It had significant negative association with fat, carbohydrate, potassium at both genotypic and phenotypic level (Table 18 and Table 19). It had also non-significant negative association with ash, fibre, at both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.2 Ash

Ash had significant positive association with fibre (G=0.334, P=0.312), potassium (G=0.476, P=0.459) at both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant positive correlation with fat, magnesium, protein at both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.3 Fat

It had significant positive correlation with chlorophyll content (G=0.501, P=0.451), at both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant positive association with fibre, potassium, phosphorus, magnesium, at both genotypic and phenotypic level (Table 18 and Table 19). It had also non-significant negative association with CHO, iron at both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.4 Fiber

Fiber had significant positive correlation potassium, magnesium, protein and at both genotypic and phenotypic level (Table 18 and Table 19). It had also non-significant negative correlation with iron at genotypic level (Table 18 and Table 19).

4.2.3.5 Carbohydrate

Carbohydrate had significant positive correlation with iron(G=0.412, P=0.369) at both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant positive correlation with phosphorus, chlorophyll content at both genotypic and phenotypic level (Table 18 and Table 19). It had also non-significant negative correlation with potassiumat both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.6 Iron

It had non-significant negative correlation with potassium, phosphorus ,magnesium, chlorophyll content at both genotypic and phenotypic level (Table 18 and Table 19). It had significant negative association with protein at both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.7 Potassium

It had significant positive correlation with magnesium (G=0.687, P=0.669) at both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant negative correlation with phosphorus, chlorophyll content at both genotypic and phenotypic level (Table 18 and Table 19). It had also non-significant positive correlation with protein at both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.8 Phosphorus

It had significant negative correlation with magnesium (G=-0.244, P=-0.239), protein at both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant negative association with chlorophyll contentat both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.9 Magnesium

It had non-significant positive correlation with proteinat both genotypic and phenotypic level (Table 18 and Table 19). It had non-significant negative association with chlorophyll contentat both genotypic and phenotypic level (Table 18 and Table 19).

4.2.3.10 Chlorophyll content

It had non-significant positive correlation with proteinat both genotypic and phenotypic level (Table 18 and Table 19).

4.2.4 Path coefficient analysis

Path coefficient analysis was showed direct and indirect effects of different characters mungbean in Table 20.

4.2.4.1 Moisture

Moisture had negative direct effect (-0.585) on protein % (Table 20) which is contributed to result non-significant positive genotypic correlation with protein% (0.150).It showed positive indirect effect with ash%, fat%, fibre%, carbohydrate%, phosphorus%, chlorophyll content. It had a negative indirect effect on iron, potassium, magnesium.

Table 18. Genotypic correlation coefficients among different pairs of quality characters for different genotype of mungbean

Character	Moisture %	Ash %	Fat %	Fibre %	CHO %	Iron (mg/100gm)	K %	P %	Mg %	CC	Protein%
Moisture %	1										
Ash %	-0.057^{NS}	1									
Fat %	-0.353**	0.055^{NS}	1								
Fibre %	-0.197^{NS}	0.334**	0.195^{NS}	1							
CHO %	-0.433**	-0.275*	-0.074^{NS}	-0.561**	1						
Iron (mg/100gm)	0.045^{NS}	-0.361**	-0.056^{NS}	-0.187^{NS}	0.412**	1					
K %	-0.298*	0.476**	0.070^{NS}	0.406**	-0.049^{NS}	-0.055^{NS}	1				
P %	0.062^{NS}	0.337**	0.105^{NS}	-0.351**	0.199^{NS}	-0.108^{NS}	-0.143^{NS}	1			
Mg %	0.095^{NS}	0.224^{NS}	0.063^{NS}	0.553**	-0.336**	-0.008^{NS}	0.687**	-0.244*	1		
CC	-0.424**	-0.355**	0.501**	0.148^{NS}	0.097^{NS}	-0.095^{NS}	-0.179^{NS}	-0.233^{NS}	-0.100^{NS}	1	
Protein%	0.150^{NS}	0.134^{NS}	0.130^{NS}	0.451**	-0.906**	-0.495**	0.047^{NS}	-0.242*	0.192^{NS}	0.025^{NS}	1

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

Table 1. Phenotypic correlation coefficients among different pairs of quality characters for different genotype of mungbean

Character	Moisture %	Ash %	Fat %	Fibre %	CHO %	Iron (mg/100gm)	K %	P %	Mg %	CC	Protein%
Moisture %	1										
Ash %	-0.063^{NS}	1									
Fat %	-0.316**	0.033^{NS}	1								
Fibre %	-0.168^{NS}	0.312**	0.125^{NS}	1							
CHO %	-0.433**	-0.248*	-0.074^{NS}	-0.538**	1						
Iron (mg/100gm)	0^{NS}	-0.285*	-0.032^{NS}	-0.132^{NS}	0.369**	1					
K %	-0.273*	0.459**	0.056^{NS}	0.369**	-0.049^{NS}	-0.051^{NS}	1				
P %	0.060^{NS}	0.302*	0.080^{NS}	-0.299*	0.187^{NS}	-0.106^{NS}	-0.141^{NS}	1			
Mg %	0.089^{NS}	0.206^{NS}	0.052^{NS}	0.468**	-0.317**	-0.015^{NS}	0.669**	-0.239*	1		
CC	-0.380**	-0.307*	0.451**	0.130^{NS}	0.098^{NS}	-0.091^{NS}	-0.170^{NS}	-0.226^{NS}	-0.104^{NS}	1	
Protein%	0.122^{NS}	0.096^{NS}	0.137^{NS}	0.389**	-0.878**	-0.453**	0.041^{NS}	-0.230^{NS}	0.191^{NS}	0.018^{NS}	1

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

4.2.4.2 Ash

It had negative direct effect (-0.231) on protein % (Table 20) which is contributed to result non-significant positive genotypic correlation with protein% (0.134).It showed positive indirect effect with moisture, carbohydrate, iron, potassium,phosphorus, chlorophyll content. It had a negative indirect effect on fat, fibre, magnesium.

4.2.4.3 Fat

Fat had negative direct effect (-0.070) on protein % (Table 20) which is contributed to result non-significant positive genotypic correlation with protein% (0.130).It showed positive indirect effect with moisture, carbohydrate, iron, potassium. It had a negative indirect effect on ash, fibre, magnesium, chlorophyll content.

4.2.4.4 Fibre

Fibre had negative direct effect (-0.389) on protein % (Table 20) which is contributed to result significant positive genotypic correlation with protein% (0.451).It showed positive indirect effect with moisture, carbohydrate, iron, potassium. It had a negative indirect effect on ash, fat, iron, phosphorus, magnesium, chlorophyll content.

4.2.4.5 Carbohydrate

Carbohydrate had negative direct effect (-1.428) on protein % (Table 20) which is contributed to result significant negative genotypic correlation with protein% (-0.906).It showed positive indirect effect with moisture, ash, fat, fibre, phosphorus, magnesium. It had a negative indirect effect on iron, potassium, chlorophyll content.

4.2.4.6 Iron

Iron had negative direct effect (-0.041) on protein % (Table 20) which is contributed to result significant negative genotypic correlation with protein% (-

0.495).It showed positive indirect effect with ash, fat, fibre, magnesium, chlorophyll content. It had a negative indirect effect on carbohydrate, potassium, phosphorus.

4.2.4.7 Potassium

Potassium had positive direct effect (0.074) on protein % (Table 20) which is contributed to result non-significantpositivegenotypic correlation with protein% (0.047).It showed positive indirect effect with moisture, carbohydrate, iron, chlorophyll content.It had a negative indirect effect on ash, fat, fibre, phosphorus, magnesium.

4.2.4.8 Phosphorus

Phosphorus had positive direct effect (0.015) on protein % (Table 20) which is contributed to result significant negative genotypic correlation with protein% (-0.242).It showed positive indirect effect with fibre, iron, magnesium, chlorophyll content. It had a negative indirect effect on moisture, ash, fat, carbohydrate, potassium.

4.2.4.9 Magnesium

Magnesium had negative direct effect (-0.62) on protein % (Table 20) which is contributed to result non-significant positive genotypic correlation with protein% (0.192).It showed positive indirect effect with carbohydrate, iron, potassium, chlorophyll content. It had a negative indirect effect on moisture, ash, fat, fibre, phosphorus.

4.2.4.10 Chlorophyll content

Chlorophyll content had negative direct effect (-0.062) on protein % (Table 20) which is contributed to result non-significant positive genotypic correlation with protein% (0.025).It showed positive indirect effect with moisture, ash, iron. It had a negative indirect effect on fat, fibre, carbohydrate, potassium, phosphorus.

Table 20. Path coefficient analysis showing direct and indirect effects of different quality characters of mungbean

Direct effect	Moisture %	Ash %	Fat %	Fibre %	CHO %	Iron (mg/100gm)	K %	P %	Mg %	CC	Protein%
Moisture %	**-0.585**	0.013	0.025	0.077	0.619	-0.002	-0.022	0.001	-0.001	0.026	0.150^{NS}
Ash %	0.033	**-0.231**	-0.004	-0.130	0.392	0.015	0.035	0.005	-0.003	0.022	0.134^{NS}
Fat %	0.207	-0.013	**-0.070**	-0.076	0.105	0.002	0.005	0.002	-0.001	-0.031	0.130^{NS}
Fibre %	0.115	-0.077	-0.014	**-0.389**	0.801	0.008	0.030	-0.005	-0.008	-0.009	0.451**
CHO %	0.254	0.063	0.005	0.218	**-1.428**	-0.017	-0.004	0.003	0.005	-0.006	-0.906**
Iron (mg/100gm)	-0.027	0.083	0.004	0.073	-0.588	**-0.041**	-0.004	-0.002	0.0001	0.006	-0.495**
K %	0.175	-0.110	-0.005	-0.158	0.070	0.002	**0.074**	-0.002	-0.010	0.011	0.047^{NS}
P %	-0.036	-0.078	-0.007	0.137	-0.284	0.004	-0.011	**0.015**	0.004	0.014	-0.242*
Mg %	-0.056	-0.052	-0.004	-0.215	0.479	0.0003	0.051	-0.004	**-0.015**	0.006	0.192^{NS}
CC	0.248	0.082	-0.035	-0.058	-0.139	0.004	-0.013	-0.003	0.001	**-0.062**	0.025^{NS}

Residual effect: 0.005

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll conten

4.2.5 Multivariate analysis for quality characters

4.2.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with six genotypes of sweet potato which gives Eigen values of principal component axes of coordination of genotypes with the first axes 28.43% of the total variation among the genotypes. First five Eigen values for five principal coordination axes of genotypes accounted for 84.54% variation showed in Table 21.

4.2.5.2 Canonical variate analysis

Inter-cluster distances was compute by Canonical Variate Analysis (CVA). The intra and inter-cluster distance (D^2) values were shown in Table 22.When inter-cluster distances were higher than the intra-cluster distances, it's indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters I and V (15.341), followed by between clusters I and IV (11.284).

In contrast, the lowest inter-cluster distance was observed between cluster I and II (9.219). However, the maximum inter-cluster distance was observed between the clusters I and V (15.341) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population.On the other hand, the maximum intra-cluster distance was found in cluster V (0.424), which contained of 2 genotypes, while the minimum distance was found in cluster I (0.339) that comprises 3 genotypes each. Inter and intra cluster distanceswere showed in Table 22. In the present study the maximum distance existence both cluster I and V at the same level. So the crosses between the genotypes belonging cluster I with cluster IV might produce high heterosis. So the genotypes belonging to cluster I and cluster V might be selected for future hybridization program.

Table 21. Eigen values and percent contribution of eleven quality characters in twenty-three genotypes of mungbean

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	3.127	28.43	28.43
II	2.0048	18.23	46.66
III	1.8213	16.56	63.22
IV	1.5103	13.73	76.95
V	0.835	7.59	84.54
VI	0.5729	5.21	89.75
VII	0.4563	4.15	93.9
VIII	0.333	3.03	96.93
IX	0.2186	1.99	98.92
X	0.1191	1.08	100
XI	0.0016	0.01	100

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

Table 22. Intra (Bold) and inter cluster distances (D^2) in quality experiment

	I	II	III	IV	V
I	**0.339**				
II	9.219	**0.387**			
III	10.751	4.538	**0.409**		
IV	11.284	8.826	4.793	**0.303**	
V	15.341	9.19	4.988	5.504	**0.424**

4.2.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as attained by principal coordinate analysis (PCO) for all possible combinations between the couple of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G4 and G23 (Table 23).The lowest distance was observed between the G11 and G19. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 23 genotypes of mungbean studied.

4.2.5.4 Non-hierarchical clustering

From covariance matrix the computations gave non-hierarchical clustering among six genotypes of sweet potatoand grouped them into three clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by principal component analysis (PCA). So, the results obtained through PCA were confirmed by non-hierarchical clustering.Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 24. Cluster III had the maximum number of 10 genotypes comprising G7, G8, G9, G10, G12, G14 and G16 respectively.

4.2.5.5 Cluster mean analysis

The cluster means of 11 different characters (Table 25) were compared and indicated considerable differences between clusters for all the characters studied. The maximum moisture was noticed in cluster V (8.4), whereas the minimum moisture was noticed in cluster IV (5.98). The maximum ash percentwas observed in cluster III (4.38), whereas the minimum ash percent in cluster I (3.84). The maximum fat was noticed in cluster IV (0.94), whereas the minimum fat was noticed in cluster II (0.69). The maximum fiber was noticed in cluster V (5.53), whereas the minimum fiber was noticed in cluster I(3.99). The maximum carbohydrate was noticed in cluster I (62.15), whereas the minimum carbohydrate was noticed in cluster V (53.6). The maximum iron was noticed in cluster I (7.17)

and the minimum (4.75) in cluster III. The maximum potassium was observed in cluster II (0.64), whereas the minimum potassium was observed in cluster V (0.55).The maximum phosphorous was observed in cluster II (0.44), whereas the minimum was observed in cluster V (0.4). The maximum (0.8) and the minimum (0.61) magnesium were observed in cluster V and I, respectively. The maximum (48.71) and the minimum (39.08) chlorophyll contentwere noticed in cluster IV and II, respectively. The maximum protein was noticed in cluster V (27.55), whereas the minimum protein was noticed in cluster I (22.24).

Table 23. Ten highest and ten lowest inter genotypic distance in quality experiment

Highest Distance			Lowest Distance		
Genotypes		**Distance**	**Genotypes**		**Distance**
G4	G23	0.765	G11	G22	0.119
G5	G23	0.723	G10	G12	0.175
G6	G23	0.712	G10	G17	0.180
G3	G23	0.686	G8	G12	0.204
G4	G13	0.684	G2	G13	0.216
G5	G13	0.672	G3	G11	0.225
G13	G17	0.662	G6	G8	0.226
G13	G15	0.655	G8	G21	0.230
G13	G20	0.651	G5	G10	0.243
G15	G23	0.651	G11	G19	0.245

Table 24. Distribution of twenty-three genotypes in different clusters

Cluster No.	Genotypes	No. of genotypes
I	**G1, G2, G13**	**3**
II	**G3, G4, G5, G6**	**4**
III	**G7, G8, G9, G10, G12, G14, G16, G18, G20, G21**	**10**
IV	**G11, G19, G22, G23**	**4**
V	**G15, G17**	**2**
	Total	**23**

Table 25. Cluster mean for eleven quality characters in twenty-three genotypes of mungbean

Characters	I	II	III	IV	V
Moisture %	6.96	7.3	7.31	5.98	8.4
Ash %	3.84	4.32	4.38	4.3	4.12
Fat %	0.7	0.69	0.73	0.94	0.8
Fibre %	3.99	4.53	4.72	5.09	5.53
CHO %	62.15	59.15	57.85	58.48	53.6
Iron (mg/100gm)	7.17	6.13	4.75	5.01	5.77
K %	0.61	0.64	0.62	0.62	0.55
P %	0.42	0.44	0.44	0.41	0.4
Mg %	0.61	0.67	0.63	0.68	0.8
CC	45.74	39.08	42.92	48.71	44.59
Protein%	22.24	24.17	25.06	25.22	27.55

CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage, CC- Chlorophyll content.

4.2.5.6 Contribution of characters towards divergence of the genotypes

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis (Jagadev*et al.,* 1991). Further Multivariate analysis is an important tool for assessing the degree of divergence and relative contribution of different characters to total divergence (Zaman*et al.,* 2005). Mian *et al*. (1989) also suggested that the multivariate analysis is an important tool to identify genetically diverse parents. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Bose and Pradhan, 2005; Rahman *et al*., 1997; Sinha *et al.*, 1996; Murty and Arunachalam,1966). Hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Recombination breeding between genotypes of different clusters had also been suggested by Sinha *et al*. (1991) and Singh *et al.* (1996).The characters contribution towards the divergence obtained from principle component analysis is presented in Table 26. The character, which gave highest absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Same as, the characters, which gave highest absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. The same character is given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation. In vector 1 (Z_1), the important characters responsible for genetic divergence in the axis of differentiation were moisture (3.008), ash (7.863), fat (6.1), fibre (4.875), carbohydrate (2.505), magnesium (0.852), chlorophyll content (0.064), protein (3.716).In vector 2 (Z_2), the second axis of differentiation moisture (4.309), ash (3.539), fat (5.241), fibre (4.418), carbohydrate (3.867), protein (3.636) were important because all these characters had positive signs. On the other hand, iron (-0.793), potassium (-1.4)possessed the negative sign in the first axis of differentiation and iron (-

Table26. Relative contributions of the eleven quality characters of twenty-three genotypes to the total divergence

Characters	Vector 1	Vector 2
Moisture %	3.008	4.309
Ash %	7.863	3.539
Fat %	6.1	5.241
Fibre %	4.875	4.418
CHO %	2.505	3.867
Iron (mg/100gm)	-0.793	-0.197
K %	-17.225	-3.364
P %	-1.4	-5.735
Mg %	0.852	-2.319
CC	0.064	-0.77
Protein%	3.716	3.636

CC- Chlorophyll content, CHO- Percentage of carbohydrate, K%- Potassium percentage, P%- Phosphorus percentage, Mg%- Magnesium percentage

0.197), potassium (-3.364), phosphorous (-5.735),magnesium (-2.319), chlorophyll content (-0.77) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence.

4.2.5.7Selection of genotypes as parent for hybridization programme

Genetically dissimilar parent selection is the fundamental works for hybridization programme. In the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G1, G2 for the maximum percentage ofiron, fibre, carbohydrate, potassium from cluster I, G15, G17for the minimum fat, carbohydrate, maximum protein percentage, maximum fibre percentage from cluster V. Therefore considering group distance and nutrient content level G1 and G15 genotypes may be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present study was undertaken at Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh with 23 mungbean genotypes during the period from March 2019 to June 2019 and lab experiment was conducted in Bangladesh Council of Science and Industrial Research during the period from July to September. Mungbean was sown to the main field in Randomized Complete Block Design (RCBD) with four replications. Data on various agro –morphological traits such as days to 50% flowering, days to maturity, plant height at vegetative stage, plant height at maturity, number of branch at maturity, number of leaf at maturity, stem length, root length, number of nodule, number of cluster per plant ,number of pod per cluster, number of pod per plant, pod length, number of seed per pod, thousand seed weight, grain weight per plant were recorded Data on various qualitative traits such as moisture (%), protein (%), fat(%), fiber (%), ash (%), carbohydrate (%), magnesium(%), potassium(%), phosphorus(%), iron (mg/g), and chlorophyll content were also recorded.

In case of agro-morphological traits, analysis of variance revealed significant differences among all the genotypes for all the characters under study. In case of qualitative traits, the analysis of variances showed significant mean squares for different characters indicated the presence of sufficient variation among the genotypes for all the characters.

Number of pod per plant showed highest range of variation in agro-morphological traits (53.77-16) that means wide range of variation present for this character. The carbohydrate content % showed highest range of variation in qualitative traits (21.02-27.75) that means wide range of variation present for this character.

Number of cluster per plant, number of pod per plant, thousand seed weight,grain weight per plant in agro-morphological traits exhibit the highest value of heritability. In case of qualitative traits, all the characters under the present study exhibit the highest value of heritability.

Correlation co-efficient among the characters were studied to define the association between yield and yield contributing components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study. The significant positive correlation with yield per plant was found in plant height at vegetative stage, number of cluster of plant, number of pod per cluster, pod length, thousand seed weight at both genotypic and phenotypic level, and number of pod per plant at phenotypic level. In case of qualitative traits, the significant positive correlation with protein percentage was found in fiberat genotypic and phenotypic level.

Path coefficient analysis showed that number of pod per plant had significant positive direct effect (2.147) on yield. It had also significant positive correlation with grain weight per plant(0.0.471).It also showed that pod length, number of seed per pod, thousand seed weight had positive direct effect on yield. It also showed that thousand seed per plant (0.569),pod length (0.592) had the positive correlation with yield. Its indicating selection would be more effective for these characters in crop improvement. In case of qualitative traits potassium %, and phosphorous % had direct positive effect on protein %.

In case of agro-morphological traits, genetic diversity of twenty three genotypes based on sixteen characters were measured through multivariate analysis. The twenty three genotypes fell into five distant clusters. The highest inter-cluster distance was observed between cluster I and II (29.53) followed by between clusters I and V (28.76). In contrast, the lowest inter-cluster distance was observed between cluster III and IV

(4.79). However, the maximum inter-cluster distance was observed between the clusters I and II (29.53) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population.

From the findings of the present study, the following conclusions could be drawn:

- In both agro-morphological and qualitative traits, technique of selection would be applied for desired characters number of pod per plant, number of cluster per plant, pod length, thousand seed weight and protein content, fiber % to develop high yielding varieties.

- In case of agro-morphological traits, wide range of genetic diversity existed among 23 genotypes which were grouped into five clusters and most diverse genotypes were G4 and G6, G9. That variability could be used for future breeding program of mungbean in Bangladesh.

- In case of agro-morphological traits, highly significant positive association of number of cluster per plant, number of pod per cluster, pod length, thousand seed weight at with grain weight per plant at genotypic and phenotypic level. In case of qualitative traits, the significant positive correlation with protein was found in fiber at genotypic and phenotypic level. This result suggested that grain weight per plant and nutrition can be increased by improving these characters.

- In case of agro-morphological traits, number of pod per plant, pod length, number seed pod per plant, thousand seed had the positive direct effect with grain weight per plant. In case of qualitative traits, potassium, and phosphorous content had direct positive effect on protein content % and fiber had significant positive correlation with protein matter content %. This result

suggested that grain weight per plant per plant and nutrition can be increased by improving these characters.

Based on the results of the study, the following recommendations may be drawn:

- Genotypes G4 and G6 could be included in future breeding program in the response of increase grain weight per plant.

- The genotypes of cluster I and II could be used as parents for the further breeding program to develop mungbean variety.

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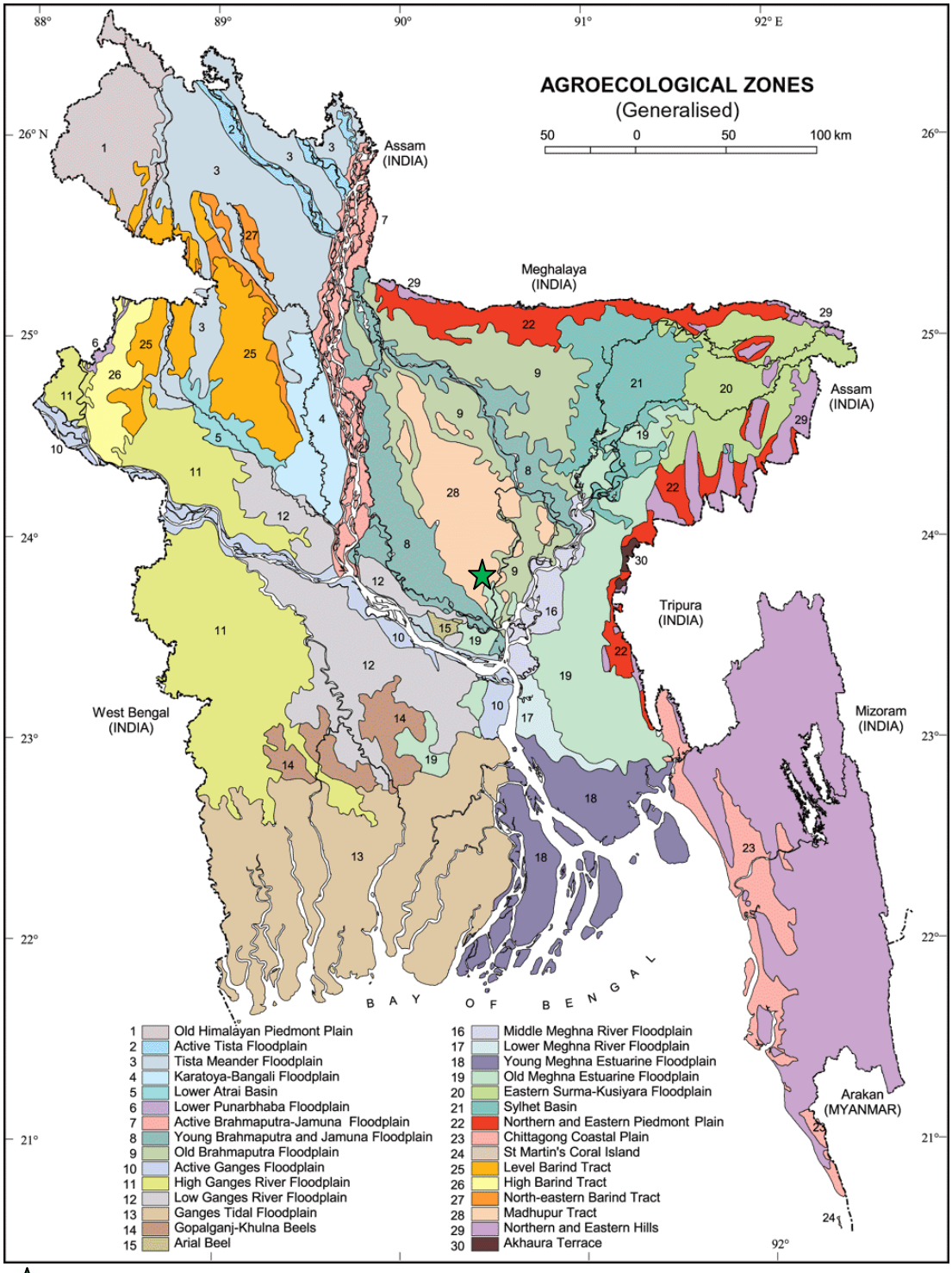
APPENDICES

Appendix I. Map showing the experimental site under the study



★ The experimental site under the study

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

A. Morphological characteristics of the experimental field

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

B. Physical composition of the soil

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

Appendix II. (Cont'd)

C. Chemical composition of the soil

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

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

Appendix III. Monthly average temperature, average relative humidity and total rainfall and average sunshine of the experimental site during the period from March, 2019 to June, 2019.

Month	Average temperature (°c)		Average RH (%)	Rainfall (mm) (total)	Average sunshine (hr)
	Minimum	Maximum			
March, 2019	19.5	28.1	68	00	6.8
April, 2019	23.2	33.4	67	78	6.9
May, 2019	25.9	34.7	70	185	7.8
June, 2019	25.5	32.4	81	228	5.7

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

Appendix IV. Pictorial view of the experimental field