

**“ IDENTIFICATION OF GENETIC STOCK OF
URDBEAN [*Vigna mungo* (L.) Hepper] FOR
YELLOW VEIN MOSAIC RESISTANCE ”**

By

Mr. JATRATE SAGAR MALLAPPA

(Reg. No. 015/035)

A thesis submitted to the

**MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
MAHARASHTRA, INDIA**

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

GENETICS AND PLANT BREEDING

**DEPARTMENT OF AGRICULTURAL BOTANY,
POST GRADUATE INSTITUTE,
MAHATMA PHULE KRISHI VIDYAPEETH
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2017

CANDIDATE'S DECLARATION

*I hereby declare that this thesis or part
there of has not been submitted
by me or any other person to
this or any other University
or Institute for a
Degree or
Diploma.*

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Dated : / /2017

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This is to certify that the thesis entitled **“IDENTIFICATION OF GENETIC STOCK OF URDBEAN [*Vigna mungo* (L.) Hepper] FOR YELLOW VEIN MOSAIC RESISTANCE”**, submitted to MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI, DIST. AHMEDNAGAR, MAHARASHTRA. STATE. for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the results of a piece of bonafide research work carried out by **Mr. JATRATE SAGAR MALLAPPA**, under my guidance and supervision and that no part of the thesis has been submitted for any other Degree or Diploma. The assistance and help received during the course of this investigation have been acknowledged.

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This is to certify that the thesis entitled, **“IDENTIFICATION OF GENETIC STOCK OF URDBEAN [*Vigna mungo* (L.) Hepper] FOR YELLOW VEIN MOSAIC RESISTANCE”**, submitted to the MAHATMA PHULE KRISHI VIDYAPEETH, RAHURI, DIST.AHMEDNAGAR, MAHARASHTRA. STATE. for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the results of a piece of bonafide research work carried out b **Mr. JATRATE SAGAR MALLAPPA**, under the guidance and supervision of **Dr. S. B. CHAUDHARY**, Assistant Professor of Agricultural Botany, Department of Agricultural Botany, P.G.I., MPKV, Rahuri and that no part of the thesis has been submitted for any other Degree or Diploma.

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Place : M.P.K.V., Rahuri

Date : / /2017

(Mr.JATRATE.S.M.)

CONTENTS	Page
CANDIDATE'S DECLARATION	iii
CERTIFICATES	
1. Research Guide	iv
2. Associate Dean (PGI)	v
ACKNOWLEDGMENT	vi-vii
LIST OF CONTENTS	viii-ix
LIST OF TABLES	X
LIST OF FIGURES	X
LIST OF ABBREVIATIONS	Xi
ABSTRACT	xii-xv
1. INTRODUCTION	1-4
2. REVIEW OF LITERATURE	5-27
2.1 Genetic Variability	5
2.2 Heritability and genetic advance	10
2.3 Correlation coefficient and path analysis	14
2.4 Genetic diversity	22
2.5 Screening for virus resistance	26
3. MATERIAL AND METHODS	28-42
3.1 Experimental material	28
3.2 Experimental methods	28
3.3 Observations recorded	29
3.4 Screening for virus resistance	32
3.5 Statistical analysis	33
4. EXPERIMENTAL RESULTS	43-72
4.1 Genetic variability and heritability	43
4.2 Correlation studies	51
4.3 Path coefficient analysis	59
4.4 Genetic divergence	64
4.5 Screening for virus resistance	67

CONTENTS	Page
5. DISCUSSION	73-86
5.1 Genetic variability and heritability	73
5.2. Correlation studies	76
5.3 Path coefficient analysis	78
5.4 Genetic divergence	82
5.5 Screening for virus resistance	86
6. SUMMARY AND CONCLUSIONS	87-91
6.1 Genetic variability and heritability	87
6.2 Correlation studies	88
6.3 Path coefficient analysis	88
6.4 Genetic divergence	89
6.5 Screening for virus resistance	90
7. LITERATURE CITED	93-104
8. VITA	105

LIST OF TABLES

Table No.	Title	Page No.
1.	List of thirty urdbean genotypes with salient features included in the study.	30
2.	Analysis of variance for twelve quantitative characters of urdbean genotypes.	45
3.	Mean values for different characters in urdbean genotypes.	48
4.	Estimates of variability parameters for thirteen different characters of urdbean.	52
5.	Estimation of genotypic and phenotypic correlation coefficients for different characters of urdbean genotypes.	57
6.	Direct and indirect effects of twelve causal variables on seed yield of urdbean genotypes.	60
7.	Composition of thirty urdbean genotypes into different clusters by Tocher's method.	68
8.	Average intra and inter cluster D^2 and cluster distance D values of urdbean genotypes.	68
9.	Cluster means for twelve characters of urdbean genotypes .	69
10.	Per cent contribution of different characters to genetic diversity of urdbean genotypes.	70
11.	Per cent disease incidence of yellow vein mosaic with resistant, moderately resistant, moderately susceptible and susceptible genotypes of urdbean.	71

LIST OF FIGURES

Sr.N.	Title	Between pages
1.	Graphical presentation of variability parameters for twelve different characters studied in urdbean.	52-53
2.	Genotypical path diagram for seed yield per plant.	60-61

LIST OF ABBREVIATIONS

b.s.	:	Broad sense
C.D.	:	Critical difference
cm	:	Centimeter
C.V.	:	Coefficient of variation
Cov,	:	Covariance
d.f.	:	Degrees of freedom
<i>et al.</i> ,	:	And others (et alia)
Fig	:	Figure
G	:	Gramme (s)
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
ha	:	Hectare
h^2	:	Heritability
i.e.	:	That is (id est)
MSS	:	Mean sum of squares
No.	:	Number
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
r	:	Correlation coefficient
S.E.	:	Standard Error
S.S.	:	Sum of squares
Via	:	By the way of, by means of
viz.	:	Namely
Vs	:	Versus
δ	:	Variance
δ^2	:	Standard deviation

ABSTRACT

**“IDENTIFICATION OF GENETIC STOCK OF URDBEAN
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(GENETICS AND PLANT BREEDING)

MAHATMA PHULE KRISHI VIDYAPEETH,

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2017

Research Guide : Dr. S.B.Chaudhary

Major discipline : Genetics and Plant Breeding

The present investigation entitled “Identification of genetic stock of urdbean (*Vigna mungo* (L.) Hepper) for yellow vein mosaic resistance ” was undertaken to study the nature and extent of genetic variability, inter relationships among various yield components, genetic divergence between different genotypes of mungbean, to group them in suitable clusters and to assess mungbean germplasm for yellow vein mosaic. Thirty genotypes of mungbean were grown at Post Graduate

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Institute, MPKV, Rahuri during *kharif* 2016 in Randomized Block Design (RBD) with two replications.

The observations were recorded on days to 50 % flowering, days to maturity, plant height (cm), plant spread (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod (cm), 100 seed weight (g), protein content (%), seed yield per plant (g) and disease incidence of yellow vein mosaic. Appreciable amount of variability was observed for various characters among genotypes under study. The phenotypic coefficient of variation estimates were higher than genotypic coefficient of variation estimates. The phenotypic coefficient and genotypic coefficients were observed highest for the seed yield per plant (64.80 and 65.67), number of pods per plant (36.92 and 37.86), number of clusters per plant (31.57 and 33.23), plant spread (31.37 and 31.72), plant height (19.96 and 20.20) 100 seed weight (19.74 and 20.57). High heritability (b.s.) was observed for all the characters under study ranged between 61.32 (number of primary branches per plant) to 97.82 (plant spread). The genetic advance ranged between (0.46) and (16.64) with lowest estimate for number of primary branches per plant and highest for plant height. High heritability accompanied with high genetic advance as a per cent of mean

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suggest additive genetic control in the inheritance of characters like number of pods per plant, number of clusters per plant, seed yield per plant which indicated scope for selection for improvement of these characters.

Correlation studies revealed that, genotypic correlation coefficients were higher than corresponding phenotypic ones. Seed yield showed significant positive genotypic correlation with number of seeds per pod (0.416), length of pod (0.473), number of pods per plant (0.546), number of clusters per plant (0.522) and number of primary branches per plant (0.554) at both genotypic and phenotypic levels. From the path analysis study, it was revealed that number of pods per plant (0.5509), showed positive highest direct effects followed by plant spread (0.4847), 100 seed weight (0.3736), number of seeds per pod (0.2247), number of primary branches per plant (0.1806), length of pod (0.1772) and protein content (0.1749). This suggests the importance of these characters while selecting the genotypes for improvement of grain yield.

The D^2 statistics showed that there was considerable variability among the genotypes with D^2 values ranging from 23.66 to 994.27. On the basis of D^2 values, the thirty genotypes of mungbean were grouped into five clusters. Cluster V and III were divergent solitary clusters having one

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genotype each. The genotypes KU-15-118, PBCUB-14, KU-15-126 and PBCUB-9 are proposed for crossing programme on the basis of genetic divergence, cluster means and per se performance of genotypes for mungbean improvement.

Thirty urdbean genotypes were studied for incidence of yellow vein mosaic disease along with susceptible to yellow vein mosaic disease mungbean variety Kopergaon-1 under natural conditions. The disease incidence occurred on 30 genotypes were observed, 13 genotypes were found resistant to yellow vein mosaic however 9 genotypes were moderately resistant, 5 were moderately susceptible and 3 genotypes were susceptible. The resistant genotypes were KU-15-118, KU-15-122, KU-15-123, KU-15-125, KU-15-126, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, KU-15-117, KU-15-131.

1. INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) ($2n=2x=22$) commonly known as urd or mash, is one of the important *kharif* pulse crops grown in India. In Agriculture, legumes have been important from the ancient times.

It is a leguminous species, grown as pulse crop principally for its protein rich edible seeds and is the fourth important pulse crop after Bengalgram, Redgram and Greengram. It is widely cultivated throughout the country as sole , mixed or intercrop with maize, sorghum, cotton, pigeonpea, bajra, groundnut and sesamum .

It is rapidly growing, erect or sub-erect annual usually 30 to 100 cm in height. It is frequently more branched with a light tendency of twining in its upper branches. It is a self-pollinated crop however, sometimes cross pollination may occur due to insects. Being a short duration crop with wider adaptability, it is grown all over the country in different seasons as a sole crop and as an intercrop or mixed crop with cereals, forming important component of crop rotations. It improves the nutrient status of soil through atmospheric nitrogen fixation and adds humus to the soil. It is also useful as fodder.

Urdbean is a source of digestible protein. The protein of urdbean is less expensive than animal protein. To improve the protein level and quality of protein; the genetics of the protein or its constituents may provide useful clue for the further desired improvement. It is nutritious containing 24 per cent protein, 59.6 per cent carbohydrates, 1.4 per cent fat, 10.69 per cent of water

and 0.9 per cent of fibre. It is rich in vitamin B is regarded as remedy for beriberi. When it is allowed to sprout, ascorbic acid (vitamin C) is synthesized and amount of riboflavin and thiamine are also increased.

Urdbean is short duration, warm season crop grown mainly in semi-arid to sub humid tropics and tropics with 600 to 1000 mm annual rainfall. It requires up to 35°C mean temperature during crop production and elevations not exceeding 1800 to 2000 m above mean sea level. For a high yield, a warm climate and deep well drained loam or sandy loam soils are desired.

In India black gram is grown in almost all states over an area at 3.06 million hectare area with total production of 1.70 million tonnes and productivity of 555 kg/ha in India (Anonymous, 2013-2014). India is primary Urdbean producer contributing about 75 per cent of world production. The major Urdbean producer states are Andhra Pradesh, Maharashtra, Gujarat, Orissa and Tamilnadu. About 70 per cent of Urdbean is cultivated during *kharif* season, while remaining 30 per cent is grown in *rabi* and summer season. In Maharashtra, it is grown over an area of 2.80 lakh hectare area with total production of 0.59 lakh tonnes and productivity of 211 kg/ha in Maharashtra (Anonymous, 2015-2016).

Though India is leading producer of black gram in world, its productivity is very low. Therefore, there is great scope for its improvement and to increase the productivity by developing high yielding, disease and pest resistance varieties with improved nutritional value. Good amount of variability has been reported in black gram for various characters such as flowering, days to

maturity, plant height, pods per plant, protein content, number of clusters per plant etc. however their utilization in breeding programme resulted in identification and release of good number of varieties in black gram. However, these released types cannot be continued longer due to genetic erosion and susceptibility to diseases and pests.

Genetic diversity is one of the criteria of parent selection for hybridization programme. The availability of transgressive segregants in any breeding programme depends upon the diversity between the parents involved. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2 statistic has made possible to choose genetically diverse parents. Recent works indicated that the Mahalanobis generalized distance (D^2 statistic) is an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The coefficient of correlation between yield and its contributing characters shows a complex relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effect and visualizes the relationship in more meaningful way.

The yellow mosaic disease of mungbean as well as urdbean was first observed in 1955 at the experimental farm of the Indian Agricultural Research Institute, New Delhi.

Urdbean yellow mosaic is the most destructive viral disease of *kharif* legumes in India. The infected plant show alternating green and yellow patches. Leaf size is generally not affected, but sometimes the green areas are slightly raised and the leaves show a slight puckering and reduction in size. The

leaves become papery white and thin. The disease is transmitted by the whitefly vector *Bemisia tabaci* (Nene, 1972).

The disease can be managed through host plant resistance but it was found that the resistant sources are limited. Keeping in view to above aspects, the present studies was undertaken to find out the resistant sources to yellow vein mosaic virus in Urdbean with the following mentioned objectives.

- 1) To study the direct and indirect effects of different characters on seed yield of urdbean.
- 2) To group the various urdbean genotypes into various clusters.
- 3) To asses urdbean germplasm for yellow vein mosaic.

2. REVIEW OF LITERATURE

The literature relevant to present study entitled “Identification of genetic stock of urdbean [*Vigna mungo* (L.) Hepper] for yellow vein mosaic resistance” has been reviewed and presented under the following sub-headings.

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation and path analysis

2.4 Genetic diversity

2.5 Screening for virus resistance

2.1 Genetic variability

Genetic variability is very important as it serves as a basis for crop improvement programme. Nilsson-Ehle (1908) gave the concept of multiple factor hypothesis to prove inheritance of quantitative characters. Johannsen (1909) was the first to demonstrate the distinction between genotype and phenotype. All these discoveries led to the fact that variability is due to the interaction between genotype and environment.

Hutchinson (1940) emphasized the utility of estimates of genetic variability in designing a more efficient breeding programme. The genotypic coefficient of variation helps to measure the range of genetic variability in a character and provides measure to compare the genetic variability present in various quantitative characters. The statistical method to calculate genetic component of variance was given by Frankel (1947), Burton (1952) and Panse and Sukthame (1985).

Power *et al.*, (1950) partitioned total variance into genotypic and phenotypic variances by using estimates of environmental variance from non-segregating population.

Veeraswamy *et al.*, (1973) reported high estimate of phenotypic coefficient of variation for pod number and plant height, and low values of genotypic coefficient of variation for seed number, days to maturity and pod length in blackgram.

Gowda *et al.*, (1997) while assessing 18 genotypes of diverse origin of blackgram found sufficient variability for grain yield per plant, pods per plant, branches per plant and plant height.

Sharma *et al.*, (2000) studied genetic variability in thirty genotypes of blackgram and found that genotypic coefficient of variation was the highest (38.9) for clusters per plant followed by pods per plant .

Yadav and Dahiya (2000) studied variability in 160 germplasm of blackgram and found the highest level of variability for seed yield per plant followed by followed by plant height and pods per plant.

Sanjeev *et al.*, (2001) assessed 670 accessions of blackggram and recorded considerable variation for all the character viz., seed yield, plant height and number of pods per plant except for seeds per pod and 100 seed weight.

Singh (2007) studied genetic variation between yield and its components and observed variation for number of secondary branches per plant followed by seeds per pod, primary branches per plant, 100-seed weight and seed yield per plant.

Kousar Makeen (2009) evaluated 22 lines of urdbean for genetic divergence and found phenotypic and genotypic correlation estimates showed that pods per plant and clusters per plant had highly significant positive correlation with seed yield per plant. In addition the trait like 100-seed weight and plant height showed moderate positive association with seed yield, suggesting that these traits may be given second priority in the selection programme.

Singh (2014) found higher estimate of phenotypic coefficient of variation (PCV of more than 20 %) were observed for plant height (29.89), seed yield (24.21), number of branches per plant (22.31) and number of pods per plant (20.97). The highest genotypic coefficient of variability was observed for plant height (26.97), seed yield (22.36) and number of branches per plant (20.89). Low estimates of phenotypic and genotypic coefficient of variation were observed for the parameters days to maturity, length of pods and 100-seed weight.

Venkateshwarlu (2011) evaluated thirty five genotypes of green gram for yield and yield attributes in rabi 2009-10. Genotypes differed significantly for all the studied characters. High genetic advance coupled with high heritability was observed for characters viz., plant height, number of pods per plant, shoot diameter per plant and seed yield per plant, indicating the preponderance of additive gene action for these characters.

Srivastava and Singh (2012) reported highly significant differences for all the studied characters. Seed yield

per plant, 100 seed weight, number of seeds per pod, number of pods per plant and number of nodes on main stem exhibited high estimates of GCV, PCV, heritability, genetic advance and genetic advance as percentage of mean.

Gadakh *et al.*, (2013) evaluated fifty diverse genotypes of mungbean for genetic variability, heritability, genetic advance and found that genotypes differ significantly for all characters studied indicating good amount of genetic variability. Higher genotypic and phenotypic coefficient of variation was observed for harvest index followed by biological yield per plant, 100 seed weight and number of branches per plant. High heritability coupled with high genetic advance was observed for biological yield per plant, harvest index, number of pods per plant, indicating importance of additive gene expression for these characters.

Garje *et al.*, (2013) studied forty genotypes of mungbean for genetic divergence. They reported that seed yield per plant recorded maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by number of pods per plant. High heritability (broad sense) was recorded for number of pods per plant. High heritability coupled with high genetic advance was observed for plant height and number of pod per plant suggesting, the role of additive gene effect and possibilities of achieving high genetic progress through selection. The genotypes KM-09-152, KM-09-156, KM-09-183, BM-2005-1, Vaibhav, KM- 09-187, KM-09-173 and KM-09-158 were identified as genetically diverse

genotypes, which can be utilized for further hybridization programme for crop improvement.

Meshram *et al.*, (2013) analysed diverse genotypes of black gram for genetic variability and recorded highest GCV and PCV and high estimates of heritability for the characters sprouting percentage, number of pods per plant and grain yield per plant (g).

Sowmini. K and Jayamani. P (2013) evaluated 130 lines of black gram for variability studies for yield and reported that higher estimates of PCV were observed for all the traits when compared with GCV, however GCV was found to be high for the traits single plant yield, number of clusters per plant and number of pods per plant.

Suresh *et al.*, (2013) reported high heritability (broad sense) along with high genetic advance as per cent of mean for plant height, number of pods per plant, number of seeds per pod, 100 seed weight and plant yield indicating that these characters would be amenable for phenotypic selection in green gram.

Reni *et al.*, (2013) recorded the highest phenotypic coefficient of variability for grain yield (40.08 %) and pods per plant (34.87 %). The highest genotypic coefficient of variability was recorded for grain yield (39.39 %) and pods per plant (33.30 %) that indicates the presence of exploitable genetic variability for these traits.

Panigrahi *et al.*, (2014) studied variability in landraces and found that high GCV was shown by number of primary branches per plant, number of clusters per plant,

number of pods per plant and yield per plant. 100 seed weight, pod length and plant height exhibited moderate GCV value where as low GCV value was recorded with characters like days to 50% flowering, days to maturity and seeds per pod.

Punia *et al.*, (2014) evaluated genetic parameters for different quantitative characters and revealed considerable variability among the existing 115 set of germplasm. Among the eight quantitative characters, pods per plant had maximum variation followed by plant height and seed yield per plant.

Mehra *et al.*, (2016) studied 75 morphologically diverse genotypes of blackgram which indicated the existence high range of variability for seeds per plant (86-342) with the mean of 188 followed by plant height (21-59) with mean of 36, pods per plant (15-51) with mean of 28, biological yield per plant (7-33) with mean of 17, days to maturity (66-83) with mean of 75 and seed yield per plant (3-13) with the mean of 7 which indicates that sufficient variability is present in the germplasm for above characters.

9.2 Heritability and genetic advance.

Heritability is a good index of transmission of quantitative characters from parents to their offspring (Falconer, 1989). More specifically it could also be defined as the proportion of total variability that is due to genetic cause. Lush (1949) classified heritability into broad sense and narrow sense heritability. Improvement in the mean genotypic value of selected plants over parental population is known as genetic

advance. The genetic advance is the product of heritability, phenotypic standard deviation and selection differential (Burton and Devene, 1953).

Veeraswamy *et al.*, (1973) reported high heritability for days to flowering, plant height, number of clusters, number of branches and days to maturity in mungbean. Lowest heritability estimates for seed yield indicated that this character was influenced by environment. A high genetic advance was noticed in respect of number of clusters, number of branches per plant, plant height and number of pods. In case of days to maturity, pod length, weight of pods and number of seeds, though heritability was moderate to high, the genetic advance was low which indicating presence of non additive gene action.

Paramsivan and Rajasekaran (1980) reported high heritability for days to 50 per cent flowering and maturity were not associated with high genetic advance in mungbean. But in case of 100 seed weight, pod length, cluster number, pod number and seed yield, high heritability was associated with the high genetic advance indicating presence of additive gene effects for these characters.

Ramana and Singh (1987) studied heritability and genetic advance in thirty seven promising varieties of green gram, grown in two different seasons i.e. in the spring (S) and rainy (R) season and observed that the seed yield per plant, pods per plant, clusters per plant and plant height had high heritability coupled with high genetic advance, suggesting that additive gene action was more important for these characters.

Tiwari *et al.*, (1996) reported high heritability with high genetic advance for clusters per plant and 100-seed weight which revealed that selection in segregating population would be more effective and reliable in mungbean.

Rajendra *et al.*, (2000) evaluated 19 genotypes of blackgram and found that the heritability estimate was the highest for plant height (99.7%) followed by number of branches per plant (97.1%). The genetic advance was high for number of clusters per plant (56.03 %) and plant height (43.39%). High heritability with high genetic advance was recorded for plant height followed by grain yield per plant, number of branches per plant and number of clusters per plant.

Reddy (2003) reported high magnitude of heritability (b.s.) for test weight followed by days to maturity, protein content, days to 50 per cent flowering, pod length and number of nodules per plant. High heritability coupled with high genetic advance was observed for days to maturity and days to 50 per cent flowering in mungbean.

Singh. I. P (2007), recorded that seed yield had positive and significant association with number of pods per plant, plant height pod length, number of seeds per pod, days to flower and days to maturity in urdbean while negative correlation with primary branches per plant, Number of pods per plant with plant height and pod length; pod length with number of seeds per pod and plant height had positive and significant correlations. Path coefficient analysis also revealed

positive direct effect of pods per plant, plant height, pod length and days to flower on seed yield per plant.

Rahim *et al.*, (2008) recorded high heritability coupled with high genetic advance in the next generation for number of pods per plant, grain yield per plant and plant height. Suggesting that these characters govern by additive genetic effect to a great extent.

Reni *et al.*, (2013) estimated high heritability for all the traits except days to 50% flowering in urdbean. In general phenotypic coefficient of variability was greater than their corresponding genotypic coefficient of variability. Higher estimates of heritability and genetic advance as percent of mean were observed for grain yield (97.0%, 79.93%), pods per plant (91.0%, 65.50% and plant height (78.0%, 31.74%) indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of grain yield in black gram.

Meshram *et al.*, (2013) recorded high heritability accompanied with high genetic advance for number of pods/plant governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve character in future in urdbean. He also found the expression for number of pods /plant is predominantly governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve this character in future.

Singh (2014) recorded high heritability (bs) values (>50%) with high genetic advance as a per cent of mean for plant height , seed yield , number of branches per plant and number of pods per plant in urdbean . Moderate (>10 %) estimates of genetic advance coupled with high heritability was recorded for the characters number of seeds per pod (11.90%) and 100-seed weight (11.17%), while high heritability coupled with low genetic advance was recorded for length of pods and days to maturity in urdbean.

Panigrahi *et al.*, (2014) evaluated 19 genotypes of blackgram for heritability and found high heritability along with high genetic advance as per cent of mean (GAM) for yield per plant (60.66), number of clusters plant (48.20) and number of pods per plan (52.11).

Mehra *et al.*, (2016) studied the heritability and genetic advance in 75 lines of urdbean and found highest heritability in days to maturity (86.0%) followed by biological yield per plant (80.3%) and seed yield per plant (76.8%). Also highest genetic advance as percent of mean was recorded in biological yield per plant (65.74%), followed by seed yield per plant (58.29%).

2.3 Correlation and path analysis

The yield is a complex character and depends on many other attributes of plant. Correlation studies help in understanding the association between such traits and for making efficient selection. Estimates of correlation coefficient are the measures of association between characters and

provide the basic information in identifying characters that have little or no importance in the selection programme.

Giriraj and Vijaykumar (1974) reported that the seed yield was positively correlated with days to flowering, plant height, number of pods per plant and seeds per pod. The character 100-seed weight exhibited significant positive correlation with pod length but was negatively correlated with seed yield, days to flowering and plant height. Further they found strong positive correlation of pods per plant with plant height and days to flowering in mungbean. The length of pod had maximum positive direct effect on seed yield followed by plant height and days to flowering. Plant height showed negative effect through pod length and 100-seed weight, while, 100-seed weight had negative direct and indirect effects via most of the characters leading to negative correlation with seed yield.

Singh and Singh (1977) observed positive correlation of seed yield with number of pods and number of clusters per plant in mungbean. The number of pods per plant was the major contributing factor for seed yield, while number of clusters per plant influenced the seed yield *via* number of pods per plant.

Patil and Narkhede (1987) studied twenty eight strains of blackgram and found that yield was significantly correlated with pods per plant, 100 seed weight, pod length and seeds per pod. Pods per plant and 100 seed weight were observed to be most reliable components in selecting high

yielding genotypes rather than plant height, despite its maximum direct effects on yield indicated by path analysis.

Ramana and Singh (1987) studied the character associations in 37 promising varieties and two checks of green gram grown in spring and rainy season and found that in both the seasons, seed yield per plant showed significant correlations with plant height, pods per plant, clusters per plant and seeds per pod. In general, phenotypic correlations were smaller than the genotypic correlations in both the seasons.

Patil and Deshmukh (1989) while studying eighteen genotypes of urdbean observed that grain yield was significantly correlated with plant height, pods per plant, grains per pod, pod length and 100 gram weight, while days to flower and day to maturity were negatively correlated with grain yield. Positive association among pods per plant, grains per pod, pod length and 100 grain weight and their positive and significant correlation with yield showed that they had positive direct contribution to the grain yield. The pods per plant had maximum positive direct effect on grain yield followed by grains per pod, 100 grain weight, pod length, days to maturity and plant height.

Raut *et al.* (1988) observed that genotypic correlation coefficients were higher than the phenotypic correlation coefficients in mungbean. They further reported positive correlation of seed yield with number of seeds per pod, number of branches per plant, clusters per plant and pods per plant at genotypic level. Number of pods per plant

exhibited negative and non-significant association with seed yield. The high positive contribution to seed yield per plant was recorded by number of clusters per plant, 100-seed weight and seeds per pod. The positive direct effect due to number of pods per plant was nullified by negative indirect effects *via* 100-seed weight, plant height and number of branches per plant.

Ghafoor *et al.* (1990) derived information on 48 genotypes and found that branches per plant, pod length, harvest index and biological yield per plant had positive and significant correlation with yield.

Renganayaki and Rangasamy (1991) studied 20 genotypes of blackgram and found that seed yield per plant showed significant positive correlation with pod length, seeds per pod and 100 seed weight. Plant height and leaf area were important factors affecting yield.

Parmeswarappa *et al.*, (1993) studied character association in blackgram and indicated that plant height, number of pods per cluster, pod length, seeds per pod, branches per plant, biological yield per plant and harvest index were positively associated with seed yield, whereas days to 50 per cent flowering was negatively associated with pod length and harvest index.

Ram and Singh (1993) reported that number of pods and number of branches per plant were positively correlated with seed yield in urdbean.

Gyanendrasingh and Majorsingh (1994) evaluated fifty two genotypes of blackgram and found that grain yield

had significant and positive association with 100 seed weight, pods per plant, pod length and plant height Path analysis indicated that 100 seed weight and pods per plant had high direct effect on grain yield indicating that these were major yield determinants

Sanjeev *et al.*, (2001) reported significant correlation between yield and pods per plant but non-significant correlation between yield and seeds per pod in urdbean. Strong positive correlation existed between number of pods per plant and branches per plant.

Gopikrishnan *et al.*, (2002) found that the characters pods per plant, clusters per plant, pod length and seeds per pod had highly significant and positive association with seed yield per plant in urdbean .Seed yield had negative association with days to 50 per cent flowering and days to maturity. Days to 50 per cent flowering had a positive association with days to maturity Path analysis revealed that pods per plant had the highest positive direct effect on seed yield and days to 50 per cent flowering, whereas clusters per plant and pods per cluster had negative direct effect on seed yield

Vaithiyalingan *et al.*, (2002) reported that seed yield in urdbean exhibited significant positive association with branches per plant, clusters per plant, pods per plant, seeds per pod. dry matter production and harvest index. Path analysis revealed that harvest index and pods per plant had maximum direct effect on seed yield.

Reddy *et al.*, (2005) reported that number of seeds per plant was significantly and positively correlated with plant height and number of branches per plant at both genotypic and phenotypic levels, whereas it was significantly and positively associated with number of seeds per pod, test weight, days to maturity and days to 50 per cent flowering at genotypic level and with number of pods per plant at phenotypic level. Path analysis indicated that plant height, days to 50 per cent flowering and test weight recorded the highest direct effect in desirable direction.

Shivade *et al.*, (2011) revealed that plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, length of pod, number of seeds per pod and dry matter per plant showed highly significant positive correlation with seed yield per plant at both phenotypic and genotypic level. Path analysis revealed that number of clusters per plant, number of pods per cluster, length of pod, 100-seed weight, dry matter per plant, harvest index, number of seeds per pod and number of branches per plant exhibited positive direct effect on seed yield per plant.

Khanpara *et al.*, (2012) studied correlation coefficients among twelve yield contributing traits with their path effects towards the seed yield in blackgram using fifty-eight genotypes of green gram. It was observed that the magnitude of genotypic correlations were higher than the corresponding phenotypic correlations. The seed yield per plant had highly significant and positive correlations both at

genotypic and phenotypic levels with number of pods per plant, number of pods per cluster, number of clusters per plant and number of seeds per pod. Seed yield per plant showed negative and highly significant correlation with days to maturity at both the levels and days to 50 per cent flowering at only genotypic level and also reported that number of pods per plant, number of clusters per plant and number of pods per cluster exert maximum direct effects.

Ahmad *et al.*, (2013) studied thirty five genotypes of mungbean along with check Shalimar Mungbean-1 elicit information on association and interrelationship for seed yield and its component traits. Seed yield per plant showed positive significant association with number of clusters per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length and 100-seed weight, negative and significant association with days to 50 per cent maturity. In path analysis, They also observed that maximum positive direct contribution to seed yield plant per plant came from number of seeds per pod (0.424) followed by 100-seed weight (0.419), number of pods plant per plant (0.339) and number of primary branches plant per plant (0.177). Significant positive indirect contribution came from all the traits *via* pod length and number of seeds per pod.

Reni *et al.*, (2013) recorded that in urdbean pods per plant and plant height had highly significant genotypic and phenotypic correlation with grain yield also results revealed that grain yield was significantly and positively correlated with pods per plant plant height and 100 seed

weight. The Path coefficient analysis revealed that the highest positive direct effect on grain yield per plant was recorded by pods per plant followed by 100 seed weight, days to maturity and days to 50% flowering.

Singh ., (2014) found that number of branches per plant, number of pods per pant, length of pod, number of seeds per pod were positively correlated with seed yield per plant. Path analysis indicated that days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod and 100-seed weight showed positive direct effect, while the traits like days to 50% flowering showed direct negative effect on seed yield in urdbean.

Panigrahi *et al.* (2014) revealed in urdbean that positive direct effect on seed yield was exhibited by days to 50% flowering, number of primary branches per plant, number of pods per plant and 100 seed weight.

Mehra *et al.*, (2016) found high degree of association in urdbean between seed yield per plant and seeds per plant (0.895**) followed by pods per plant (0.832**), biological yield per plant (0.811**), plant height (0.578**) and 100 seed weight (0.465**) whereas days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and harvest index were not significant, path analysis found that seeds per plant (0.442) exhibited highest positive direct effect on seed yield followed by 100 seed weight (0.237) and high direct effect and positive association of seeds per plant (0.442) was observed on seed yield.

2.4 Genetic diversity

Genetic diversity is the genetic differences as observed between the individuals as genetic stocks with respect to individual trait or an array of traits. It is a result of inherent genetic variations present in the germplasm. The knowledge of nature and degree of genetic divergence is useful in selecting the desirable parents for breeding programme. The selection based on the genetic divergence has been successfully utilized by different workers in various crops. D^2 statistics, as a tool for quantitative estimates of genetic divergence between the populations was described by Mahalanobis (1936). While Rao (1952) suggested more flexible method which would replace the measurement on large number of characters, all of which contribute in some degree towards discrimination by relatively few measurements.

Murthy and Arunachalam (1966) revealed that geographical distribution and genetic diversity could not be directly related in any of the crop.

Gyanendrasingh and Majorsingh (1994) on the basis of D^2 grouped fifty two genotypes of urdbean into cluster, with greatest contribution to divergence being made by days to maturity (36.1%) followed by weight (34.8%) and seed yield (15.5%); The greatest number of genotypes in a single cluster was 35 (cluster I) Minimum intracluster distance was 6.19.

Renganayaki and Rangasamy (1995) studied D^2 statistics indicating that 100 seed weight, pod length and seed yield were characters causing divergence in urdbean.

Ganesh *et al.*, (1997) grouped 30 strains of urdbean into 8 clusters. The characters, pod yield and seeds per pod were major contributors to divergence

Pariya *et al.*, (1997) grouped 70 genotypes collected from 12 Indian states into 8 clusters, by using multivariate analysis, in which cluster I was the largest with 55.6 per cent genotypes whereas clusters VI, VIII and VIII were monogenotypic. Genotypes from Gujarat exhibited the maximum diversity and were represented in all clusters except V. No parallelism was observed between geographic diversity and genetic diversity.

Ram *et al.*, (1997) evaluated thirty strains of urdbean for genetic divergence on the basis of D^2 analysis for 8 yield related traits and grouped them into eight clusters. Pod yield and seeds per pod were important contributors to genetic divergence. Clustering pattern was independent of geographic distribution

Verma and Kanta (1997) analysed 41 genotypes of urdbean and grouped them into 9 diverse clusters, with majority of genotypes in cluster I. Plant height contributed the most towards divergence.

Manivannan *et al.*, (1999) grouped 30 genotypes of urdbean into six clusters in which number of pods per cluster, number of pods per plant and number of clusters per plant contributed maximum towards the genetic divergence, whereas pattern of D^2 clusters demonstrated that geographical distribution was not related to genetic diversity.

Asrat *et al.*, (2001) analysed 42 cultivars of urdbean using Mahalanobis D^2 statistics to group into 7 clusters, clustering pattern being irrespective of ecogeographical distribution. Number of pods per plant, plant height, number of clusters per plant and grain yield per plant contributed significantly to genetic divergence among cultivars.

Ghafoor *et al.* (2001) categorised 484 accessions into 5 clusters based on linkage in which cluster II, III and IV were clearly separated from cluster I and V.

Manikannan *et al.*, (2001) grouped 31 genotypes into six clusters, in which cluster I and II were the largest with nine genotypes and cluster V was the smallest with two genotypes. Intracluster distance ranged from 9.4 to 41.61 being maximum in cluster VI. Intercluster distance was maximum between I and II.

Singh (2001) assessed 50 genotypes for 8 quantitative traits and grouped them into 7 clusters cluster I was the largest containing 24 genotypes, cluster II, IV,V and VII being monogenotypic Pods per plant had the highest contribution (34.61%), followed by days to 50 per cent flowering (30.61%) and seed yield per plant (21.16%) towards genetic diversity.

Ahmad *et al.*, (2013) studied genetic divergence in 35 genotypes of mungbean. They found that there is relationship between geographical origin and genetical divergence in cluster formation.

Garje *et al.*, (2013) studied forty genotypes of green gram for the nature and magnitude of genetic divergence using Mahalanobis's D^2 analysis. The forty green gram genotypes were grouped into thirteen clusters. Cluster III was largest with ten genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster VIII and IV, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters *viz.* seed yield per plant (g), number of pod per plant, and Pod length (cm) contributed maximum in manifestation of genetic diversity.

Jayamani and Sathya (2013) grouped 50 genotypes of urdbean into 10 clusters, cluster I was formed with 25 genotypes and the clusters VI, VII, VIII, IX and X were represented by each with one genotype. The contribution of number of pods per plant was the maximum (25.71%) followed by pod length (21.63%).

Panigrahi *et al.*, (2014) investigated 19 genotypes of urdbean and grouped them into six distinct clusters as Cluster I had maximum 8 genotypes (8) followed by cluster IV with 5 genotypes whereas cluster II and III were digenotypic. Cluster V and VI had solitary genotype.

Rathod *et al.*, (2014) studied thirty two genotypes of green gram for the nature and magnitude of genetic divergence using Mahalanobis's D^2 analysis. The thirty two green gram genotypes were grouped into four clusters. Cluster I was largest with twenty two genotypes followed by cluster II with

five genotypes. The maximum inter-cluster distance was observed between cluster II and IV suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters.

Mehra *et al.*, (2016) grouped seventy five genotypes into seventeen clusters. The varietal composition of the clusters I, II, III, IV, V, VI, VII, VIII, IX,X, XI, XII, XIII, XIV, XV, XVII and XVII had 11, 2, 5, 2,2, 8, 9, 2, 3, 2, 2, 10, 13, 1, 1, 1 and 1 genotypes respectively.

10.5 Screening for virus resistance

Bashir and Zubair (2002) evaluated breeding line cultivars of urdbean against MYMV under field conditions and found that out of 132 genotypes 53 were highly resistant and rest were moderately resistant.

Ganapathy *et al.* (2003) evaluated 71 genotypes of black gram against the mungbean yellow mosaic virus and found that RV-229, VGB-86, VGB-89, 2KV-54, SU-16, were highly resistant to MYMV.

Peerajade *et al.*, (2004) tested 85 genotypes against mungbean yellow mosaic virus (MYMV) at MARS, Dharwad. Among them GG-41 and GG-42 were found resistant and GG-52 showed moderate resistance.

Pathak and Jhamaria (2004) evaluated fourteen mungbean varieties for resistance against yellow mosaic virus at ARS, Navagaon. They found that ML-5 and MUM-2, were resistant with only 2.22 and 3.12 per cent infection as against per cent infection in K-851 a check cultivar.

Bashir *et al.*, (2006) screened mungbean germplasm lines against the mungbean yellow mosaic begomovirus, out of 110 mungbean lines 85 were found highly resistant (HR), 14 resistant (R), 5 moderately resistant (MR), only 6 accessions were graded as susceptible (S).

Singh *et al.*, (2008) screened forty mungbean genotypes under natural epiphytotic conditions to identify the source of resistance against mungbean yellow mosaic virus (MYMV). Out of forty genotypes the genotypes DPM 90-1, DPM 90-2, HUM-1, IPM-04-2, and IPM-04-3 were found highly resistant.

Iqbal (2011) screened of 100 mungbean genotypes for resistance against MYMV and found four genotypes viz; 014043, 014133, 014249, 014250 were resistant to MYMV.

Panduranga (2011) carried out field screening of 22 mungbean genotypes for resistance against whitefly and mungbean yellow mosaic virus (MYMV) and found four lines viz; LGG 407, MGG 356, KM 200 and NM 1 resistant against MYMV.

Muhammad (2014) identified sources of resistance against MYMV. Out of 64 mungbean six lines were found as resistant lines viz; AZRI-1, NCM-15-11, NCM-21, NCM-11-8, 14063, AZRI-06 and 35 moderately resistant.

3. MATERIAL AND METHODS

The present study on “Identification of genetic stock of urdbean [*Vigna mungo* (L.) Hepper] for yellow vein mosaic resistance” was conducted during kharif 2016 at Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri. The details of the material used and methods followed to carry out the experiments and statistical procedures are presented in this chapter.

3.1 Material

The material used in the present study consisted of 30 genotypes obtained from the Oilseed Specialist, Oilseed Research Station, Jalgaon (MS). The salient features of 30 genotypes of urdbean are given in Table-1.

3.2 Methods

3.2.1 Experimental design

Total 30 genotypes of the black gram were grown in *Kharif* 2016. The field experiment was laid out in Randomized Block Design with two replications. In each replication the plot size was 3.00 m x 1.20 m with 30 cm spacing between the rows and 10 cm between plants.

3.2.2 Cultivation practices

The fertilizer dose was applied at the rate of 25 kg Nitrogen and 50 kg Phosphorus per hectare at the time of sowing. All other cultivation practices like weeding, irrigation etc. were carried out regularly as per need and stage of crop growth.

3.2.3 Harvesting

The pods were harvested after attaining their physiological maturity.

3.3 Details of observations -

The following observations were recorded on five randomly selected competitive plants from each treatment in each replication and averages were worked out.

3.3.1 Days to 50 per cent flowering

Number of days required for flowering initiation of 50 per cent plants in a plot from the date of sowing was recorded.

3.3.2 Days to maturity

The number of days required from the date of sowing till physiological maturity, were considered as days to maturity.

3.3.3 Plant height (cm)

Plant height was measured in centimeter from the ground level to the tip of the main branch of plant at physiological maturity.

3.3.4 Plant spread (cm)

The plant spread was measured at maturity stage in centimeter.

3.3.5 Number of primary branches per plant

The total number of primary branches were counted, the average was worked out and recorded at the time of harvesting.

Table1. List of Urdbean genotypes along with salient features included in the studies.

Sr. No.	Name of genotypes	Salient feature	Sr. No.	Name of genotypes	Salient features
1.	KU-15-107	More number of pods per cluster	16.	KU-15-132	Early flowering
2.	KU-15-109	Early flowering	17.	PBCUB-5	More pod length
3.	KU-15-110	Resistant to YVM	18.	PBCUB-6	Late flowering
4.	KU-15-114	Early flowering	19.	PBCUB-7	Resistant to YVM
5.	KU-15-116	Long pod length	20.	PBCUB-8	Early, Bold seeded
6.	KU-15-117	Early flowering	21.	PBCUB-9	More number of primary branches per plant
7.	KU-15-118	Bold seeded	22.	PBCUB-11	More number of pods per cluster
8.	KU-15-122	More protein content	23.	PBCUB-12	Resistant to YVM
9.	KU-15-123	More number of seeds per pod	24.	PBCUB-13	Leaves light green
10.	KU-15-125	More number of primary branches per plant and Tall	25.	PBCUB-14	More number of clusters per plant, more seed yield
11.	KU-15-126	More plant height	26.	PBCUB-15	Profuse growth, Resistant to YVM
12.	KU-15-127	Leaves light green	27.	PBCUB-18	More number of seeds per pod
13.	KU-15-128	More number of clusters per plant, High protein content	28.	PBCUB-19	More number of seeds per pod
14.	KU-15-130	Early flowering	29.	PBCUB-25	More number of primary branches per plant
15.	KU-15-131	More number of clusters per plant	30.	PBCUB-27	Tall, late

3.3.6 Number of clusters per plant

The total number of clusters were recorded at maturity the average was worked out.

3.3.7 Number of pods per cluster

The total number of pods per cluster was counted and the average was worked out.

3.3.8 Number of pods per plant

The total number of pods were counted and the average was worked out.

3.3.9 Length of pod (cm)

The length of pod was measured in centimeter and the average was worked out.

3.3.10 Number of seeds per pod

The seeds of randomly selected plants were counted and the average was worked out.

3.3.11 100 seed weight (g)

The weight of randomly selected 100 seeds was taken in grams of the observational plants and the average was worked out for recording 100 seed weight.

3.3.12 Seed yield per plant (g)

The seed yield per plant was measured in grams by taking the total seed weight per plant after drying.

3.3.13 Protein content (%)

The protein content was estimated by using spectro photo analyser machine.

3.3.14 Disease incidence of yellow vein mosaic

The disease incidence was recorded on 30 urdbean genotypes under natural condition and grouped into three categories.

3.4 Screening for virus resistance

Thirty genotypes of urdbean were studied at Post Graduate Institute Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri for screening virus resistance. The infected rows of mungbean variety Kopargaon-1 was sown three weeks before normal sowing of experimental material for sufficient occurrence of yellow vein mosaic disease. The per cent disease incidence was observed on these genotypes on 45 DAS and grouped into three categories, according to Bashir (2005)

3.4.1 Per cent disease incidence

$$\text{PDI} = (\text{Total number of infected plants} / \text{Total number of plants}) \times 100$$

The plants were grouped as per following disease rating scale (Bashir 2005)

Sr no	Per cent infection	Infection category
1	All plants are disease free	Highly resistant
2	1-10 % infection	Resistant
3	11-20 % infection	Moderately resistant
4	21-30 % infection	Moderately susceptible
5	30-50% infection	Susceptible
6	More than 50% infection	Highly susceptible

3.5 Statistical analysis

The mean values of five randomly selected plants for thirteen different traits were used for statistical analysis. The following statistical parameters were worked out for presentation of the data on different quantitative attributes.

3.5.1 Analysis of Variability

a. Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in the following form.

$$Y_{ij} = \mu + G_i + R_j + E_{ij}$$

Where,

$$i=1,2,\dots,\dots\dots g$$

$$j=1,2,\dots,\dots\dots r$$

Y_{ij} = Observation on i th genotype in j th replication

μ = General mean

G_i = Effect of i th genotype

R_j = Effect of j th replication

E_{ij} = Random error associated with Y_{ij} observation

Sr.No.	Sources of variation	D.F.	Expected means sum of square
1	Replications	($r-1$)	$\sigma^2_e + t\sigma^2_r$
2.	Treatments	($t-1$)	$\sigma^2_e + 2\sigma^2_t$
3.	Error	($r-1$) ($t-1$)	σ^2_e
	Total	($rt-1$)	

Where,

D.F.= Degrees of freedom

r =Number of replications

t=Number of treatment

Estimation of S.E. and C.D.

$$\text{S.E. of mean (S.E.m)} = \sqrt{\sigma^2_e}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \times \sqrt{2}$$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the Σ total by corresponding number of observations:

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where,

$\bar{X}$ = Mean of the character

ΣX_i = Total of all the observations for the character

n= Number of observations

The lowest and highest values of mean of character represented the range.

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated by using the respective mean squares from the variance ANOVA Table (Johnson *et al*, 1955) as below.

$$\text{Environmental variance } (\sigma^2_e) = \text{EMS}$$

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

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated by using the following formulae given by Burton (1952).

i. Genotypic Coefficient of Variation (GCV)

$$\text{GCV} = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

$\sigma^2_g = Vg$ = Genotypic variance

$\bar{X}$ = General mean of the character

ii. Phenotypic Coefficient of variation (PCV):

$$\text{PCV} = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

$\sigma^2_p = Vp$ = Phenotypic variance and,

$\bar{X}$ = General mean of the character

e. Heritability percentage

Heritability percentage(broad sense) was calculated as for Burton (1952).

$$h^2 \text{ (b.s.)} = (Vg/Vp) \times 100$$

$$h^2 \text{ (b.s.)} = (\sigma^2_g / \sigma^2_p) \times 100$$

Where,

$h^2 \text{ (b.s.)}$ = Heritability in broad sense

$\sigma^2_g = V_g$ = Genotypic variance

$\sigma^2_p = V_p$ = Phenotypic variance

Heritability estimates were classified as high, medium and low on the basis of values given by Robinson (1966):

Low Heritability = < 30 %

Medium Heritability = 30.1 to 60 %

High Heritability = > 60 %

f. Genetic advance

Genetic advance was calculated as given by Johnson et al. (1955).

$$G.A. = K \times \frac{\sigma^2_g}{\sigma^2_p} \times \sigma_p \text{ or } GA = k \times h^2 \times \sigma^2_p$$

Where,

K = Selection differential which is 2.06 at 5 per cent

selection intensity

$\sigma^2_g = V_g$ = Genotypic variance

$\sigma^2_p = V_p$ = Phenotypic variance

σ_p = Phenotypic standard deviation

G.A. as percentage of mean (GAM).

$$GAM = (G.A./X) \times 100$$

Where,

G.A.= Genetic advance

X = Character mean

Low : 10 %

Medium : 10.1 to 20 %

High : > 20 %

3.5.2 Correlations

To understand the association among the characters, genotypic and phenotypic correlation coefficient were worked out as given by Singh and Chaudhary (1977).

i. Phenotypic correlation coefficient (rp)

It is derived by using formula as follows

$$r_{p_{1,2}} = \frac{(COV.p_{1,2})}{\sqrt{(\sigma^2_{p_1}) . (\sigma^2_{p_2})}}$$

Where,

$r_{p_{1,2}}$ = Phenotypic correlation between character 1 and 2.

COV. $p_{1,2}$ = Phenotypic covariance between character 1 and 2.

$\sigma^2_{p_1}$ and $\sigma^2_{p_2}$ = Phenotypic variance of character 1 and 2 respectively.

ii. Genotypic correlation coefficient (rg)

It is derived by

$$r_{g_{1,2}} = \frac{(COV.g_{1,2})}{\sqrt{(\sigma^2_{g_1}) . (\sigma^2_{g_2})}}$$

Where,

$rg_{1.2}$ = Genotypic correlation coefficient between character 1 and 2.

COV. G1.2 = Genotypic covariance between character 1 and 2.

$\sigma^2_{g_1}$ and $\sigma^2_{g_2}$ = Genotypic variance of character 1 and 2 respectively.

The significance of genotypic and phenotypic Correlation coefficient were tested by 't' test (Panse and Sukhatme, 1985).

$$t = r \sqrt{(n-2) / (1 - r^2)}$$

Where,

r = Correlation coefficient

n = Total number of observations

The calculated 't' value was tested with Table 't' value for respective (n-2) degrees of freedom for significance.

3.5.3 Path analysis

Path coefficient analysis was done according to procedure suggested by Dewey and Lu (1959). If y is the effect 'x_i' is the cause, path coefficient for the path from cause x_i to the effect y is $\partial x_i / \partial y$. Direct and indirect effects were worked out by using genotypic correlation as below.

Direct effect of x₁ on y = $P_{x_1.y}$

Where,

P_{x_1} = Path coefficient of x₁ on y. Similarly, direct effects

of other attributes on yield were calculated.

Indirect effect of x_1 via x_2 on $y = p_{x_2.y} \times r_{x_1.x_2}$

Where,

$p_{x_2.y}$ = Path coefficient of the component character x_2 on y .

$r_{x_1.x_2}$ = Genotypic correlation between x_1 and x_2 .

Similarly, indirect effects in all possible combinations were calculated for all component characters. The residual effect (R) was calculated below.

$$R = [1 - (P_{x_1y} \cdot r_{x_1y}) - (P_{x_2y} \cdot r_{x_2y}) - \dots - (P_{x_ny} \cdot r_{x_ny})]^{1/2}$$

Where,

P_{x_1y} , P_{x_2y} , P_{x_ny} = Direct effects of respective character on seed yield.

r_{x_1y} , r_{x_2y} , r_{x_ny} = Correlation coefficient between respective characters and seed yield.

3.5.4 Mahalanobis generalized distance (D^2)

The generalized distance between two populations was defined by Mahalanobis (1936) as :

$$D^2 = \sum \sum \lambda_{i,j} \cdot \delta_i \cdot \delta_j$$

Where,

$\lambda_{i,j}$ = Reciprocal matrix to the common dispersion matrix

δ_i = Difference between the mean values of the two populations for the i^{th} character.

Estimation of D^2 value from the above formula is very complicated in the present study. Since, it requires the

inversion of thirteen order determinants and then the evaluation of $B(BH)/2$ terms whose sum is D^2 . It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variables reduces to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation elements.

3.5.5 Determination of gene constellations

Tochers method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for findings the clusters because a cluster is not a well defined term. The only criterion appears to be that any two groups belonging to the same cluster should be at least on an average shows a smaller D^2 than those belonging to two different clusters. A simple device suggested by K.D. Tocher is to start with two closely associated groups and find the third group which has the smallest D^2 from the first three and so on. If at the any stage the average D^2 of group from those already listed appears to be high, then these groups does not fit in with the former groups and is therefore taken outside the former cluster.

The group of first cluster then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to the inclusion of an additional group. If the changes are appreciable then the newly added group has to be considered as outside the

cluster.

3.5.6 Average intra and inter cluster D^2 and D value

3.5.6.1 Average intra cluster D^2

$$D^2 = \sum D_i / n$$

Where,

D_i is the sum of distance between all possible combinations (n) of the population included in a cluster.

3.5.6.2 Average inter cluster D^2

$D^2 = \sum \text{Distance between the population of cluster } i \text{ and } j / n_i \cdot n_j$

Where,

n_i = Number of population in cluster i

n_j = Number of population in cluster j

3.5.6.3 Average intra and inter cluster distance

$$D = \sqrt{D^2}$$

3.5.7. Cluster means

Cluster mean were calculated for individual characters on the basis of mean performance of the genotypes included in that cluster.

3.5.8 Genetic diversity as an index for selecting desirable parents for hybridization

Bhatt (1970) advocated the use of multivariate analysis for the selection of parents. He also stated that Statistical distance of all possible cluster combination may be considered arbitrarily as guideline and suggested that it

would be logical to effect crosses between genotypes belonging to the clusters separated by high estimated statistical distance.

4. EXPERIMENTAL RESULTS

The results of the present investigation i.e. “Identification of genetic stock of urdbean (*Vigna mungo* (L.) Hepper) for yellow vein mosaic resistance” which was carried out to assess the diversity and incidence of yellow vein mosaic between thirty urdbean genotypes, presented in this chapter under following sub-heads.

4.1 Variability and genetic parameters

4.1.1 Analysis of variance

The analysis of variance for thirteen characters studied are presented in Table 2. The analysis revealed that all genotypes exhibited highly significant differences for all of the characters under study.

4.1.2 Mean performance and the range of variability

Mean values of the genotypes for different characters studied are presented in Table 3, while the estimates of range for each of the character are given in Table 4.

4.1.2.1 Days to 50 % flowering

The variation in days to 50% flowering ranged between 37.10 (KU-15-109) to 42.90 (PBCUB-8) with a general mean of 39.71. The genotypes KU-15-116, KU-15-118, KU-15-123, KU-15-126, KU-15-132, PBCUB-5, PBCUB-6, PBCUB-7, PBCUB-9, PBCUB-12, PBCUB-15, PBCUB-18, PBCUB-19, PBCUB-25, PBCUB-27 are statistically significant superior over population mean.

4.1.2.2 Days to maturity

The number of days to maturity ranged between 65.80 (KU-15-131) to 74.00 (PBCUB-27) with a general mean of 69.28. KU-15-116, KU-15-118, KU-15-123, KU-15-126, PBCUB-6, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-11, PBCUB-12, PBCUB-15, PBCUB-18, PBCUB-25 genotypes were statistically significant superior over population mean.

4.1.2.3 Plant height (cm)

The genotypes KU-15-126 was the tallest genotype for plant height of 60.20 cm followed by PBCUB-14 (58.50 cm) whereas the genotype KU-15-128 (26.00 cm) was dwarfest. The general mean for plant height was 40.96 cm. The genotypes KU-15-116, KU-15-125, KU-15-132, PBCUB-6, PBCUB-7, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-14, PBCUB-18, PBCUB-25, PBCUB-27 were statistically significant superior over population mean.

4.1.2.4 Plant spread (cm)

Highest plant spread was observed in PBCUB-14 (43.00 cm) and lowest plant spread in KU-15-114 (13.50 cm) with mean value 23.98 cm. The genotypes KU-15-122, KU-15-126, KU-15-131, PBCUB-5, PBCUB-6, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, PBCUB-25, PBCUB-27 were statistically significant superior over population mean.

4.1.2.5 Number of primary branches per plant

The mean number of primary branches per plant was 2.43. It was varied from 2.00 (KU-15-116 and KU-15-132)

Table 2. Analysis of variance for thirteen different quantitative characters of urdbean genotypes

Sr.No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to 50 % flowering	0.080	5.262**	0.437
2.	Days to maturity	0.066	8.922**	0.210
3.	Plant height (cm)	1.176	135.374**	1.632
4.	Plant spread (cm)	0.864	114.455**	1.262
5.	No. of primary branches per plant	0.192	0.216**	0.051
6.	No. of cluster per plant	2.320	11.874**	0.606
7.	No. of pods per cluster	0.416	0.518**	0.110
8.	No. of pods per plant	3.266	119.106**	2.990
9.	Length of pod (cm)	0.200	0.401**	0.058
10.	No. of seeds per pod	0.486	0.589**	0.132
11.	100 seed weight (g)	0.000	1.655**	0.068
12.	Seed yield per plant (g)	0.106	16.550**	0.222
13.	Protein content (%)	0.346	0.445**	0.191

* and ** indicates significant at 5 and 1 percent level of significance respectively.

to 3.50 (PBCUB-9). The genotype KU-15-109, KU-15-117, KU-15-126, PBCUB-6, PBCUB-8, PBCUB-12, PBCUB-13, PBCUB-24, PBCUB-25 were statistically significant superior over population mean.

4.1.2.6 Number of clusters per plant

The variation in number of clusters per plant ranged between 3.50 (KU-15-128) to 14.90 (PBCUB-14) with

7.51 as general mean. The genotypes KU-15-109, KU-15-122, KU-15-125, KU-15-126, KU-15-131, KU-15-132, PBCUB-5, PBCUB-9, PBCUB-11, PBCUB-12, PBCUB-13, PBCUB-15, PBCUB-18, PBCUB-27 were statistically significant superior over population mean.

4.1.2.7 Number of pods per cluster

The mean number of pods per cluster was 3.17. It was varied from 2.20 (PBCUB-15) to 3.90 (PBCUB-11). The genotypes KU-15-107, KU-15-118, KU-15-122, KU-15-125, KU-15-126, KU-15-130, KU-15-132, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-14, PBCUB-18, PBCUB-25, PBCUB-27 were statistically significant superior than population mean.

4.1.2.8 Number of pods per plant

Maximum number of pods per plant was found in PBCUB-14 (39.10) and minimum number of pods per plant was found in KU-15-128 (10.1) with mean value 20.63. The genotypes KU-15-107, KU-15-126, KU-15-131, KU-15-132, PBCUB-5, PBCUB-9, PBCUB-11, PBCUB-12, PBCUB-13, PBCUB-18, PBCUB-27 were statistically significant superior over population mean.

4.1.2.9 Number of seeds per pod

The genotype PBCUB-18 was having maximum number of seeds per pod (7.30) followed by PBCUB-6 (6.70). The genotype KU-15-126 has minimum number of seeds per pod (5.00). The general mean seeds per pod were 5.84. KU-15-107, KU-15-110, KU-15-116, KU-15-117, KU-15-130, KU-15-131, PBCUB-6, PBCUB-8, PBCUB-9, PBCUB-11,

PBCUB-12, PBCUB-14, PBCUB-15, PBCUB-27 genotypes were statistically significant superior over population mean.

4.1.2.10 Seed Yield per plant (g)

It varied from 1.39 t 11.93 g with population mean of 4.40 g. Lowest seed yield per plant was observed in the genotype KU-15-126 (1.39 g) while highest seed yield per plant was recorded in the genotype PBCUB-14 (11.93 g). The genotypes KU-15-107, KU-15-109, KU-15-132, PBCUB-5, PBCUB-6, PBCUB-9, PBCUB-12, PBCUB-15, PBCUB-27 were statistically significant superior over population mean.

4.1.2.11 100 seed weight (g)

The mean of 100 seed weight was 4.51 g. The variation in 100 seed weight ranged between 3.12 g (KU-15-109) to 8.05 g (KU-15-118). The genotypes KU-15-110, KU-15-116, KU-15-123, KU-15-125, PBCUB-6, PBCUB-8, PBCUB-14, PBCUB-18, PBCUB-25, PBCUB-27 were statistically significant superior over population mean.

4.1.2.12 Length of pod (cm)

The length of pod varied from 3.45 cm (KU-15-114) to 5.28 cm (PBCUB-5) with mean value 4.34 cm. The genotypes KU-15-109, KU-15-116, KU-15-122, KU-15-131, KU-15-132, KU-15-6, KU-15-7, KU-15-8, KU-15-9, KU-15-11, KU-15-14, KU-15-15, KU-15-18, KU-15-25, KU-15-27 were statistically significant superior over population mean.

4.1.2.13 Protein content (%)

The protein content varied from 23.45 % (KU-15-118) to 26.18 % (KU-15-130) with mean value 24.29 %. The

Table 3. Mean values of different yield contributing characters of urdbean genotypes.

Sr.No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of cluster per plant	No. of pods per cluster	No.of pods per plant	No. of seeds per pod	Seed yield per plant (g)	100 seed weight (g)	Length of pod (cm)	Protein content (%)
1.	KU-15-107	37.70	68.20	31.00	22.20	2.40	7.20	3.30	21.70	6.10	7.20	4.08	3.72	24.36
2.	KU-15-109	37.10	66.30	35.10	18.20	2.50	8.20	3.10	18.30	5.30	5.14	3.12	4.45	23.99
3.	KU-15-110	37.60	67.50	34.60	17.70	2.30	4.80	2.40	14.60	5.90	2.64	4.58	4.24	23.83
4.	KU-15-114	37.50	67.50	30.20	13.50	2.10	5.10	2.50	11.30	5.70	1.65	3.53	3.45	24.15
5.	KU-15-116	40.20	69.50	47.70	17.40	2.00	5.70	2.50	14.20	6.60	3.53	4.84	4.90	24.56
6.	KU-15-117	38.50	68.70	30.70	17.00	2.50	4.20	3.10	11.60	6.20	2.81	4.26	4.30	23.98
7.	KU-15-118	40.30	70.10	35.20	18.10	2.20	6.80	3.30	17.60	5.30	3.59	8.05	4.17	23.45
8.	KU-15-122	37.40	67.30	39.70	25.00	2.30	7.80	3.90	18.80	5.10	1.65	3.60	4.49	24.88
9.	KU-15-123	40.40	69.40	39.80	22.20	2.40	6.00	2.60	13.30	5.50	3.64	5.65	4.33	23.80
10.	KU-15-125	38.80	67.90	41.90	18.00	2.40	8.60	3.50	18.60	5.50	2.86	4.66	3.61	23.93
11.	KU-15-126	40.50	69.60	60.20	31.30	3.00	10.00	3.40	27.40	5.00	1.39	3.6	3.69	24.47
12.	KU-15-127	39.60	68.10	31.00	17.60	2.30	6.50	2.60	14.20	5.50	2.61	3.48	4.04	24.02
13.	KU-15-128	38.70	67.30	26.00	14.30	2.10	3.50	3.00	10.10	5.50	1.81	4.31	3.58	26.18
14.	KU-15-130	37.50	67.00	36.60	20.10	2.40	5.60	3.50	14.90	6.00	1.80	3.94	4.20	24.41
15.	KU-15-131	38.70	65.80	34.90	29.50	2.30	11.30	2.60	27.00	6.30	3.16	3.69	4.76	24.40

Table 3. contd...

Sr.No.	Genotypes	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of cluster per plant	No. of pods per cluster	No.of pods per plant	No. of seeds per pod	Seed yield per plant (g)	100 seed weight (g)	Length of pod (cm)	Protein content (%)
16.	KU-15-132	38.90	66.90	45.10	17.30	2.00	7.60	3.90	22.30	5.70	4.56	4.24	4.36	24.12
17.	PBCUB-5	40.70	68.20	40.20	30.50	2.40	9.10	2.50	23.00	5.10	8.16	4.48	5.28	24.62
18.	PBCUB-6	42.20	71.10	49.70	38.90	2.80	5.50	3.00	18.00	6.70	11.2	5.16	4.40	24.37
19.	PBCUB-7	41.70	70.20	42.30	25.50	2.30	7.20	3.50	18.20	5.60	2.39	4.37	4.53	24.14
20.	PBCUB-8	42.90	73.20	40.50	25.40	2.60	7.40	3.60	20.30	6.30	2.08	5.08	4.71	24.18
21.	PBCUB-9	40.50	71.20	44.30	30.30	3.50	11.10	3.60	35.50	6.00	7.96	4.14	4.48	24.16
22.	PBCUB-11	39.40	70.60	40.10	20.60	2.20	7.60	3.90	35.00	5.90	2.77	3.99	4.48	23.85
23.	PBCUB-12	40.20	70.70	47.70	34.30	2.90	9.20	3.50	33.40	6.30	7.43	4.34	4.29	24.67
24.	PBCUB-13	38.80	68.70	46.30	25.20	2.50	8.10	3.10	24.90	5.40	4.36	4.48	3.99	24.25
25.	PBCUB-14	39.60	68.40	58.50	43.00	3.00	14.90	3.80	39.10	6.10	11.93	5.32	4.96	24.66
26.	PBCUB-15	40.40	72.70	38.90	31.50	2.20	10.00	2.20	16.70	6.00	5.37	4.54	4.37	24.39
27.	PBCUB-18	41.60	70.70	42.90	18.80	2.40	7.60	3.50	23.50	7.30	3.87	5.24	4.62	24.37
28.	PBCUB-19	39.80	69.0	35.70	15.40	2.20	3.70	2.70	10.90	5.10	1.86	4.35	4.31	24.12
29.	PBCUB-25	41.90	72.80	48.80	29.40	2.50	7.00	3.60	18.10	5.80	3.94	5.13	4.58	24.57
30.	PBCUB-27	42.40	74.00	53.20	31.20	2.20	8.20	3.60	26.40	6.500	8.91	4.98	5.17	24.08
	Mean	39.71	69.29	40.96	23.98	2.43	7.51	3.17	20.63	5.84	4.40	4.51	4.34	24.29
	S.E. ±	0.46	0.32	0.90	0.79	0.16	0.55	0.23	1.22	0.25	0.33	0.18	0.17	0.30
	C.D. 5%	1.35	0.93	2.61	2.29	0.46	1.59	0.67	3.53	0.74	0.9	0.53	0.49	0.86

genotypes KU-15-107, KU-15-116, KU-15-122, KU-15-126, KU-15-130, KU-15-131, PBCUB-5, PBCUB-6, PBCUB-11, PBCUB-12, PBCUB-14, PBCUB-15, PBCUB-18, PBCUB-25 were statistically significant superior over population mean.

4.1.3 Estimates of genetic components of variation

The estimates of genotypic, phenotypic and environmental components of variation for different characters are presented in Table 4. The estimate of genotypic variance was highest for plant height (66.87) followed by number of pods per plant (58.05) and lowest for number of primary branches per plant (0.08). The phenotypic variance ranged between 0.13 (number of primary branches per plant) to 68.50 (plant height), environmental variance ranges from 0.05 (length of pod and number of primary branches per plant) to 2.99 (number of pods per plant).

4.1.4 Genotypic and phenotypic coefficients of variation

The estimates of genotypic and phenotypic coefficients of variation are presented in Table 4.

The value of genotypic coefficient of variation was highest for seed yield per plant (64.80) followed by number of pods per plant (36.92) and number of cluster per plant (31.57). The lowest value of GCV recorded for protein content (1.49).

The phenotypic coefficient of variation was least for protein content (2.30) and highest for seed yield per plant (65.67), followed by number of pods per plant (37.86), number cluster per plant (33.23), plant spread (31.72). In general, the

phenotypic coefficient of variations were greater than genotypic coefficient of variation.

4.1.5 Heritability and genetic advance

The estimates of heritability in broad sense and genetic advance for different characters studied are presented in Table 4. All characters showed high heritability. Maximum heritability was observed for plant spread(97.82 %), followed by plant height(97.62 %), seed yield per plant (97.35 %), seed yield per plant (95.10 %), days to maturity (95.00 %) and 100 seed weight (92.07 %).

The genetic advance ranged between (0.46) and (16.64) with lowest estimate for number of primary branches per plant and highest for plant height and GA as a percent of mean highest for seed yield per plant (131.71), followed by number of pods per plant (74.18), plant spread (63.91), number of clusters per plant (61.81), plant height (40.63), 100 seed weight (39.03) and number of primary branches per plant (32.37).

The estimates of both heritability and predicted genetic gain differed among the characters. It is evident that heritability and genetic advance as a percent of mean were high for seed yield per plant, number of pods per plant, plant spread, and number of clusters per plant . However, protein content and number of pods per cluster heritability but comparatively lower estimates of genetic advance.

4.2 Correlation studies

The genotypic and phenotypic correlation for thirteen characters studied are presented in Table 5. In general

Table 4. Estimates of variability parameters for thirteen different characters of urdbean genotypes

Sr.No.	Characters	COMPONENTS								
		Range	σ^2g	σ^2p	σ^2e	GCV %	PCV %	Heritability (%) (b.s.)	Genetic advance	Genetic advance as % of mean
1.	Days to 50 % flowering	37.10-42.90	2.41	2.85	0.43	3.91	4.25	84.00	2.94	7.41
2.	Days to maturity	65.80-74.00	4.35	4.56	0.21	3.70	3.79	95.00	4.19	7.46
3.	Plant height (cm)	26.00-60.20	66.87	68.50	1.63	19.96	20.20	97.62	16.64	40.63
4.	Plant spread (cm)	13.50-43.00	56.59	57.85	1.26	31.37	31.72	97.82	15.32	63.91
5.	No. of primary branches per plant	2.00-3.50	0.08	0.13	0.05	20.07	25.63	61.32	0.46	32.37
6.	No. of cluster per plant	3.50-14.90	5.63	6.24	0.60	31.57	33.23	90.29	4.64	61.81
7.	No. of pods per cluster	2.20-3.90	0.20	0.31	0.11	14.21	17.64	64.86	0.74	23.58
8.	No. of pods per plant	10.1-39.10	58.05	61.04	2.99	36.92	37.86	95.10	15.30	74.18
9.	No. of seeds per pod	5.00-7.30	0.22	0.36	0.13	8.18	10.28	63.23	0.78	13.40
10.	Length of pod (cm)	3.45-5.28	0.17	0.22	0.05	9.52	11.02	74.68	0.73	16.95
11.	100 seed weight (g)	3.12-8.05	0.79	0.86	0.06	19.74	20.57	92.07	1.76	39.03
12.	Seed yield per plant (g)	1.39-11.93	8.16	8.38	0.22	64.80	65.67	97.35	5.80	131.71
13.	Protein content (%)	23.45-26.18	0.13	0.31	0.18	1.49	2.30	42.32	0.48	2.00

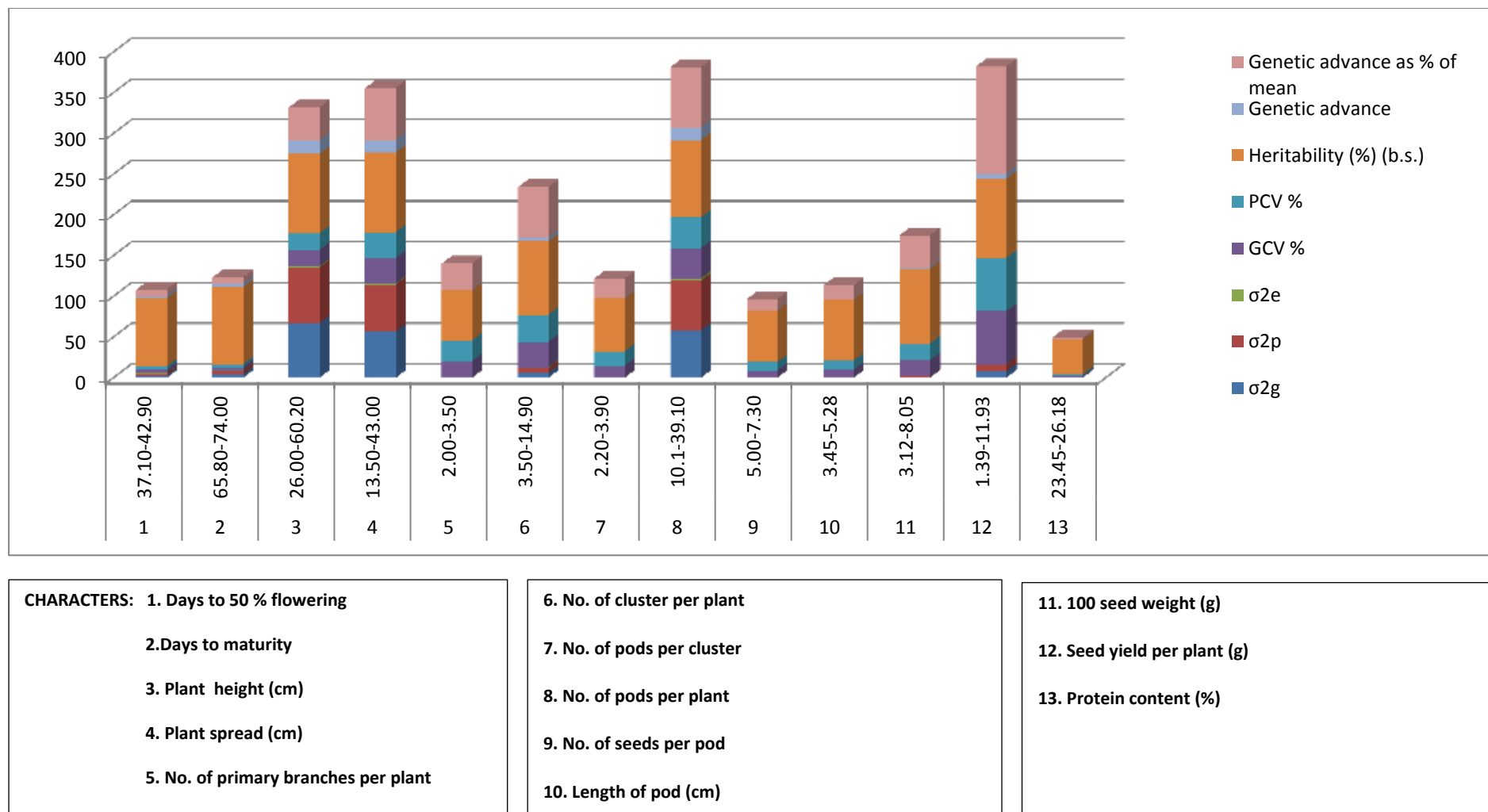


Fig1. Variability parameters for thirteen different characters studied in urdbean.

phenotypic correlation coefficients were higher than their corresponding genotypic correlation coefficients.

4.2.1 Association of grain yield with it's components

It was observed from Table 5, that seed yield per plant had significant positive correlation with number of seeds per pod, number of clusters per plant, number of pods per plant, number of primary branches per plant, length of pod, days to 50% flowering, plant height, plant spread and days to maturity at both genotypic and phenotypic levels while characters like 100 seed weight, protein % and number of pods per cluster were non significantly positive correlated with both genotypic and phenotypic levels.

4.2.2 Inter relationship of yield components.

1. Days to 50 % flowering

Days to 50 % flowering showed high significant and positive correlation with plant height ($r_p = 0.284$), ($r_g = 0.333$) and days to maturity ($r_p = 0.806$), ($r_g = 0.876$) and plant spread ($r_p = 0.445$), ($r_g = 0.504$) and 100 seed weight ($r_p = 0.464$), ($r_g = 0.500$) and length of pod ($r_p = 0.446$), ($r_g = 0.517$) and number of seeds per pod ($r_p = 0.307$), ($r_g = 0.423$), while number of primary branches per plant ($r_p = 0.216$), ($r_g = 0.255$), number of cluster per plant ($r_p = 0.122$), ($r_g = 0.167$), number of pod per cluster ($r_p = 0.0.124$), ($r_g = 0.163$), number of pods per plant ($r_p = 0.192$), ($r_g = 0.223$), showed non-significant positive correlation at genotypic level, while protein content ($r_g = -0.071$), ($r_g = -0.010$), showed negative correlation at both genotypic and phenotypic level.

2. Days to maturity

Days to maturity had highly significant and positive correlation with plant height ($r_p = 0.441$), ($r_g = 0.456$), plant spread ($r_p = 0.401$), ($r_g = 0.432$), number of seeds per pod ($r_p = 0.342$), ($r_g = 0.448$), 100 seed weight ($r_p = 0.424$), ($r_g = 0.429$), length of pod ($r_p = 0.313$), ($r_g = 0.371$) at both genotypic and phenotypic level, while number of primary branches per plant ($r_p = 0.214$), ($r_g = 0.257$) had significant positive correlation at genotypic only and number of cluster per plant ($r_p = 0.100$), ($r_g = 0.095$), number of pods per cluster ($r_p = 0.172$), ($r_g = 0.235$), number of pods per plant ($r_p = 0.221$), ($r_g = 0.224$), while it had negative correlation with protein content ($r_p = -0.129$), ($r_g = -0.141$), at both genotypic and phenotypic level.

3. Plant height

Plant height showed highly positive and significant correlation with plant spread ($r_p = 0.699$), ($r_g = 0.715$), number of primary branches per plant ($r_p = 0.418$), ($r_g = 0.580$), number of cluster per plant ($r_p = 0.553$), ($r_g = 0.585$), number of pods per cluster ($r_p = 0.375$), ($r_g = 0.483$), number of pods per plant ($r_p = 0.598$), ($r_g = 0.619$), length of pod ($r_p = 0.364$), ($r_g = 0.420$) at both genotypic and phenotypic level and number of seeds per pod ($r_p = 0.178$), ($r_g = 0.177$), 100 seed weight ($r_p = 0.170$), ($r_g = 0.190$) and protein content ($r_p = 0.002$), ($r_g = 0.008$) have non-significant, but positive correlation with plant height at both genotypic and phenotypic level.

4. Plant spread

Plant spread showed highly significant and positive correlation with seed yield ($r_g = 0.727$), ($r_g = 0.732$), number of primary branches per plant ($r_g = 0.561$), ($r_g = 0.744$), number of clusters per plant ($r_g = 0.687$), ($r_g = 0.735$), number of pods per plant ($r_p = 0.644$), ($r_g = 0.660$), and length of pod ($r_p = 0.426$), ($r_g = 0.501$), plant height ($r_g = 0.699$), ($r_g = 0.715$), days to 50% flowering ($r_g = 0.445$), ($r_g = 0.504$), days to maturity ($r_g = 0.401$), ($r_g = 0.432$), at both genotypic and phenotypic level, 100 seed weight ($r_p = 0.110$), ($r_g = 0.114$), number of pods per cluster ($r_p = 0.200$), ($r_g = 0.232$) and number of seeds per pod ($r_p = 0.197$), ($r_g = 0.253$), protein content ($r_g = 0.144$), ($r_g = 0.213$), had non significant and positive correlation with plant spread at both genotypic and phenotypic level.

5. Number of primary branches per plant

Number of primary branches per plant showed strong and highly significant positive correlation with number of clusters per plant ($r_p = 0.472$), ($r_g = 0.630$), seed yield per plant ($r_p = 0.416$), ($r_g = 0.554$), number of pods per plant ($r_p = 0.519$), ($r_g = 0.706$), plant height ($r_p = 0.418$), ($r_g = 0.580$), plant spread ($r_p = 0.561$), ($r_g = 0.764$), while it showed negative correlation with 100 seed weight ($r_p = -0.015$), ($r_g = -0.073$), at both genotypic and phenotypic level.

6. Number of clusters per plant

Number of clusters per plant showed strong and highly significant positive correlation with seed yield per plant ($r_p = 0.502$), ($r_g = 0.522$), number of pods per cluster ($r_p =$

0.268), (rg = 0.350), number of pods per plant (rp = 0.795), (rg = 0.848), number of primary branches per plant (rp = 0.472), (rg = 0.630), plant height (rp = 0.553), (rg = 0.585), plant spread (rp = 0.687), (rg = 0.735), negative correlation with 100 seed weight (rp = -0.035), (rg = -0.012), at both genotypic and phenotypic level.

7. Number of pods per cluster

Number of pods per cluster showed strong and highly significant and positive correlation with number of pods per plant (rp = 0.485), (rg = 0.619), number of clusters per plant (rp = 0.268), (rg = 0.350), plant height (rp = 0.375), (rg = 0.483), at both genotypic and phenotypic level while protein content (rp = -0.006), (rg = 0.105) showed negative non significant correlation at phenotypic level only.

8. Number of pods per plant

Number of pods per plant showed strong and highly significant positive correlation with seed yield per plant (rp = 0.539), (rg = 0.546), length of pod (rp = 0.337), (rg = 0.378), plant spread (rp = 0.644), (rg = 0.660), number of primary branches per plant (rp = 0.519), (rg = 0.706), number of clusters per plant (rp = 0.795), (rg = 0.848), number of pods per cluster (rp = 0.485), (rg = 0.619) at both genotypic and phenotypic level while 100 seed weight (rp = -0.008), (rg = -0.025), protein content (rp = -0.002), (rg = -0.041) showed negative correlation at both genotypic and phenotypic level

9. Number of seeds per pod

It showed highly significant positive correlation with seed yield per plant (rp = 0.315), (rg = 0.416), length of pod

Table 5. Estimates of genotypic and phenotypic correlation coefficients for different characters of urdbean genotypes.

Characters		Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per Plant	No. of cluster per plant	No. of pods per cluster	No. of pods per plant	No. of seeds per pod	100 seed weight (g)	Length of pod (cm)	Protein content (%)	Seed yield peer plant (g)
Days to 50 % flowering	P	1.000	0.806**	0.497**	0.445**	0.216	0.122	0.124	0.192	0.307*	0.464**	0.446**	-0.071	0.284*
	G	1.000	0.876**	0.557**	0.504**	0.255*	0.167	0.163	0.223	0.423**	0.500**	0.517**	-0.010	0.333**
Days to maturity	P		1.000	0.441**	0.401**	0.214	0.100	0.172	0.221	0.342**	0.424**	0.313*	-0.129	0.268*
	G		1.000	0.456**	0.4327	0.2578	0.095	0.235	0.224	0.448**	0.429**	0.371***	-0.141	0.290*
Plant height (cm)	P			1.000	0.699**	0.418**	0.553**	0.375**	0.598**	0.178	0.170	0.364**	0.000	0.472**
	G			1.000	0.715**	0.580**	0.585	0.483**	0.619**	0.177	0.190	0.420**	0.008	0.481**
Plant spread(cm)	P				1.000	0.561**	0.687**	0.200	0.644**	0.197	0.110	0.426**	0.144	0.727**
	G				1.000	0.744**	0.735**	0.232	0.660**	0.253	0.114	0.501**	0.213	0.732**
No. of primary branches per Plant	P					1.000	0.472**	0.234	0.519**	0.017	-0.015	0.030	0.007	0.416**
	G					1.000	0.6301	0.442**	0.706**	0.213	-0.073	0.108	0.057	0.554**
No. of cluster per plant	P						1.000	0.2681*	0.795**	0.019	-0.035	0.353**	0.001	0.502**
	G						1.000	0.350**	0.848**	0.123	-0.012	0.377**	0.014	0.522**
No. of Pods per cluster	P							1.000	0.485**	0.032	0.072	0.099	-0.006	0.118
	G							1.000	0.619**	0.163	0.060	0.086	0.105	0.135
No. of pods per plant	P								1.000	0.187	-0.008	0.337**	-0.002	0.539**
	G								1.000	0.241	-0.025	0.378**	-0.041	0.546**
No. of seeds per pod	P									1.000	0.152	0.264*	0.049	0.315*
	G									1.000	0.194	0.448**	-0.049	0.416
100 seed weight	P										1.000	0.191	-0.201	0.212
	G										1.000	0.225	-0.354**	0.229
Length of pod	P											1.000	-0.026	0.430**
	G											1.000	-0.128	0.473**
Protein content (%)	P												1.000	0.050
	G												1.000	0.051
Seed yield peer plant (g)	P													1.000
	G													1.000

*and ** indicates significant at 5 % and 1% level of significance respectively.

($r_p = 0.264$), ($r_g = 0.448$), days to 50% flowering ($r_p = 0.307$), ($r_g = 0.423$), days to maturity ($r_p = 0.342$), ($r_g = 0.448$), at both genotypic and phenotypic level while 100 seed weight ($r_p = 0.152$), ($r_g = 0.194$), showed non significant positive correlation at both genotypic and phenotypic level. It showed negative correlation with protein content ($r_p = 0.049$), ($r_g = -0.049$), at genotypic level.

10. 100 seed weight

It showed highly significant and positive correlation with days to 50% flowering ($r_p = 0.464$), ($r_g = 0.500$), days to maturity ($r_p = 0.424$), ($r_g = 0.429$), and negative correlation with number of primary branches per plant ($r_p = -0.015$), ($r_g = -0.073$), number of clusters per plant ($r_p = -0.035$), ($r_g = -0.012$), number of pods per plant ($r_p = -0.008$), ($r_g = -0.025$), at both genotypic and phenotypic level.

11. Length of pod (cm)

It showed significant and positive correlation with seed yield per plant ($r_p = 0.430$), ($r_g = 0.473$), days to 50% flowering ($r_p = 0.446$), ($r_g = 0.517$), plant height ($r_p = 0.364$), ($r_g = 0.420$), plant spread ($r_p = 0.426$), ($r_g = 0.501$), number of pods per plant ($r_p = 0.337$), ($r_g = 0.378$), and negative correlation with protein content ($r_p = -0.026$), ($r_g = -0.128$), at both genotypic and phenotypic level.

12. Protein content (%)

It showed non-significant and positive correlation with plant height ($r_p = 0.002$), ($r_g = 0.008$), plant spread ($r_p = 0.144$), ($r_g = 0.213$), number of cluster per plant ($r_p = 0.001$), ($r_g = 0.014$) and negative correlation with days to 50 %

flowering ($r_p = -0.071$), ($r_g = -0.010$), days to maturity ($r_p = -0.129$), ($r_g = -0.141$), number of pods per plant ($r_p = -0.002$), ($r_g = -0.041$), 100 seed weight ($r_p = -0.201$), ($r_g = -0.354$), length of pod ($r_p = -0.026$), ($r_g = -0.128$), at both genotypic and phenotypic level.

4.3 Path coefficient analysis

Path coefficient analysis was carried out to find out the direct and indirect contribution of each characters towards the seed yield per plant. The genotypic correlation coefficient being more important, were only partitioned into direct and indirect effects which are presented in Table 6 and Fig. 2.

4.3.1 Seed yield Vs days to 50% flowering

The character days to 50% flowering showed negative direct effect (-0.4842) on seed yield and indirect effect through plant spread, number of pods per plant and 100 seed weight while negative effect through number of clusters per plant and protein content. The total correlation with seed yield per plant was 0.3332.

4.3.2 Seed yield Vs days to maturity

This character had positive direct effect (0.0952) on seed yield. It showed negative indirect effect through days to 50% flowering, number of clusters per plant, number of pods per cluster and protein content while positive indirect effects through number of primary branches per plant, plant height, number of pods per cluster and number of seeds per pod. The total correlation with seed yield per plant was 0.2900.

Table 6. Direct and indirect effects of twelve casual variables on seed yield of urdbean genotypes .

Sr.No	Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of cluster per plant	No. of pods per cluster	No. of pods per plant	No. of seeds per pod	100 seed weight (g)	Length of pod (cm)	Protein content (%)	Seed yield per plant (g)
1.	Days to 50 % flowering	-0.4842	0.0835	0.0719	0.2443	0.0461	-0.0643	-0.0594	0.1233	0.0951	0.187	0.0917	-0.0017	0.3332**
2.	Days to maturity	-0.4244	0.0952	0.0588	0.2097	0.0465	-0.0365	-0.0854	0.1236	0.1008	0.1604	0.0659	-0.0248	0.2900*
3.	Plant height (cm)	-0.27	0.0434	0.129	0.3466	0.1047	-0.2247	-0.1752	0.341	0.04	0.0711	0.0745	0.0015	0.4819**
4.	Plant spread (cm)	-0.244	0.0412	0.0922	0.4847	0.1344	-0.2821	-0.0842	0.3639	0.0569	0.0429	0.0889	0.0373	0.7320**
5.	No. of primary branches per plant	-0.1235	0.0246	0.0748	0.3606	0.1806	-0.2417	-0.1602	0.3892	0.0479	-0.0273	0.0192	0.0100	0.5542**
6.	No. of cluster per plant	-0.0812	0.0091	0.0756	0.3563	0.1138	-0.3836	-0.1269	0.4673	0.0278	-0.0048	0.067	0.0026	0.5228**
7.	No. of pods per cluster	-0.0794	0.0225	0.0624	0.1127	0.0799	-0.1345	-0.3622	0.3413	0.0368	0.0226	0.0153	0.0184	0.1359
8.	No. of pods per plant	-0.1084	0.0214	0.0799	0.3202	0.1276	-0.3254	-0.2244	0.5509	0.0543	-0.0096	0.067	-0.0072	0.5463**
9.	No. of seeds per pod	-0.2049	0.0427	0.023	0.1227	0.0385	-0.0475	-0.0593	0.1332	0.2247	0.0726	0.0794	-0.0086	0.4163**
10.	100 seed weight(g)	-0.2423	0.0409	0.0246	0.0557	-0.0132	0.0049	-0.0219	-0.0141	0.0436	0.3736	0.0399	-0.0619	0.2298
11.	Length of pod(cm)	-0.2507	0.0354	0.0542	0.2431	0.0196	-0.145	-0.0313	0.2085	0.1006	0.0842	0.1772	-0.0225	0.4734**
12.	Protein content (%)	0.0048	-0.0135	0.0011	0.1033	0.0103	-0.0056	-0.0381	-0.0227	-0.011	-0.1323	-0.0228	0.1749	0.0483**

* and ** indicates Significant at 5 and 1 percent level of significance respectively.

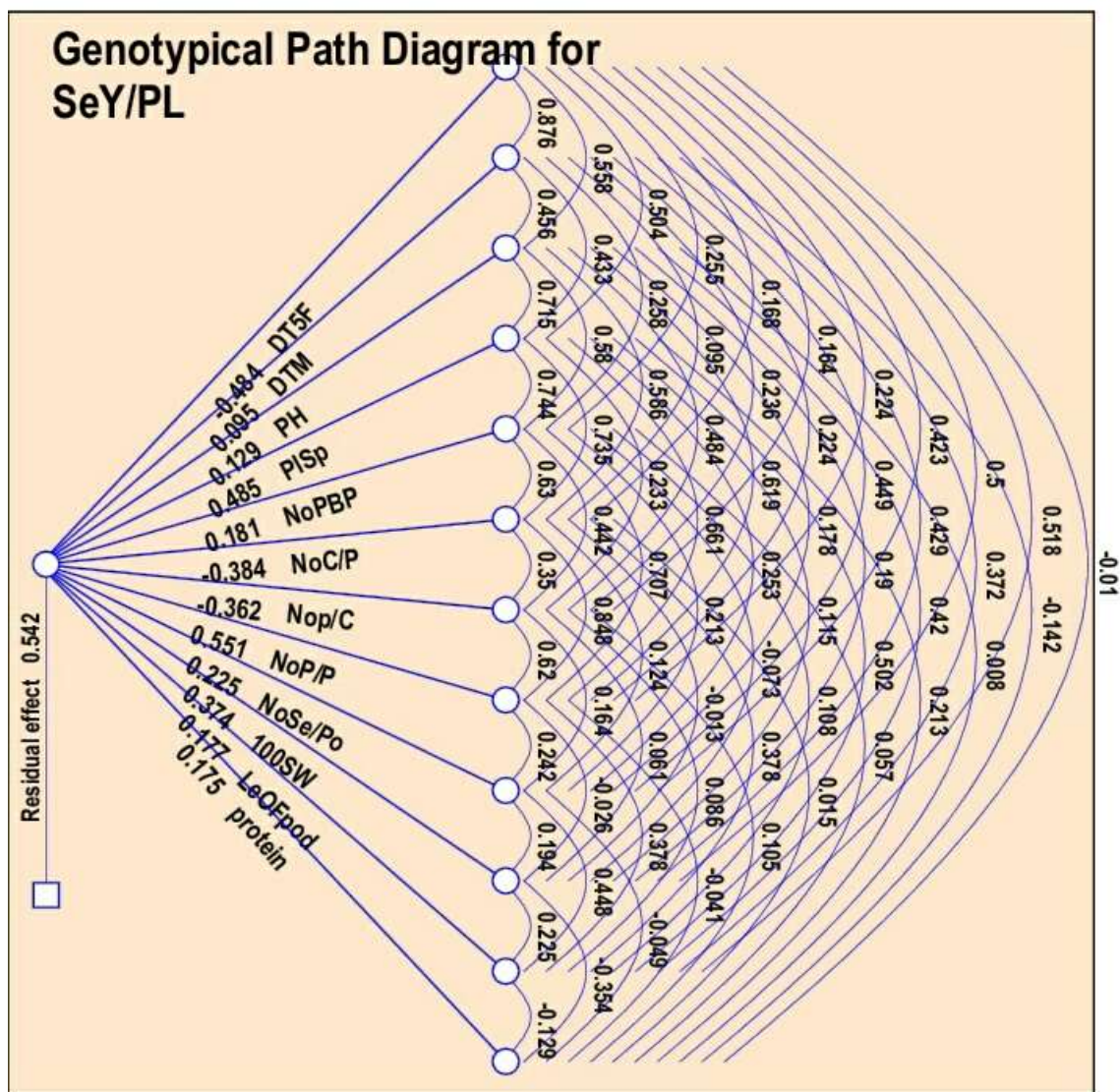


Fig. 2. Genotypic path diagram for seed yield.

4.3.3 Seed yield vs. plant height

This character showed positive direct effect (0.129) on seed yield. It had positive indirect effect through days to maturity, plant spread, number of primary branches per plant, number of pods per cluster, 100 seed weight, number of seeds per pod, protein content (%) and negative indirect effect through days to 50% flowering number of pods per plant, number of clusters per plant, The total genotypic correlation with seed yield was 0.4819.

4.3.4 Seed yield Vs plant spread

This character showed positive direct effect (0.4847). It had positive indirect effect through days to maturity, plant height, number of pods per plant, number of primary branches per plant, number of clusters per plant, number of pods per cluster, protein content, 100 seed weight and negative indirect effect through number of clusters per plant, number of pods per cluster and number of seeds per pod .. The genotypic correlation with seed yield was 0.7320.

4.3.5 Seed yield Vs primary branches per plant

This character had positive direct effect (0.1806) on seed yield. It had negative indirect effect through days to 50% flowering, number of clusters per plant, number of pods per cluster, number of seeds per pod, while positive indirect effect through days to maturity, plant height, plant spread, number of pods per plant, protein content and 100 seed weight. The total genotypic correlation with seed yield was 0.5542.

4.3.6 Seed yield Vs clusters per plant

This character had negative direct effect -0.3836 on seed yield. It had positive indirect effects through plant spread, plant height, number of pods per plant, number of seeds per pod, protein content, number of primary branches per plant, and negative indirect effect through day to maturity, number of pods per cluster and 100 seed weight. The correlation with seed yield per plant was 0.5228.

4.3.7 Seed yield Vs pods per cluster

This character had negative direct effect (-0.3622) on seed yield. It had positive indirect effects through, plant height, number of pods per plant, number of seeds per pod, protein content (%) , days to maturity, plant spread, number of primary branches per plant, 100 seed weight and negative indirect effects through days to 50 % flowering and number of clusters per plant. The total correlation with seed yield per plant 0.1359.

4.3.8 Seed yield Vs pods per plant

This character had positive direct effect (0.5509) on seed yield. It had positive indirect effects through, plant height, number of seeds per pod ,protein content (%), days to maturity, plant spread, number of primary branches per plant, number of pods per plant, 100-seed weight and negative indirect effects through, days to 50% flowering, number of pods per cluster and number of clusters per plant. The correlation with grain yield per plant was 0.5463.

4.3.9 Seed yield Vs seeds per pod.

This character had positive direct effect (0.2247) on seed yield. It had positive indirect effects through, number of pods per plant, plant height, plant spread, number of primary branches per plant, number of pods per cluster, and negative indirect effects through days to maturity, number of clusters per plant, 100 seed weight and protein content (%). The correlation with seed yield per plant was 0.4163.

4.3.10 Seed yield Vs 100 seed weight

This character had positive indirect effect (0.3736) on seed yield. It had negative indirect effects through days to 50 % flowering, number of pods per plant, number of pods per cluster, protein content and positive indirect effects through plant height, plant spread, number of primary branches per plant, number of clusters per plant, days to maturity and number of seeds per pod. The genotypic correlation with seed yield was 0.2298.

4.3.11 Seed yield Vs Length of pod.

This character had positive indirect effect (0.1772) on seed yield. It had negative indirect effects through days to 50 % flowering, number of clusters per plant, number of pods per plant, protein content and positive indirect effects through plant height, plant spread, number of primary branches per plant, number of pods per cluster, days to maturity and number of seeds per pod. The genotypic correlation with seed yield was 0.4734.

4.3.12 Seed yield Vs protein content

This character had positive indirect effect (0.1749) on seed yield. It had negative indirect effect through, number of pods per cluster, 100 seed weight., days to maturity, number of pods per plant, number of seeds per pod. It had positive indirect effect through, plant spread, number of primary branches per plant, number of clusters per plant, days to 50 % flowering and plant height. The correlation with seed yield per plant was 0.0483.

4.4 Genetic divergence

The data obtained for each of thirteen characters of urdbean was subjected to Mahalanobis (1936) D^2 analysis to calculate genetic distance between them.

4.4.1 Mahalanobis's generalized distance (D^2)

Wilk's (1932) criterion showed significant differences between the genotypes for pooled effect of 13 characters studied. Therefore the analysis was further extended to calculate D^2 values. The D^2 values for all the possible pairs of comparison between 30 genotypes were calculated. The calculated D^2 values ranged from 23.66 to 994.27. The maximum and minimum D^2 values were observed between the pair of genotypes (KU-15-117 and KU-15-109) and (KU-15-114 and PBCUB-14), respectively which clearly reveal diversity among the genotypes studied.

4.4.2 Clustering pattern of the genotypes

The clustering pattern obtained on the basis of D^2 value is presented in Table 7. Thirty genotypes were grouped into five clusters. Cluster I consisted maximum number of

genotypes (20) followed by clusters II (7), however clusters III, IV and VII were solitary clusters including only one genotype each .

4.4.3 Intra and inter cluster distances.

The average intra and inter cluster D^2 and D values are represented in Table 8. Maximum statistical distance (inter cluster distance) was observed between cluster V and III (30.40) followed by cluster IV and III (27.33), cluster IV and I (25.32), cluster III and II (25.30), cluster V and I (23.88) and cluster V and II (20.83), cluster II and I (20.10), cluster V and IV (19.91), cluster IV and II (18.53), cluster III and I (16.66) and others were comparatively low. Intra cluster divergence among the five clusters revealed that cluster II had maximum intra cluster distance (12.56) followed by cluster I (12.15) . As the clusters III, IV and V were solitary so there was no intra cluster distance between them.

Average Intra and inter cluster D^2 and cluster

4.4.4 Cluster means for twelve different characters.

Cluster means for thirteen different characters studied were presented in Table 9. A considerable inter cluster variation in respect of cluster was observed among the various clusters for all 13 characters studied in urdbean.

The cluster means for days to 50% flowering varied from 41.50 (Cluster II) to 39.60 (cluster IV). The cluster means for days to maturity varied from 72.24 (Cluster II) to 68.24 (Cluster I). Highest cluster mean for plant height was recorded for cluster V (60.20) and lowest was recorded for cluster III (35.20). The cluster means for plant spread varied from 18.10

(Cluster III) to 43.00 (Cluster IV). Cluster IV and cluster V exhibited highest value for number primary of branches per plant (3.00) and cluster III exhibited lowest value (2.20).

Cluster mean for number of clusters per plant varied from 6.77 (cluster I) to 14.90 (Cluster IV). Cluster mean for number of pods per cluster varied from 3.09 (cluster I) to 3.80 (Cluster IV). Cluster mean for number of pods per plant varied from 17.60 cluster (III) to 27.40 (Cluster IV). Cluster mean for number of seeds per pod varied from 3.69 (Cluster V) to 4.57 (cluster II) and Cluster mean for 100 seed weight was minimum in case of cluster V (3.60) and maximum in case of cluster IV (5.32). In case of protein content, variation was observed from 24.30 (cluster I) to 24.66 (cluster IV). Cluster mean for number of seeds per pod varied from 3.69 (Cluster V) to 4.96 (cluster IV). The cluster mean for length of pod varied from 1.40 (cluster V) to 11.93 (cluster IV).

4.4.5 Per cent contribution of different characters to genetic diversity

The utility of D^2 analysis was enhanced by its application to estimate the relative contribution of various plant characters to genetic divergence. The per cent contribution of thirteen characters studied is given in Table 10. It was observed that plant spread (39.31%), seed yield per plant (17.47 %), plant height (14.02 %) 100 seed weight (11.95%) contributed maximum for genetic divergence followed by number of pods per plant (6.21%), days to maturity (3.68%), length of pod (2.30%), number of seeds per pod

(2.07%), number of clusters per plant (1.84%), protein content (0.92%) and days to 50% flowering (0.23%).

4.5 Screening for virus resistance

Per cent disease incidence of yellow vein mosaic

Thirty urdbean genotypes were studied for screening for yellow vein mosaic disease under natural condition at Post Graduate Institute M.P.K.V. Rahuri. The disease incidence occurred on 30 genotypes were observed as presented in Table 11.1 to 11.4. Thirteen genotypes were found resistant to yellow vein mosaic however 9 genotypes were moderately resistant, 5 were found moderately susceptible and 3 genotypes were susceptible. The resistant genotypes were KU-15-118, KU-15-122, KU-15-123, KU-15-125, KU-15-126, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, KU-15-117, KU-15-131.

However, genotypes KU-15-107, KU-15-109, KU-15-116, KU-15-110, KU-15-132, PBCUB-14, PBCUB-18, PBCUB-19 and PBCUB-25 were found moderately resistant while KU-15-114, KU-15-127, KU-15-130, PBCUB-6, PBCUB-11, were moderately susceptible to YVM virus. More over three genotypes viz., KU-15-128, PBCUB-5 and PBCUB-27 exhibited susceptible reaction towards YVM virus.

Table 7. Composition of thirty Urdbean genotypes into different clusters by Tocher's method.

Cluster No.	No. of genotypes included	Name of genotypes
Cluster I	20	KU-15-117, KU-15-127, KU-15-114, KU-15 - 110,PBCUB-19, KU-15-128, KU-15-130, KU-15-109, KU-15-107, KU-15-125, KU-15-123, PBCUB-18, KU-15-116, KU-15-132, PBCUB-13, KU-15-122,PBCUB-7,PBCUB-5,PBCUB-11, KU-15-131
Cluster II	7	PBCUB-9,PBCUB-12,PBCUB-25,PBCUB-8,PBCUB-15,PBCUB-27.PBCUB-6
Cluster III	1	KU-15-118
Cluster IV	1	PBCUB-14
Cluster V	1	KU-15-126

Table 8. Average inter and intra cluster D^2 and cluster distance (D) values of Urdbean genotypes.

Sr. No.	Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
1.	Cluster I	147.62 (12.15)	404.01 (20.10)	277.55 (16.66)	641.10 (25.32)	570.25 (23.88)
2.	Cluster II		157.75 (12.56)	640.09 (25.30)	343.36 (18.53)	433.88 (20.83)
3.	Cluster III			(0.00)	746.92 (27.33)	924.16 (30.40)
4.	Cluster IV				0.00 (0.00)	396.40 (19.91)
5.	Cluster V					0.00 (0.00)

Table 9. Cluster means for 13 characters of urdbean genotypes

Sr. No.	Clusters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of cluster per plant	No. of pods per cluster	No. of pods per plant	No. of seeds per pod	Seed yield per plant (g)	100 seed weight (g)	Length of pod (cm)	Protein content (%)
1.	Cluster I	39.03	68.24	37.59	20.30	2.30	6.77	3.09	18.33	4.28	5.77	4.25	3.42	24.30
2.	Cluster II	41.50	72.24	46.16	31.57	2.67	8.34	3.30	24.06	4.57	6.23	4.77	6.70	24.35
3.	Cluster III	40.30	70.10	35.20	18.10	2.20	6.80	3.30	17.60	4.17	5.30	8.06	3.59	23.45
4.	Cluster IV	39.60	68.40	58.50	43.00	3.00	14.90	3.80	39.10	4.96	6.10	5.32	11.93	24.66
5.	Cluster V	40.50	69.60	60.20	31.30	3.00	10.00	3.40	27.40	3.69	5.00	3.60	1.40	24.47

Table10. Per cent contribution of diferent characters to genetic diversity of urdbean genotypes

Sr. no.	Characters	Percent contribution
1	Days to 50% maturity	0.23 %
2	Days to maturity	3.68 %
3	Plant height (cm)	14.02 %
4	Plant spread(cm)	39.31 %
5	No of primary branches per plant	0.00 %
6	No. of cluster per plant	1.84 %
7	No. of pods per cluster	0.00 %
8	No. pods per plant	6.21 %
9	No of seeds per pod	2.07 %
10	Seed yield per plant	17.47 %
11	100 seed weight (g)	11.95 %
12	Length of pod (cm)	2.30 %
13	Protein content (%)	0.92 %

Table 11.1. Urdbean genotypes resistant to yellow vein mosaic.

Sr. No.	Name of the genotypes	Per cent disease incidence (%)
1.	KU-15-118	3.33
2.	KU-15-122	4.99
3.	KU-15-123	6.66
4.	KU-15-125	6.66
5.	KU-15-126	4.99
6.	PBCUB-7	6.66
7.	PBCUB-8	4.99
8.	PBCUB-9	3.33
9.	PBCUB-12	8.33
10.	PBCUB-13	8.33
11.	PBCUB-15	3.33
12.	KU-15-117	4.99
13.	KU-15-131	6.66

Table 11.2. Urdbean genotypes moderately resistant to yellow vein mosaic.

Sr.No.	Name of the genotypes	Per cent disease incidence (%)
1.	KU-15-107	18.33
2.	KU-15-109	16.66
3.	KU-15-116	10.00
4.	KU-15-110	18.33
5.	KU-15-132	18.33
6.	PBCUB-14	16.66
7.	PBCUB-18	16.66
8.	PBCUB-19	20.00
9.	PBCUB-25	16.66

Table 11.3.Urdbean genotypes moderately susceptible to yellow vein mosaic.

Sr.No.	Name of the genotypes	Per cent disease incidence (%)
1.	KU-15-114	26.66
2.	KU-15-127	23.33
3.	KU-15-130	26.66
4.	PBCUB-6	26.66
5.	PBCUB-11	23.33

Table 11.4.Urdbean genotypes Susceptible to yellow vein mosaic

Sr. No.	Name of the genotypes	Per cent disease incidence (%)
1.	KU-15-128	33.33
2.	PBCUB-5	38.33
3.	PBCUB-27	36.33

5. DISCUSSION

Plant breeding deals with the management and utilization of genetic variability. It is, therefore necessary to classify and utilize this variability systematically for genetic up-gradation of biological population. Similarly, the assessment of the magnitudes and direction between yield contributing characters especially with yield is useful in selecting desired genotypes on the basis of phenotypic values. Hence, it is important to study the cause and effect relationship between yield and its component characters.

In the present investigation, thirty genotypes of urdbean were obtained from the Oil Seed Specialist, Oilseed Research Station, Jalgaon (MS) were evaluated for genetic variability, correlations, direct and indirect effects of the component characters and disease incidence of yellow vein mosaic on seed yield.

The results obtained are discussed in this chapter under appropriate headings.

5.1 Variability and genetic parameters

5.1.1 Range of variability

Wide range of variability was observed for almost all the characters. Variation observed for seed yield per plant ranged between 1.39 to 11.93 g. The other yield contributing characters also observed variability viz., days to 50 % flowering (37.10- 42.90), days to maturity (65.80- 74.00), plant height (26.00-60.20 cm), plant spread (13.50- 43.00cm), number of clusters per plant (3.50-14.90),

number of pods per cluster (2.20-3.90), number of pods per plant (10.1-39.10), number of seeds per pod (5.00-7.30), Length of pod (3.45-5.28 cm) 100 seed weight (3.12-8.05 g) and protein content (23.45-26.18 %).

The characters viz., plant height, plant spread, number of pods per plant, seed yield per plant exhibited higher degree of genotypic variances than rest of the characters, while plant height, plant spread, number of pods per plant, seed yield per plant also exhibited higher phenotypic variances. Moderate estimate of variability was noticed for characters viz., days to maturity, number of clusters per plant.

These results are in agreement with finding of Garje *et al.* (2013), Meshram *et al.* (2013) and Venkateshwarlu *et al.* (2011). Srivastava and Singh (2012) also reported wide range of variability for different characters. Gadakh *et al.* (2013) and Mehra *et al.* (2016) reported that genotypes differ significantly for different characters studied.

5.1.2 Genotypic and phenotypic coefficients of variation.

The estimates of GCV and PCV for all the characters studied showed little differences, PCV being slightly greater than the former, indicating the variability existing in these characters was mainly due to genetic factor. The estimates of genotypic as well as phenotypic coefficients of variation in the present study were highest for

seed yield per plant followed by number of pods per plant, number of clusters per plant, plant spread, number of primary branches per plant, plant height, 100 seed weight, number of pods per cluster and protein content whereas lowest for protein content followed by days to maturity, days to 50 % flowering, number of seeds per pod.

Srivastava and Singh (2012) reported highest GCV and PCV for the grain yield per plant, pods per plant, 100 grain weight, number of primary branches per plant, number of seeds per pod and moderate variability was found for pod length, number of clusters per plant, and lowest for days to 50 % flowering and days to first picking maturity. Suresh *et al.* (2013) also observed similar results for grain yield per plant followed and number of pods per plant and number of seeds per pod, moderate for plant height and 100 grain weight and lowest for days to 50 % flowering and days to maturity. Gadakh *et al.* (2013) and Panigrahi *et al.* (2014) also reported maximum GCV was found for 100 seed weight, number of primary branches per plant and grain yield per plant. Thus these traits offered scope for genetic improvement. The remaining traits however, showed lower values of GCV.

5.1.3 Heritability (broad sense) and genetic advance

Genotypic coefficient of variations alone does not indicate the proportion of total heritable variation. The heritability indicates are better indicator in this respect. The broad sense heritability includes the contribution of additive

gene effect. In the selection programme, heritability values as well as estimates of genetic advance are more useful than heritability alone.

In the present investigation number of pods per plant, number of primary branches per plant, number of pods per cluster, number of pods per plant, number of clusters per plant, plant height, plant spread, 100 seed weight, seed yield per plant expressed high estimates of heritability (bs) accompanied by high genetic advance as a percent of mean (Table 4) indicating that these traits were predominantly governed by additive gene action and selection for these traits would be more effective for desired genetic improvement. However, protein content, length of pod, number of seeds per pod, days to 50% flowering, days to maturity, bearing medium heritability but comparatively lower estimates of genetic advance indicated limited scope for improvement of these characters through phenotypic selection.

Rajendrakumar *et al.* (2000) and Panigrahi *et al.* (2014) reported similar results in black gram, Garje *et al.* (2013) and Suresh *et al.* (2013) reported similar results for all yield contributing characters in green gram.

5.2 Correlation studies

Correlated characters are of interest for three chief reasons, firstly in connection with genetic cause of correlation through the pleiotrophic action of the genes, secondly in connection with the change brought by

selection. It is important to know how the improvement of one character will cause simultaneous changes in other character and thirdly in connection with natural selection.

The value of correlation coefficients cannot be constant. It varies considerably according to kind of material handled and environmental conditions in which material grown even though the material used is the same the environmental including fertilization, plant population and cultural practices changes the values of correlation coefficients considerably. All correlations depend upon poor soil and increased fertility stands to decrease variability.

It was revealed from the present study, the genotypic correlation coefficients between most of the characters were higher than the phenotypic correlation coefficients. This indicates that there was a strong inherent association between various characters studied and less influenced by environmental conditions.

The seed yield per plant was significantly and positively correlated with number of seeds per pod, length of pod , number of pods per plant, number of clusters per plant and number of primary branches per plant at both genotypic and phenotypic levels.

Similar results were found by Mehra *et al.* (2016) and Singh *et al.* (2014) for number of primary branches per plant, number of pods per plant, length of pod, pods per cluster, number of seeds per pod and 100 seed weight in black gram. Shivade *et al.* (2011) found similar results for

number of clusters per plant, number of pods per plant, number of seeds per pod, number of branches per plant, number of seeds per pod in black gram. Khanpara (2012) for number of pods per plant, number of pods per cluster, number of clusters per plant and number of seeds per pod in green gram. Biradar *et al.* (2009) and Gadakh *et al.* (2013) also reported the number of clusters per plant, number of pods per cluster, pod length, seeds per pod and 100 seed weight were significant and positively related with seed yield per plant for mungbean.

Protein content showed positive correlation with seed yield per plant at genotypic level while, plant spread showed significant positive correlation at genotypic and phenotypic level. Suresh *et al.* (2013) also reported the similar findings.

Thus, to summarize, the characters viz., number of seeds per pods, number of pods per plant, number of clusters per plant and number of primary branches per plant were significantly and positively related with the seed yield per plant and each other. Therefore, desirable plant type in urdbean with high seed yield potential should have more number branches per plant, more number of clusters per plant, more number of pods per plant and more number of seeds per pod.

5.3 Path coefficient analysis

The overall correlation observed between any two attributes is a function of a series of direct and indirect

relationship between that attributes. Seed yield is a product interactions of component traits. Apart from correlation studies path coefficient analysis is important to obtain the information about different ways in which component characters influence the seed yield. Thus, path analysis provides the base to the breeder for designing the most effective selection programme based on few reliable component characters.

Path coefficient analysis outlined by Wright (1921) was carried out to find the direct and indirect effects of yield components on seed yield. Direct effect of any component characters on seed yield gives an idea about the reliability of indirect selection to be made through those characters to bring improvement in seed yield. If the correlation coefficient between causal factor and the effect is equal to the direct effect, then correlation explains the true relationship and a selection for traits will be effective.

If final correlation coefficient is positive, but the direct effect is negative or negligible, in such relation the indirect causal factors are to be considered simultaneously for selection. When correlation coefficient is negative but the direct effect is positive and high, a restricted simultaneous selection model to be followed that is restriction to be imposed to emulsify the undesirable effect in order to make direct effects (Singh and Kaker, 1977). The residual effect determines how best the causal factors accounts for

variability of the dependent factor, the grain yield per plant in this case.

In the present investigation, plant spread, number of primary branches per plant, number of pods per plant, protein content ,seeds per pod, 100 seed weight ,length of pod and days to maturity showed positive direct effects, while days to 50% flowering, number of pods per cluster and number of cluster per plant showed negative direct effect on grain yield per plant.

Number primary branches per plant had positive direct effects on grain yield . It's association with seed yield was positive and highly significant. It's positive indirect effects through days to maturity, plant height, plant spread, number of pods per plant, protein content and 100 seed weight. Parveen *et al.* (2011), Panigrahi *et al.* (2014) and Mehra *et al.* (2016) reported similar results in urdbean. Biradar *et al.* (2009), Gadakh *et al.* (2013) and Parmeshwarappa (2007) also reported the similar results in mungbean.

Number of pods per plant had high positive direct effect on seed yield (0.5509), while it's association with seed yield was positive and highly significant. It may be due to the positive indirect effects through plant height, number of seeds per pod ,protein content (%), days to maturity, plant spread, number of primary branches per plant, number of pods per plant and 100-seed weight .

Parveen *et al.* (2011), Panigrahi *et al.* (2014) and Mehra *et al.* (2016) reported same results in urdbean.

Hundred seed weight had high positive direct effects on seed yield (0.3736), while its association with seed yield was positive and highly significant. Its positive indirect effects through plant height, plant spread, number of primary branches per plant, number of clusters per plant, days to maturity and number of seeds per pod were positive. Panigrahi. *et al.* (2014) , Singh *et al.*(2014) and Mehra, *et al* (2016) also reported similar results in urdbean. Venkateshwarlu *et al.* (2011) also reported the similar results in mungbean.

The characters like days to 50% flowering, number of clusters per plant, number of pods per cluster showed positive association with yield per plant. However, partitioning of these correlations indicated that these traits exhibited negative direct effect. The correlation simply measures mutual association without regards to causation, where as path analysis specifies the cause and measures the relative importance of traits studied.

Based on the present investigation considering both correlation coefficients, it can be concluded that number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight are the important yield contributing characters and should be given due importance during selection as they were correlated

significantly with seed yield and also high direct path effect on yield per plant.

5.4 Genetic Divergence

Genetically diverse parent when crossed known to produce heterotic F1 and yield a spectrum of transgressive segregates in segregating generation. A set of 30 genotypes of urdbean under study were therefore assessed for genetic diversity for yield and yield contributing characters.

5.4.1 Diversity based on set of thirteen characters

Analysis of variance (Table 2) revealed highly significant differences among the genotypes for all the characters under study. Hence, the D^2 values were estimated as per Mahalanobis (1936) and described by Rao (1952). The estimates of D^2 values ranged from 23.66 to 994.27 which shows diversity among the genotypes studied. The maximum and minimum D^2 values were observed between the pair of genotypes (KU-15-117 and KU-15-109) and (KU-15-114 and PBCUB-14), respectively.

5.4.2 Cluster formation

The aim of cluster formation and estimation of intra and inter cluster divergence is to provide the basis for selecting better parents for hybridization programme.

The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to different clusters (Rao, 1952) and thus crossing between the genotypes belonging to the different clusters

can give desired heterotic response and desired segregants in further generations. Thus, cluster formation and finding out intra clusters and inter cluster divergence provide the base for the selecting the parents for hybridization, greater the distance between two clusters, wider is the genetic variability between the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decreased heterosis (Moll et al., 1961). Therefore, while selecting the parents on the basis of divergence, the per se performance and cluster means for the characters also needs due consideration in the crop improvement. Thirty genotypes were grouped into five clusters. Cluster I consisted maximum number of genotypes (20) followed by clusters II(7), however clusters III, IV and VII were solitary clusters including only one genotype each .

Panigrahi *et al.* (2014) studied 19 genotypes of urdbean and grouped them into VI clusters. Mehra, et al (2016) evaluated 75 accessions of urdbean and grouped them into seventeen clusters. Fourty genotypes of mungbean studied by Garje et al. (2013) were grouped into thirteen clusters. Fifty genotypes of mungbean classified into seven clusters by Gadakh et al. (2013). The average intra and inter cluster D^2 and D values are represented in Table 8. Maximum statistical distance (inter cluster distance) was observed between cluster V and III (30.40) followed by cluster IV and III (27.33), cluster IV and I (25.32), cluster III and II (25.30), cluster V and I (23.88) and cluster V and II

(20.83), cluster II and I (20.10), cluster V and IV (19.91), cluster IV and II (18.53), cluster III and I (16.66) and others were comparatively low. Intra cluster divergence among the five clusters revealed that cluster II had maximum intra cluster distance (12.56) followed by cluster I (12.15) . As the clusters III, IV and V were solitary so there was no intra cluster distance . The cluster means are presented in Table 9. Considering the cluster means for various clusters from which selection of the desired parent for future hybridization programme should be done for the improvement in the characters shown against them as listed below. The value on the basis of inter cluster distance, cluster means per se performance the tentative future hybridization programme is suggested. So, as to obtain better recombinants in the segregating generations and similarly, as the most of the characters are showing the additive gene action, selection for these characters is more effective. The D^2 analysis thus proved to be a very useful technique in isolating diverse parents from the genotypes under the study.

5.5 Relative contribution of different characters towards the divergence

The cluster mean and contribution of each character towards divergence is given in Table 9 and 10, respectively. The data revealed considerable differences among the clusters for most of the characters studied.

The present study showed that plant spread (39.31%), seed yield per plant (17.47 %), plant height (14.02 %) and 100 seed weight (11.95%) contributed highest for genetic divergence followed by number of pods per plant (6.21%), days to maturity (3.68%), length of pod (2.30%), number of seeds per pod (2.07%), indicating that these characters may be responsible for genetic divergence in the material under study. This is in consonance with findings of earlier work Panigrahi *et al.* (2014) for plant height ,seed yield per plant number of clusters per plant ,100 seed weight, number of pods per plant, length of pod.

Traits like days to maturity, number of clusters per plant (1.84%), protein content(0.92%) and days to 50% flowering (0.23%) contributed least to divergence. Gadakh *et al.* (2013) also reported the similar findings.

Considering the present results and work done by earlier workers, it can be concluded that there is genetic divergence in the present set of urdbean genotypes. This may be attributed to use of different set of material suggested by Bain and Sood (1984), who also pointed out that a positive contribution of genetic divergence of yield components, like number of pods per plant and plant height may help in selecting genotypes for seed yield and other economic trait. The knowledge on characters influencing total divergence is an important aspect to a breeder, which was estimated by D² analysis. This provides information of

different characters towards ultimate character, of seed yield.

5.5 Screening for virus resistance

5.5.1 Per cent disease incidence of yellow vein mosaic

Thirty urdbean genotypes were studied at Post Graduate farm M.P.K.V. Rahuri under natural conditions. The disease incidence occurred on 30 genotypes were observed, 13 genotypes were found resistant to yellow vein mosaic however 9 genotypes were moderately resistant, 5 were moderately susceptible and 3 genotypes were susceptible. The resistant genotypes were KU-15-118, KU-15-122, KU-15-123, KU-15-125, KU-15-126, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, KU-15-117 and KU-15-131.

However, genotypes KU-15-107, KU-15-109, KU-15-116, KU-15-110, KU-15-132, PBCUB-14, PBCUB-18, PBCUB-19 and PBCUB-25 were found moderately resistant while KU-15-114, KU-15-127, KU-15-130, PBCUB-6, PBCUB-11, were moderately susceptible to YVM virus. Moreover three genotypes viz., KU-15-128, PBCUB-5 and PBCUB-27 exhibited susceptible reaction towards YVM virus.

6. SUMMARY AND CONCLUSION

The present investigation “Identification of genetic stock of urdbean [*Vigna mungo* (L.) Hepper] for yellow vein mosaic resistance” conducted during *kharif* 2016 to study variability, heritability, correlations, path analysis, diversity and assessment of urdbean germplasm lines for yellow vein mosaic among thirty genotypes of urdbean. The experiment was laid in randomized block design with two replications.

The observations were recorded on days to 50 % flowering, days to maturity, plant height, plant spread, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod, 100 seed weight, protein content, seed yield per plant and disease incidence of yellow vein mosaic. The results obtained are summarised as under.

6.1 Summary

6.1.1 Variability and genetic parameters

Adequate variability was observed among the genotypes under study. Wide range of variations was observed for plant height, number of pods per plant, plant spread, seed yield per plant, days to 50 % flowering, protein content, 100 seed weight and number of seeds per pod.

The estimates of genotypic and phenotypic coefficients of variation were highest for the seed yield per plant followed by number of pods per plant, number of clusters per plant, plant spread, number of primary branches

per plant, plant height, 100 seed weight, number of pods per cluster and protein content, whereas lowest for protein content followed by days to maturity, days to 50 % flowering, number of seeds per pod.

In the present investigation, number of pods per plant, number of primary branches per plant , number of pods per cluster, number of pods per plant, number of clusters per plant, plant height, plant spread, 100 seed weight, seed yield per plant expressed high estimates of heritability (bs) accompanied by high genetic advance as a percent of mean indicating that these traits were predominantly governed by additive gene action and these traits would be improved through selection only.

6.1.2 Correlations

In the present study, it was observed that seed yield per plant was significantly and positively correlated with number of seeds per pod (0.416), length of pod (0.473), number of pods per plant (0.546), number of clusters per plant (0.522) and number of primary branches per plant (0.554) at both genotypic and phenotypic levels.

6.1.3 Path coefficient analysis

Path analysis revealed number of primary branches per plant (0.1806), 100 seed weight (0.3736), plant spread (0.4847) number of pods per plant (0.5509), number of seeds per pod (0.2247), length of pod (0.1772) and protein content (0.1749) showed positive highest direct effects, while days to 50% flowering (-0.4842), number of clusters per plant

(-0.3836), number of pods per cluster (-0.3622) showed negative direct effect on grain yield per plant.

6.1.4 Genetic divergence

D² values ranging from 23.66 to 994.27 which indicates diversity among the genotypes. Thirty genotypes were grouped into five clusters. Cluster I consisted maximum number of genotypes (20) followed by clusters II(7), however clusters III, IV and VII were solitary clusters including only one genotype each .

The maximum and minimum D² values were observed between the pair of genotypes (KU-15-117 and KU-15-109) and (KU-15-114 and PBCUB-14), respectively. Clustering pattern of these genotypes did not necessarily follow the geographical distribution.

6.1.5 Screening for virus resistance

Per cent disease incidence of yellow vein mosaic of mungbean

In the present study, it was observed that disease incidence of yellow vein mosaic varies from genotypes to genotype i.e. 3.33 % to 36.66 % causing reduction in the yield. The disease incidence occurred on 30 genotypes were observed, 13 genotypes were found resistant to yellow vein mosaic however 9 genotypes were moderately resistance, 5 were moderately susceptible and 3 genotypes were susceptible.

The resistant genotypes were KU-15-118, KU-15-122, KU-15-123, KU-15-125, KU-15-126, PBCUB-7, PBCUB-

8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, KU-15-117 and KU-15-131.

6.2 Conclusion

6.2.1 Variability

High genotypic coefficients of variation for seed yield per plant followed by number of pods per plant, plant spread, plant height and number of pods per plant suggested presence of more variability.

High heritability accompanied with high genetic advance as a per cent of mean suggest additive genetic control in the inheritance of characters like number of pods per plant, number of clusters per plant, seed yield per plant which indicated scope for selection for improvement of these characters.

6.2.2 Correlations

Number of primary branches per plant, number of pods per plant, number of clusters per plant, number of seeds per pod and length of pod had strong positive correlations with seed yield per plant.

6.2.3 Path analysis

Number of primary branches per plant , plant spread , number of seeds per pod and 100 seed weight showed high positive direct effects on seed yield so these are important yield components in urdbean

6.2.4 Genetic divergence

- Substantial genetic diversity was observed among the genotypes studied.
- Thirty genotypes grouped into five clusters.

- The pair of genotypes *viz.*, (KU-15-118 and KU-15-126) was mostly divergent from one another.
- On the basis of inter cluster distances, cluster means and *per se* performance, the genotypes KU-15-118, PBCUB-14, KU-15-126 and PBCUB-9 should be used in future hybridization for urdbean improvement.
- The genotype KU-15-128 can be used in breeding programme with yellow vein mosaic resistant varieties.
- The crosses suggested are : KU-15-118 X PBCUB-14, KU-15-128 X PBCUB-9.

6.2.5 Screening for virus resistance

Per cent disease incidence of yellow vein mosaic of mungbean

Thirty urdbean genotypes were studied at Post Graduate farm M.P.K.V. Rahuri under natural conditions. The disease incidence occurred on 30 genotypes were observed, 13 genotypes were found resistant to yellow vein mosaic however 9 genotypes were moderately resistant, 5 were moderately susceptible and 3 genotypes were susceptible. The resistant genotypes were KU-15-118, KU-15-122, KU-15-123, KU-15-125, KU-15-126, PBCUB-7, PBCUB-8, PBCUB-9, PBCUB-12, PBCUB-13, PBCUB-15, KU-15-117 and KU-15-131.

However, genotypes KU-15-107, KU-15-109, KU-15-116, KU-15-110, KU-15-132, PBCUB-14, PBCUB-18, PBCUB-19 and PBCUB-25 were found moderately resistant while KU-15-114, KU-15-127, KU-15-130, PBCUB-6, PBCUB-11, were moderately susceptible to YVM virus. More ever three

genotypes viz., KU-15-128, PBCUB-5 and PBCUB-27 exhibited susceptible reaction towards YVM virus.

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8. VITA

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