“GENETIC DIVERSITY IN RICE BEAN (*Vigna umbellata* (Thumb) Ohwi and Ohashi)”

A Thesis submitted to the

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

by

Mr. SAWANT GANESH APPASAHEB
(Reg. No. 11/049)

in partial fulfilment of the requirements for the degree
of

MASTER OF SCIENCE (AGRICULTURE)

In

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE
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DEPARTMENT OF AGRICULTURAL BOTANY
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MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722
2013

CANDIDATE'S DECLARATION

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

Place : MPKV, Rahuri
Date : / / 2013

(G. A. SAWANT)

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CERTIFICATE

This is to certify that the thesis entitled, "**GENETIC DIVERSITY IN RICE BEAN (*Vigna umbellata* (Thumb) Ohwi and Ohashi)**", submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr. SAWANT GANESH APPASAHEB,** under my guidance and supervision and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : MPKV, Rahuri (S. S. Dodake)
Date : / /2013. Research Guide

Dr. S. G. Borkar,
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Post Graduate Institute,
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Maharashtra State (India).

CERTIFICATE

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Place : MPKV, Rahuri (S. G. Borkar)
Date : / /2013. (Associate Dean)

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Place: Rahuri

Date: / /2013

(Ganesh A. Sawant)

CONTENT

3.4 Genetic diversity

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LIST OF ABBREVIATIONS

% : Percent
°C : Degree celcius
µg : Microgram
C.D. : Critical difference
C.V. : Critical varience
cm : Centimetre
et al. : et alli (and others)
Fig. : Figure
g : Gram
ha. : hectare
hrs. : Hours
i.e. : that is
kg : kilogram
kg/hl : kilogram/hectolitre
mg : milligram
min. : minute
ml : millilitre
nm : nonometre
OD : Optical density
ppm : Parts per million
S.E. : Standard Error
sec : Seconds
viz., : Videlicet (Namely)

ABSTRACT

“GENETIC DIVERSITY IN RICE BEAN (*Vigna umbellata* (Thumb) Ohwi and Ohashi)”

by

Mr. GANESH APPASAHEB SAWANT

A candidate for the degree
of
MASTER OF SCIENCE (AGRICULTURE)
2013

Research Guide : **Prof. S.S. Dodake**
Department : **Agricultural Botany**
Major discipline : **Genetics and Plant Breeding**

The present investigation entitled “GENETIC DIVERSITY IN RICE BEAN (*Vigna umbellata* (Thumb) Ohwi and Ohashi).)” was undertaken to study the extent of genetic variability, heritability (broad sense), genetic advance, correlation and genetic divergence in 54 genotypes of rice bean. The material was evaluated in randomized block design with two replication during *Kharif*, 2012 at underutilized crop project field, department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri.

Observations were recorded on eleven characters *viz.,* days to 50 per cent flowering, days to maturity, plant height, length of pod, number of pods per cluster, number of seeds per pod, number of branches per plant, seed yield per plant, 1000 seed weight, seed yield per plot and seed yield per hectare.

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contd...

Significant treatment means sum of squares for all characters studied. High GCV and PCV found for seed yield per plant, plant height at maturity, days to 50 per cent flowering, days to maturity, number of pods per cluster and for number of branches per plant, while it is moderate for number of seeds per pod and for 1000 seed yield. Least GCV and PCV recorded for length of pod.

Few character shows high broad sense heritability with high genetic advance. It means that character governed by additive gene action. In correlation, all character shows positive and significant correlation with each other except 1000 seed weight, which was negatively and significantly correlated.

Substantial amount of genetic diversity was observed among 54 genotype of rice bean. D values ranges between 20.75 and 103.71. Cluster VIII and cluster IX were most divergent cluster. 1000 seed weight and days to maturity contributed maximum in divergence.

The tentative hybridization programme involving 10 potent parents identified for hybridization are listed below.

1. RRBG-11-03
2. RRBG-11-13
3. RRBH-11-16
4. RRBG-11-23
5. RRBG-11-23-03
6. RRBG-11-27
7. RRBG-11-36
8. RRBG-11-37
9. LRB-459
10. LRB-467

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1. INTRODUCTION

The grain legumes assume great importance as a source of protein rich food, particularly in the tropics. The advisory committee on Technology Innovation, Board of Science and Technology for International Development, National Academy of Science, U.S.A. identified several underutilizedand under-exploited tropical legumes which have potential. Apart from the traditional tropical legumes like chickpea, pigeonpea, mung bean, lentil and peas etc. rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) is one of the legume so identified and gaining attention as supplementary food crop in India (Chandel and Singh, 1984).

Rice bean is native of South East Asia (Burkill, 1935 Ohwi, 1965) and grown in India, Burma, Malaysia, China, Korea, Indonesia and Phillipines (Sastrapradja and Sutarno, 1977 and Thomas, *et al.* 1983). It has been introduced as garden and cover crop in Fiji, Shrilanka, Mauritius, Sierra Leone, Ghana, Zaire, Tanganyika, Jamaica, Haiti and Mexico. It is also cultivated to a limited extent in West Indies, U.S.A. Queensland (Australia) and in East Africa (Burkill, 1935).

Rice bean was originally described by Roxburgh (1974) as *Phaseolus calcaratus* Roxb. (Baker, 1979). Recent taxonomist retains this species under *Vigna spp.* (Verdcourt, 1971). The correct nomenclature of rice bean suggested by Marchal *et al.* 1981 is referred as *Vigna umbellata* (Thumb) Ohwi and Ohashi.

In India, rice bean is distributed mainly to the tribal regions of North-Eastern hills, Western and Eastern Ghats in

Peninsular India, often hilly tracts (Arora *et al.* 1980). Although it is found in different parts of the country, it is grown as an important pulse crop only in North-Eastern Santhal paraganas in Orissa and Chhotanagpur in Jharkhand.It is used as a food, fodder, green manure and cover crop (Thomas *et al.* 1983). In West-bengal, it is recommended as a fodder crop (Verma and Singh, 1985). Rice bean has been found growing wild in Himalayas (Chandel, 1981). Apart from Himalyan ranges, the plant also occurs wild in humid belt of the Western Ghats and in the hilly tracts of eastern / north eastern region upto the elevation of 1500 m (Arora *et al.* 1980, Chandel *et al.* 1978 a, 1978 b, 1982 a and 1982 b). It's distribution pattern indicates it's adaptive polymorphism for diverse distributional range with climatic variation ranging from humid sub tropical to warm cool temperate climate.

It is truly diploid species with 2n =22 (Kumar, 1945, Darlington and Wylie, 1955; Joseph and Bouwkamp, 1978; Sarbhoy, 1978). In India rice bean is known by various common names like Ghurush, Meth, Paumia, Shiltong, Sitamash, Rajmung, Khasiamung in various regions. It is also known as Japanese rice bean, climbing mountain bean and the Jerusalem pea etc.

The species *Vigna umbellata* has cultivated and wild forms. Cultivated forms are annual, stem-erect / sub-erect of flexuose, tending to viny usually covered with fine deciduous deflexed hairs, medium sized flowers and pod glabrous cylindrical, while wild forms are perennial, very viny, roots thick, leaves are more variable in shape, size and location. Flowers smaller as compared to cultivated, pods are slightly curved, shatter on maturity, seeds 8-10 per pod seeds very small, seed colour brownish black or mottled, seed coat impermeable to water.

The nutritional value of rice bean is exceptionally high. The dried seeds contain high amount of protein. Limiting amino acids like methionine and tryptophan are quite high. Phytin-phosphorus content occurs in low quantity in rice bean. Because of these facts, the nutritional quality of rice bean is better than traditional pulse (Chandel *et al.* 1978 a & b). The total starch content of rice bean varieties is higher than that of green gram and black gram.

There are five taxonomically distinct botanical varieties of rice bean.

1. Variety 'Major' found in the hills of Northern India and Myanmar having large flowers.
2. Variety 'Rumbaiya' cultivated in the hills of Myanmar, with short erect or spreading stems.
3. Variety 'Gracilis' a wild form with slender smooth stems and narrow leaflets.
4. Variety 'Glaber' with smooth stems and leaves.
5. '*Phaseolus torosus* Roxb.' cultivated in Nepal having short and sub cylindrical reddish pods (Chandel 1978b).

The rice bean is adapted to hot humid climate and is fairly well distributed in the sub-tropical hilly regions. It does well in soils varying from sandy loam to heavy. It is moderately drought tolerant and photo-thermo-sensitive in terms of flowering and reproduction.

Rice bean is cultivated for food, animal feed, cover crop, green manure etc. It is consumed alone or mixed with rice. The tender pods (long pod varieties) are cooked as vegetable, besides the green shelled seeds are also consumed like green peas or beans. It is also good cover crop and can be used to check soil erosion. It is helpful to improve soil fertility through symbiotic nitrogen fixation. It is ideally suited as short rotation forage crop in areas where there is acute competition for land to be utilized for food and fodder production (Chatterjee *et al.* 1977) in humid subtropics of India. The whole plant is used as forage. Rice bean at pre-flowering stage is quite palatable (Banarjee *et al.* 1974) and at flowering stage the proportion of Ca and P is reported to be balanced (Mujumdar *et al.* 1968). The DCP is 8.06 and TDN is 52.84 per cent, respectively.

This is new pulse crop with high nutritional qualities. It is rich in protein (20-24 %), fat (0.6 %), having 59 per cent carbohydrate and 5.2 % fiber (Chauhan 1981). The amino acid profile of rice bean has been reported to have the highest amount of methionine, lysine, histidine and stands top with respect to cystein, argenine, leusine, tryptophan, tyrosine and valine content among all legumes of worlds economic importance (Duke, 1981).

Rice bean is free from the common pests and diseases associated with pulses. It showed resistance to mung bean yellow mosaic virus (MYMV) which is the most serious disease affecting production of other *kharif* pulses like mung bean, urd bean, moth bean, soybean and cowpea (Arora *et al.* 1980, Verma and Singh, 1985). It also has very high levels of resistance to cercospora leaf spot. Rice bean is least attacked by bean fly. It has shown very high degree of resistance to pulse beetle attack which is the most important store grain pest (Muniyappa *et al.* 1977, Sandhu *et al.* 1985).

In spite of varied uses and a potential grain legume, rice bean is not fully exploited for it's potential. Thus, there is a need to improve and exploit the genetic potential of this crop through systematic assessment of variability and it's utilization in hybridization programme by using proper selection criterion. The research work on genetic diversity and cause and effect relationship through path analysis in this crop is scanty and the situation calls for more detailed studies.

It is a well known fact that breeding for high yield is the major objective in any breeding programme. Plant yield is the ultimate criterion which plant breeder has always to keep in view in his attempts to evolve, superior varieties. Genetic diversity which is heritable is pre-requisite for any successful breeding programme. Genetic divergence among the parents play vital role in cultivar improvement because a cross involving genetically diverse parents is likely to produce high heterotic effects and also more variability in segregating generations, which can be exploited for the desired improvement. The choice of diverse parents in the hybridization programme is of a paramount importance.

The Mahalanobis's (1936) D^2 statistic is powerful tool for quantifying the divergence between two populations. It thus, gives better idea about the magnitude of divergence and is independent of size of sample and provides the basis for selection of parental lines for future breeding programme. Many studies indicated that geographical isolation is not necessarily related to genetic diversity.

Plant yield is not unitary character but is the result of interaction of a number of factors both inherent in the plant as well as the environmental. It therefore becomes difficult to evaluate or select for this complex character directly. Resources must then be more on indirect methods such as determination of the association existence between other less variable plant characters and yield. Association among the characters influenced by a large number of genes is elaborated statistically by estimating correlation coefficient which provides a measure of genotypic correlation between characters selection pressure may then be easily exerted on those variables which show close association with yield.

The method of partitioning the correlation into direct and indirect effects by path coefficient analysis suggested by Wright (1921) provides useful information on the relative merits of the trait under selection.

The present investigation is therefore proposed to study genetic diversity in rice bean with the following objectives.

1. To measure genetic diversity in quantitative characters.
2. To study the nature and extent of genetic diversity.

2. REVIEW OF LITERATURE

The literature pertaining to the present investigation has been reviewed,

2.1 Origin, botany and cytological studies in rice bean

2.1.1 Origin

Rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi) Syn *Phaseolus calcaratus* Roxb] is a native of south and south East Asia (Ohwi Jisabura, 1965). As a cultigen, rice bean occurs in India, Burma, Malaysia, China, Korea, Indonesia and the Philippines. It has been introduced as a garden and cover crop in Fiji, Sri lanka, Mauritius, Sierra, Leone, Ghana, Zaire, Tanganyika, Jamaica, Haiti and Mexico. It is also cultivated to a limited extent in West Indies, U.S.A., Gueensland (Australia) and in East Africa (Burkill, 1935).

Out of the 230 species of *Phaseolus,* 20 are cultivated and on the basis of their origin they are divided into Asiatic and American type. Out of five Asiatic species, *P. mungo* and *P. aureus* are oldest and not found in wild state, both of these species originated in India. Rice bean belongs to *P. calcaratus* which has been introduced into cultivation very recently and is found under cultivation as well as in wild form in Indian Origin. (Dana, 1976).

2.1.2 Botany

The rice bean was originally described by Roxburgh (1974) under *Phaseolus calcaratus* Roxb (Baker, 1979). In the recent classification of *Phaseolus* species, all Asiatic *Phaseolus* groups are included in the genus *Vigna* and now rice bean is botanically known as *Vigna umbellata* (Thumb) Ohwi and Ohashi and it's significant synonyms are *Dolichos umbellatus* Thumb, *Phaseolus calcaratus* Roxb. *P. pubescens* Blume, *P. ricciardiarus* Ten and *Azukia umbellata* (Thumb) Ohwi (Thomas *et al.* 1983).

Rice bean is quite distinct from other Asiatic *Phoseolus* species now under *Vigna,* having elongated seeds with long linear and straight, prominent, concave hilum raised above the surface and crinkled at margins, rounded ends of seed, hypogeal germination and beaked pods. It is a highly branched bushy annual growing 80-100 cm in height. The early habit is erect but with the progress of growth it gives off twining branches 80-100 cm long. The stem is glaucous but the leaves are young branches have short hair. Leaves are bold and pinnately trifoliate. The root system is very extensive with a number of fine deep rooting branches. The tap root goes down very deep (100-150 cm) and it bears a number of small nodules. Flowers are yellow and occur in clusters on auxiliary racemes. Pods are curved, thin 9-10 cm long, ripe pods are white, seeds are oval, bold and yellow colored with white hilum.

2.1.3 Cytological studies

Similar to other *Vigna* species of Asian origin rice bean is also truly diploid species with 2n = 22 chromosomes (Kumar, 1945; Darlington and Wylie, 1955; Joseph and Baukanp, 1978 and Sarbhay, 1978). However, the primary basic number for *Vigna umbellata* is n = 11. Rice bean has a highly symmetrical Karyotype (Singh and Rao, 1970). Rao and Chandel (1991) carried out karyomorphological studies in the cultivated and wild *Vigna* species and found chromosome number 2n = 2x = 22 indicating that the basic number of genus *Vigna* is X = 11.

Flowers of the rice bean are self fertile, but some natural out crossing occurs and the plant will cross even with other legume species (Sewa, 1974; Dana, 1966 a and 1967). Das and Dana (1987) observed the out crossing frequency varying from 0.27-0.81 among crosses of 6 *Vigna umbellata* and the percentage of lines within a cross that showed out crossing ranged from 86.8 to 100.

Biswas and Dana (1975) recorded completely seed sterile hybrids with 0.5-1.1 % pollen fertility and highly irregular meiosis in crosses of rice bean with *Phaseolus aureus* and *P. mungo*. Evidences of interchange, inversion heterozygosity and reverse types of duplication have been collected from pachytene and later stages of meiosis in the diploid and triploid hybrids of rice bean. It was concluded that the chromosomes of rice bean might have been differentiated through interchange, inversion and reverse repeats (Dana, 1966 b and Biswas and Dana, 1975).

2.2 Genetic diversity and variability in rice bean

Das (1979) reported high heritability for number of seeds perplant (89.2 %) and seed size (99.8 %).

Thomas *et al.* (1983) made 170 collections from Nepal, Sikkim and Himalaya and probably it was the first report of an effort towards genetic improvement in rice bean. They observed good range of variability with regard to seed yield and its components. But none of the types as such possessing high seed yield and other agronomic traits was found suitable under Delhi conditions.

Das and Dana (1985) reported narrow sense heritability estimates of 12.4, 30.4, 95.8 and 85.6 per cent for plant height, number of branches, days to flower and number of pods respectively. Their study indicated that the inheritance and days to flower and number of pods are mostly determined by additive gene effects. They suggested that the conventional breeding procedures involving crosses between high yielding parents having different values for these two characters followed by selection in segregating generations would lead to the development of early variety with higher number of pods per plant.

Styan *et al.* (1988) induced the genetic variability in amphidiploid generation of mung bean and rice bean crosses of the amphidiploid progenies from an inter specific hybrids between mung bean and rice bean studied in C_1, C_2 and C_3 generations, many showed resistance to mung bean yellow mosaic virus and powdery mildew. Much variability was also observed in the three generations for seed yield and it’s components.

Gadekar and Dhumale (1990 a) studies twenty two genotypes of *Vigna umbellata* for grain yield, number of branches per plant, number of seeds per pod and other five characters. Grain yield, number of branches per plant and number of seeds per pod expressed considerably high PCV and GCV and appeared more stable characters. Number of pods per plant was having high PCV but moderate GCV, indicating more influence of environment. It was also been reflected in lower heritability. Very high estimates of heritability were obtained for days to flowering (97.64 %), number of branches per plant (78.40 %) and number of seeds per pod (78.12 %). The heritability was moderate for 100 seed weight (65.19 %), length of pod (64.98 %) and grain yield per plant (55.56 %).

Sharma *et al.* (1991) evaluated 19 rice bean germplasm lines collected from Meghalaya and Mizoram for yield and it's eight components. Heritability (broad sense) estimates were high for 100 seed weight, days to maturity and pod length. At the phenotypic level, seed yield showed highly significant positive correlations with plant height, branches and pods per plant. At the genotypic level, seed yield was also strongly correlated with these traits and in addition with seeds per pod and days to 50 % flowering. High yield potential (1002 to 1203 kg / ha) was shown by 8 of the 19 lines. Highly significant differences between genotypes for year and genotype x year interaction were observed.

Mishra *et al.* (1995) studied genetic variability in 10 germplasm lines of rice bean. They observed high genotypic coefficients of variation for all the traits except grain per pod. Moderate to high heritability and high genetic gain were reported for seed yield, days to 50 % flowering, plant height, 1000 seed volume and test weight.

Roquib and Das (1995) recorded data from seven yield and forage yielding characters in 63 strains of rice bean (*Vigna umbellata*) and the data analyzed using Mahalanobis D^2 statistics. the relative merits of days to 50 % flowering, dry matter and green forage yield in contributing towards total divergence in both the years were stable enough while days to 50% flowering has more profound effect on genetic divergence than other characters under study.

Kumar *et al.* (1996) studied thirty radiation induced *Vigna umbellata* M_4 mutants and the control variety IC 156431 were grouped into 8 clusters by D^2 analysis of data on quantitative characters from plant grown in Banglore.

Sharma *et al.* (1996) studied the genetic diversity of 28 genotypes of *Vigna umbellata* of indigenous and exotic origin was studied by subjecting data on 9 yield components to Mahalanobis D^2 analysis. The genotypes were grouped into 6 clusters. Clusters II, III and V were the most divergent, with a high mean yield expression and thus are suitable for use in breeding programme. No relationship was established between geographic origin and genetic diversity.

Jadhav (1996) studied genetic variability in 50 genotypes of rice bean and reported that GCV and PCV were higher for all traits except days to 50 % flowering, days to maturity and pod length for which it was least. The heritability in broad sense was the highest for plant height at 50 % flowering. High heritability associated with genetic gain is per cent of mean were observed in shattering percentage at 10 days at maturity, grain yield per plant, number of clusters per plant and number of pods per plant.

Chaudhari (1997) evaluated 60 rice bean genotypes for genetic variability and reported a wide range and variation for most of the yield components except for pod length, branches per plant, 100 grain weight and grain protein content. Heritability in broad sense was the highest for grain protein contents followed by grain yield per plant and plant height. High heritability with high genetic advance were observed for grain protein content, plant height, grain yield per plant, 100 grain weight, days to maturity and 50 % flowering.

Singh *et al.* (1999) studied genetic divergence of thirty-one local rice bean cultivars of Manipur hills and genotype $CXM_{12}P_3$ from the N.B.P.G.R., Based on Mahalanobis D^2 values, the genotypes were classified into five different clusters following Tocher's method. Depending upon the inter cluster distance, cluster mean value and mean per se performance of the best genotype within the cluster, cross combinations involving different selected parents for various breeding objectives were suggested : RBM1 x RBM10 for shorter plant height, early flowering and higher number of seeds per pod, RBM10 x RBM17 for higher primary branches per plant, RBM11 x RBM17 for higher number of pods per plant and grain yield per plant, RBM31 x RBM17 for higher length of pod and seed weight.

Singh *et al.* (1998) studied genetic divergence using D^2 statistic of 100 rice bean (*Vigna umbellata*) cultivars of different eco-geographical origins revealed existence of considerable diversity. The cultivars were grouped into 15 clusters. The cluster I was the largest containing 40 cultivars followed by cluster II with 14 cultivars. Cluster III, IV and VI had nine cultivars each, whereas cluster V had only five cultivars. The diversity among the cultivars measured by inter cluster distance was adequate for improvement of rice bean by hybridization and selection. The cultivars included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregates in rice bean.

2.3 Correlation.

The yield is a complex character dependent of many attributes of plants. The correlation studies helps in understanding the association between the traits. The chief genetic cause of correlation is pleiotropy and linkage (Falconer, 1960). Because of which it becomes difficult to get the actual idea about positive or negative effect of genes.

Robinson *et al.* (1951) observed that the correlation values are of potential importance since selection is usually concerned with changing two or more traits simultaneously. Dewey and Lu (1959) used these correlation coefficients first time in plant for path analysis by following Wright (1921).

Gadekar *et al.* (1990) reported pods per plant and seeds per pod as chief contributors to seed yield per plant.

Gadekar and Dhumale (1990 b) studied 22 genotypes for path analysis during kharif, 1987 at Akola. Pods per plant and length of pod showed higher direct effects (0.45 and 0.612 respectively) on grain yield at genotypic as well as phenotypic level (0.666 and 0.232 respectively). Number of seeds per pod is a third important trait with significant correlation mainly due to its indirect effect via length of pod.

Gadekar and Dhumale (1990 a) studied 22 genotypes of *Vigna umbellata* (Thumb), Ohwi and Ohashi for grain yield, number of branches per plant and number of seed per pod. Grain yield, number of branches per plant and number of seed per pod. Grain yield, number of branches per plant and number of seeds per pod expressed considerable high PCV and GCV and seemed to be more stable characters. Number of pods per plant was having high PCV but moderate GCV; indicating more influence of environment. It had also reflected in lower heritability. Very high estimates of heritability were obtained for days to flowering (97.64 %), number of branches per plant (78.40 %) and number of seeds per pod (78.12 %). The heritability was moderate for 100 seed weight (65.19 %), length of pod (64.98%) and grain yield per plant (55.56 %).

Sharma *et al.* (1991) evaluated rice bean germplasm in upland terraces of Meghalaya. Heritability estimates were high for 100 seed weight, days to maturity and pod length. At the phenotypic level, seed yield showed highly significant positive correlations with plant height and branches and pods per plant. At the genotypic level, seed yield was also strongly correlated with these traits and in adoption with seeds per pod and days to 50 % flowering.

Baisakh (1992) studied inter-relationship between yield and it’s attributes in 12 genotypes of rice bean. Genotypic correlations were found to be higher than phenotypic correlations. The character pods per plant showed significant positive correlation with yield both at phenotypic and genotypic levels, whereas plant height and clusters per plant only at genotypic level. These characters also had significant positive association among themselves, indicating that selection for these characters may improve the grain yield simultaneously.

Singh *et al.* (1992) studied correlation coefficients derived from data on 14 yield related agronomic characters in 42 diverse genotypes of rice bean. They reported that grain yield showed significant positive correlations with number of pods per plant and number of seeds per pod. Heritability estimates were high for 100 seed weight, days to flowering, days to maturity, nodules per plant and plant height. Path coefficient analysis indicated that pods per plant, days to maturity and seeds per pod have high direct positive effects on grain yield.

Mishra *et al.* (1995) studied inter-relationships between yield and it’s components in 10 germplasm lines of rice bean. They reported that seed yield was significant positively associated only with pods per plant.

Thaware *et al.* (2000) from assessment of the genotypic and phenotypic correlation estimated from pooled data over 4 environments regarding yield and yield attributes of 60 genotypes of rice bean revealed that plant height, days to initiation of flowering, days to 50 % flowering, peduncles per plant, pods per plant and grains per plant showed consistently positive and significant correlation with grain yield in all 4 environments and on pooled basis. At phenotypic level yield did not show significant association with pods per peduncles, pod length and 100 grains weight on pooled basis. Thus, plant height, days to initiation of flowering, days to 50 % flowering, peduncles per plant, pods per plant and grains per plant are the major yield attributes and therefore deserve adequate consideration while constructing selection indices in rice bean.

Chaudhari *et al.* (2000) estimated genotypic and phenotypic correlation coefficients in rice bean. They found that genotypic correlation coefficient had higher magnitude than their corresponding phenotypic correlation indicating inherent relationship between the characters. In their studies all different traits showed positive correlation with grain yield per plant except grain protein content which showed significant negative correlation (r = - 0.32) with grain yield per plant. The character plant height (r = 0.38), number of branches per plant (r = 0.27) and pod length (r = 0.36) showed significant positive association with grain yield. However, the highest value of correlation coefficient between grain yield and pods per cluster (r = 0.75) and pods per plant (r = 0.93) indicated the close association with yield. From the observations, it was concluded that the characters, plant height, number of branches per plant, clusters per plant, pods per cluster, pods per plant and pod length were the principle yield components of rice bean. Therefore, simultaneous selection for these traits might bring an improvement in grain yield.

3. MATERIAL AND METHODS

The present investigation on "Genetic Diversity in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi)" was carried out at All India Co-ordinated Research project on underutilized crop project field, Department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri. The details of the material used, methods adopted and statistical procedure followed during the present experiment are given under following heading.

3.1 Experimental material

The fifty four genotypes of *Vigna umbellata* for the present investigation were obtained from the Plant Breeder, AICRP on Underutilized Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri. The list of genotypes used is given in Table 3.1.

3.2. Method

3.2.1Experimental design

These fifty four genotypes of rice bean, were evaluated in a Randomized Block Design (RBD) with two replications. Each genotype was represented by four row, of 3.0 meter length in each replications. The sowing on medium soil was done on 28th July, 2012. The row to row spacing was 30 cm while plant to plant spacing was 15 cm. A light irrigation was given after sowing to get good germination. The crop was fertilized with 20 kg N and 40 kg P_2O_5 and 20 kg K_2O per ha. All the standard cultural practices such as fertilizer application, interculturing, weeding etc., were followed to raise good crop.

Table 3.1 : List of rice bean genotypes

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	RRBG-11-02	19.	RRBG-11-35	37.	LRB-464
2.	RRBG-11-03	20.	RRBG-11-36	38.	LRB-465
3.	RRBG-11-04	21.	RRBG-11-37	39.	LRB-467
4.	RRBG-11-05	22.	RRBG-11-37-1-2	40.	LRB-470
5.	RRBG-11-07	23.	RRBG-11-39	41.	LRB-472
6.	RRBG-11-11	24.	RRBG-11-40	42.	LRB-477
7.	RRBG-11-13	25.	RRBG-11-40-1-3	43.	LRB-478
8.	RRBG-11-14	26.	LRB-319	44.	LRB-480
9.	RRBG-11-16	27.	LRB-325	45.	LRB-481
10.	RRBG-11-18	28.	LRB-447	46.	LRB-482
11.	RRBG-11-20	29.	LRB-448	47.	LRB-484
12.	RRBG-11-23	30.	LRB-455	48.	LRB-487
13.	RRBG-11-23-3	31.	LRB-456	49.	RBL-1 (C)
14.	RRBG-11-25	32.	LRB-457	50.	RBL-6 (C)
15.	RRBG-11-27	33.	LRB-458	51.	RBL-35 (C)
16.	RRBG-11-30	34.	LRB-459	52.	RBL-50 (C)
17.	RRBG-11-32	35.	LRB-460	53.	Chandrapur local

18.	RRBG-11-34	36.	LRB-463	54.	Bhandara local

3.2.2Observations recorded

Observations in each replication were recorded on five randomly selected plants for the following quantitative characters. The data averaged over the five plants were used for statistical analysis.

1. Days to 50 % flowering (No.)

Number of days from sowing to the date when 50 % plants in each plot flowered recorded and average number of days for fifty per cent flowering was estimated.

2. Days to maturity (No.)

The number of days required from sowing to the date of maturity was recorded, when most of the pods on the plants in a plot were dry and matured.

3. Plant height at maturity (cm)

Plant height was measured at maturity and was recorded in centimeter from ground level to the top of main shoot and average was worked out.

4. Length of Pod (cm)

The length of five randomly selected pods was measured in centimeter in each of the five observational plants and averaged.

5. Number of pods per cluster.

Total number of pods per cluster counted at maturity and averaged.

6. Number of branches per plant.

Number of branches on each of the five randomly selected plants was counted and average was worked out.

7. Seed yield per plant (g)

The seeds obtained from five observational plants were weighed, totaled and average yield per plant was calculated by dividing by number of plants.

8. 1000 seed weight (g)

The weight of 1000 seeds from randomly selected observational plant for each genotype was recorded in grams.

9. Seed yield per plot.

Seed collected from one plot of one genotype is calculated and weight was recorded.

10. Seed yield per hectare.

Grain yield per hectare was calculated by multiplying the plot yield by hectare factor.

3.3 Statistical analysis.

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

3.3.1 Analysis of variance (ANNOVA).

The average data on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomly Block Design (Panse and Sukhatme, 1985).

Sr. No.	Source of variation	Degree of freedom	Expected mean sum of square
1.	Replication	r-1	$\sigma e^2 + t\sigma^2 r$
2.	Treatment	t-1	$\sigma e^2 + r\sigma^2 t$
3.	Error	(r-1)(t-1)	$\sigma^2 e$
4.	Total	(rt-1)	

Where,

t = Number of genotypes and

r = Number of replications

The characters showing significant treatment differences were only subjected to further analysis.

3.3.2 Estimation of Mean and range

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

$$m = \frac{\sum_{i=1}^{n} x_i}{n}$$

Where,

m = Mean of character

n = Number of observations

Σ = Total of all the observations for a characters.

The lowest and highest values represent the range.

3.3.3 Estimation of components of variations

The Genotypic and phenotypic variances were calculated by using respective mean squares from analysis of variance table (Johnson *et al.* (1955) as follow

1. Environmental variance (σ^2e) = EMS
2. Genotypic variance (σ^2g) = $\frac{\text{GMS-EMS}}{r}$
3. Phenotypic variance (σ^2p) = $\sigma^2g + \sigma^2e$

Where,

GMS = Genotypic mean sum of squares.

EMS = Error mean sum of squares.

r = Number of replications.

3.3.4 Estimation of coefficients of variation

The phenotypic and genotypic coefficient of variation were computed, as the ratio of corresponding standard deviation to the mean of the character, expressed as percentage, as per the formulae given by Burton (1952).

1. Genotypic coefficient of variation **(GCV)**

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

Where,

σ^2g = Genotypic variance and

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

2. Phenotypic coefficient of variation (PCV)

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

Where,

$\sigma^2 p$ = Phenotypic variance and

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

The high, medium and low GCV and PCV estimates were classified as :

Low = 0 to 10

Moderate = 10 to 20

High = 20 and above

3.3.5 Estimation of heritability

Heritability in broad sense was calculated as per the formula given by Burton (1952) and for each character was estimated as suggested by Hanson *et al.* (1956).

$$h^2 \text{ (b.s.)} = \frac{\sigma^2 g}{\sigma^2 p} \times 100 \quad \text{or} \quad h^2 \text{ (b.s.)} = Vg/Vp \times 100$$

Where,

$\sigma^2 g$ or Vg = Genotypic variance and

$\sigma^2 p$ or Vp = Phenotypic variance

Heritability estimates were classified into the high, medium and low classes (Robinson, 1966) as below

Low = 0 to 10

Medium = 10 to 30

High = 30 and above

3.3.6 Genetic advance

Genetic advance (at 5 % selection intensity) was estimated using the formula given by Allard (1960) as below.

$$1.\ G.A. = K \times \frac{\sigma^2 g}{\sigma^2 p} \times 6p$$

or

$$G.A. = K \times h^2 \times \sigma p$$

where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

k = Selection differential (at 5 % selection intensity, (k = 2.06)

σp = Phenotypic standard deviation

The high medium and low GA as per cent of mean estimates were classified as below

Low = 0 to 10

Moderate = 10 to 20

High = 20 and above

3.4 Genetic diversity

3.4.1 Wilk's criteria

After testing the differences between the populations for the characters, a simultaneous test of significance of differences in the mean values of a number of correlated variables with regard to the pooled effect of the characters considered together, was carried out using wilk's criterion (Wilks, 1932) which was estimated using relationship that

$$\text{Wilks criteria} = \frac{l\,E\,l}{l\,E + Vl}$$

Where,

lEl = Was the determinant of the experimental error sum of squares and sum of products matrix

lE+Vl = The determinant of experimental error sum of squares and sum of products, plus the population sum of squares and product matrix.

Significance of Wilks criteria was estimated by x^2 as

$$X^2pq = \quad V = - m \log \overline{e \quad \circledR}$$

Where,

$$m = n - \frac{p + q + 1}{2}$$

$n = N_1 + \text{---------------} + Nk - 1$ = Total Number of observations – 1.

p = Number of characters

q = K-1

k = Number of genotypes

3.4.2 Mahalanobis'sgeneralized distance (D^2)

The analysis of diversity was carried out by D^2 statistic of Mahalanobis's (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D. to test the significance of differences among the genotypes as described in section 3.4.1. The character exhibiting significant differences were only used for further analysis of D^2 statistic. The Co–variance analysis for character pairs, based on plot average was carried out (Cocharan and Cox, 1957).

The generalized distance between any two populations is defined as

$$D^2 = \Sigma\lambda i.j\ .\delta i.\ \delta j$$

Where,

$\lambda i\ j$ = Reciprocal matrix to the common dispersion matrix.

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

$\delta\ j$ = Difference between the mean values of the two populations for j^{th} character.

This quantity is estimated by D^2 statistic (Mujumdar and Rao, 1958) as

$$D^2 = \Sigma\ Sij.di.dj$$

Where,

Sij, di and dj are the sample estimate of $\lambda\ i\ j$, $\delta\ i$ and $\delta\ j$. This formula for computation requires inversion of twelveth order determinant and then evaluation of 12 (12 + 1) terms whose sum is D^2

3.4.3 Computation of D^2 values

Estimation of D^2 values from the above formula is very complicated in the present study. Since, it requires the inversion of a thirteenth order determinant 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 transformed variables reduces to the evaluation of a simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977). The coefficients for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.4 Determination of population constellation

No rules can be laid down for finding the clusters because cluster is not a well defined term. The only criterion appears to be that any two groups belonging to the same cluster showed at least, on an average show a smaller D^2 value than those belonging to two different clusters. A simple device or method suggested by Tocher's (Rao, 1952) for cluster formation is to start with two closely related genotypes and find third genotype which had the smaller average D^2 from the first two. Similarly, the fourth genotypes is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further for the cluster formation, if at any stage, the average D^2 value of a genotype appears to be high than those already listed, then this genotype does not fit in that former group and it is to be taken out side of that cluster. The genotype included in first cluster, are then omitted and the rests are treated similarly to form next cluster.

3.4.5 Average intra cluster distances

The intra-cluster distances were calculated as

$$D^2 = \frac{\Sigma D^2 i}{n}$$

Where,

$\Sigma D^2 i$ = Sum of distances between all possible combinations of the genotypes included in a cluster.

n = Number of genotypes included in a cluster

3.4.6 Average inter cluster distances

The procedure followed for calculating inter cluster distances was first to measure the distance between cluster I and II, between I and III, between I and IV and so on. Likewise the clusters were taken one by one and the distances between other clusters were calculated as :

$$D^2 = \Sigma D^2 i \,/\, ni.nj$$

Where,

ni = Number of genotypes in cluster i and

nj = Number of genotypes in cluster 'j'

The intra and inter cluster distances (D values) were obtained by taking square root of average D^2 values of the respective groups.

3.4.7 Cluster diagram

With the help of D Values between the clusters, a diagram showing the relationship between different populations was drawn.

3.4.8 Correlation

Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic co-variances were then calculated as per the formulae described by Singh and Chaudhari (1977) as below.

Environmental covariance (cov $e_{1.2}$) = EMP.

Genotypic covariance (cov. $g_{1.2}$) = GMP-EMP / r

Phenotypic covariance (cov $p_{1.2}$) = (cov.$g_{1.2}$) + (cov. $e_{1.2}$).

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

The appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.* 1955).

The phenotypic correlation coefficients (rp) was calculated as :

$$rp_{1.2} = \frac{\text{Cov. } p_{1.2}}{\sqrt{(6^2 p_1 \text{ x } 6^2 p_2)}}$$

Where,

$rp_{1.2}$ = Phenotypic correlation coefficient between character 1 and 2

Cov $p_{1.2}$ = Phenotypic co-variance between character 1 and 2

The genotypic correlation coefficient (rg) was calculated as :

$$\text{Cov. } g_{1.2}$$

$$rg_{1.2} = \frac{}{\sqrt{(6^2g_1 \text{ x } 6^2g_2)}}$$

Where,

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

Cov. $g_{1.2}$ = Genotypic co-variance between character 1 and 2.

6^2g_1 and 6^2g_2 = Genotypic variance of character 1 and 2, respectively.

The significance and phenotypic and genotypic correlation coefficients was tested against 'r' values given by Fisher and Yates (1963) at (t-2) degrees of freedom at 5 per cent and 1 per cent levels of significance.

4.EXPERIMENTAL RESULTS

The results obtained in present investigation entitled "Genetic diversity in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi)" are presented below.

4.1. Analysis of variance

The analysis of variance presented in table 4.1, revealed that mean squares due to genotypes were significant indicating that the genotypes under evaluation differed significantly for all the characters under study.

4.2. Mean performance

The mean values of the 54 genotypes for 11 different characters studied are presented in table-4.2.

4.2.1. Days to 50 % flowering

The variation in days for 50 % flowering ranged between 55.50 (LRB-484) and 121.50 (RRBG-11-02) days. The overall mean for days to 50 % flowering was 88.27 days.

4.2.2 Days to maturity

The variation in days to maturity ranged between 101.50 (LRB-455, LRB-456, LRB-457, LRB-470, LRB-481 and RBL-1) and 179.00 (RRBG-11-03) days whereas the general mean was 135.23 days.

4.2.3 Plant height at maturity

Mean plant height among the genotypes studied ranged from 55.50 cm (LRB-463) to 177.00 cm (RRBG-11-37-1-2). The mean plant height was 115.83 cm.

Table No. 4.1: Analysis of variance (MSS) for 11 characters in rice bean.

Sr. No.	Characters	Mean Sum of Squares		
		Replication (r-1)= 1	Treatment (t-1) = 53	Error (r-1) (t-1)= 53
1.	Days to 50% flowering	2.67593	1811.97572	1.99668
2.	Days to maturity	12.67593	2257.63609	3.12876
3.	Plant height at maturity (cm)	12.00000	3541.56000	9.55019
4.	Pod length (cm)	0.00232	1.03948	0.011183
5.	No. of pods/cluster	0.02676	1.21498	0.01563
6.	No. of seeds/pod	0.00009	2.97936	0.04292
7.	No. of branches/plant	0.12676	1.66538	0.03506
8.	Seed yield/plant (g)	1.04037	43.37578	0.41169
9.	1000 seed weight (g)	0.45370	108.71718	0.10257
10.	Seed yield/plot (kg)	0.00180	0.25804	0.00111
11.	Seed yield/ha (q)	2.58231	197.46663	0.64647

Table. 4.2 : Mean performance of 54 genotypes of rice bean for eleven characters.

Sr. No.	Entries	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Pods/ cluster	Seeds /pod	Branch-es/plant	Seed yield /plant (g)	1000 seed weight (g)	Seed yield / plot (kg)	Seed yield / (q) ha
1	RRBG-11-02	121.5	174.0	144.8	7.4	3.64	7.81	4.4	8.9	52.45	0.71	19.67
2	RRBG-11-03	120.0	179.0	162.2	8.6	4.02	9.28	5.3	12.0	43.80	0.95	26.46
3	RRBG-11-04	120.5	177.0	162.5	7.5	4.20	8.32	4.9	13.6	43.85	1.03	28.51
4	RRBG-11-05	119.5	172.5	148.9	7.4	4.40	8.12	5.2	13.5	40.75	1.02	28.41
5	RRBG-11-07	120.0	177.0	148.2	8.8	4.36	9.61	4.8	10.5	35.90	0.84	23.25
6	RRBG-11-11	118.0	168.5	167.0	8.2	4.16	8.64	5.7	12.3	49.90	0.96	26.61
7	RRBG-11-13	118.5	172.0	159.6	8.6	4.22	9.30	4.4	11.5	52.75	0.87	24.13
8	RRBG-11-14	116.5	166.5	137.6	8.0	3.84	8.72	4.5	10.9	46.40	0.83	23.00
9	RRBG-11-16	117.5	166.5	142.8	8.5	4.74	9.94	4.5	10.9	42.10	0.80	22.31
10	RRBG-11-18	117.5	170.5	172.5	8.9	3.72	9.62	4.4	10.1	44.25	0.84	23.24
11	RRBG-11-20	117.0	167.0	169.8	7.2	3.46	8.78	5.0	11.0	46.10	0.83	23.16
12	RRBG-11-23	117.0	163.5	168.7	8.3	4.36	8.88	4.6	14.2	38.10	1.14	31.68
13	RRBG-11-23-3	116.0	161.0	174.9	9.7	3.58	9.84	4.2	14.2	38.85	1.08	30.05
14	RRBG-11-25	116.5	162.0	159.5	8.4	4.58	9.16	5.6	10.9	48.20	0.86	23.77
15	RRBG-11-27	116.5	170.5	148.7	7.9	4.26	8.66	5.1	12.1	48.65	0.96	26.80
16	RRBG-11-30	117.5	171.0	154.8	7.7	4.12	8.40	4.6	12.6	42.60	0.90	25.04
17	RRBG-11-32	118.5	162.5	132.7	7.5	3.75	8.24	4.8	7.3	44.75	0.58	16.22
18	RRBG-11-34	117.5	162.0	144.7	9.0	3.50	9.98	5.9	7.3	50.50	0.58	16.06
19	RRBG-11-35	115.0	162.0	148.0	9.0	4.66	9.70	4.2	11.7	49.45	0.95	26.33
20	RRBG-11-36	115.5	164.0	141.5	8.8	4.42	10.02	4.2	14.2	46.05	1.11	30.91

Table. 4.2 continued…

Sr. No.	Entries	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Pods/ cluster	Seeds /pod	Branch-es/plant	Seed yield /plant (g)	1000 seed weight (g)	Seed yield / plot (kg)	Seed yield / (q) ha
21	RRBG-11-37	117.0	165.0	150.4	8.9	3.66	8.96	5.4	16.2	43.70	1.28	35.56
22	RRBG-11-37-1-2	119.5	172.0	177.0	8.5	3.96	9.30	5.0	9.6	44.60	0.77	21.45
23	RRBG-11-39	118.5	162.0	158.8	6.7	3.50	9.42	5.1	8.5	49.10	0.67	18.68
24	RRBG-11-40	118.5	173.0	166.7	7.8	3.86	8.50	5.1	8.0	43.25	0.69	19.27
25	RRBG-11-40-1-3	120.0	170.5	175.0	8.2	3.88	8.80	5.2	13.9	48.55	1.06	29.53
26	LRB-319	61.5	102.5	73.5	6.8	2.28	7.06	3.7	2.3	54.75	0.19	5.20
27	LRB-325	61.5	102.0	96.2	6.9	2.28	6.60	3.1	2.2	50.50	0.17	4.59
28	LRB-447	59.5	102.0	101.9	7.0	2.16	6.10	3.7	2.2	54.75	0.17	4.80
29	LRB-448	56.5	102.5	60.2	6.9	2.48	6.16	3.6	3.4	45.50	0.27	7.58
30	LRB-455	56.5	101.5	85.0	6.9	2.52	6.26	2.9	1.9	45.10	0.15	4.15
31	LRB-456	58.0	101.5	73.7	7.7	2.84	7.22	3.4	4.5	54.90	0.36	9.88
32	LRB-457	65.5	101.5	79.1	8.0	2.96	7.25	3.9	2.5	45.00	0.20	5.61
33	LRB-458	59.5	102.0	84.2	7.5	2.68	6.93	3.8	2.1	60.25	0.18	4.90
34	LRB-459	56.0	102.0	92.8	9.3	3.47	8.19	3.3	3.1	55.25	0.25	7.02
35	LRB-460	56.0	102.5	92.2	7.6	3.05	7.00	3.9	2.6	65.20	0.21	5.88
36	LRB-463	59.5	102.5	55.5	6.8	3.16	6.08	4.6	3.0	40.00	0.24	6.54
37	LRB-464	60.5	102.0	57.5	7.4	2.67	6.68	3.1	1.8	55.00	0.16	4.38
38	LRB-465	58.0	102.0	73.2	7.6	3.01	6.88	3.2	2.8	50.00	0.22	6.24
39	LRB-467	62.0	102.5	63.7	8.2	2.88	7.28	3.7	3.0	70.00	0.26	7.26
40	LRB-470	57.0	101.5	73.3	7.6	2.74	6.92	3.4	3.6	65.00	0.29	8.10

Table. 4.2 continued...

Sr. No.	Entries	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Pods/ cluster	Seeds /pod	Branch-es/plant	Seed yield /plant (g)	1000 seed weight (g)	Seed yield / plot (kg)	Seed yield / (q) ha
41	LRB-472	57.5	102.5	80.1	7.4	2.67	6.50	3.9	2.0	64.75	0.17	4.71
42	LRB-477	62.5	102.0	82.4	7.5	2.96	7.61	5.1	4.3	54.85	0.34	9.57
43	LRB-478	59.5	102.5	85.1	7.5	2.99	6.66	3.8	2.3	54.60	0.19	5.27
44	LRB-480	58.5	103.0	67.1	7.2	2.63	6.60	3.9	2.3	45.00	0.19	5.29
45	LRB-481	56.5	101.5	76.8	6.8	2.50	6.66	2.1	3.7	60.00	0.29	8.04
46	LRB-482	57.5	102.0	64.8	7.7	2.63	7.54	4.6	4.1	59.75	0.30	8.37
47	LRB-484	55.5	103.0	66.2	6.8	2.44	6.30	3.3	1.8	54.75	0.15	4.29
48	LRB-487	58.5	102.0	65.2	7.5	2.42	6.90	2.7	1.7	50.00	0.14	3.83
49	RBL-1 (C)	56.0	101.5	89.4	7.7	2.48	6.73	4.2	3.7	54.90	0.30	8.27
50	RBL-6 (C)	57.5	102.5	70.4	8.3	2.52	7.48	2.9	2.2	55.50	0.18	4.94
51	RBL-35 (C)	56.5	102.0	66.9	7.6	2.72	7.46	2.7	4.0	55.00	0.33	9.04
52	RBL-50 (C)	56.5	103.0	75.7	8.0	2.66	7.52	2.2	2.8	45.15	0.23	6.39
53	Bhandara local	119.0	169.5	135.6	7.5	3.90	8.34	5.1	7.3	48.20	0.57	15.79
54	Chandrapur local	117.5	163.5	150.0	8.7	5.12	9.34	4.4	13.0	44.15	0.99	27.38
	Mean	88.27	135.2	115.8	7.85	3.38	7.97	4.2	7.08	49.86	0.56	15.43
	S.E.±	0.999	1.25	2.185	0.075	0.088	0.146	0.132	0.454	0.226	0.023	0.568
	C.D. at 5%	2.834	3.547	6.198	0.212	0.25	0.415	0.375	1.287	0.642	0.067	1.612

4.2.4 Length of pod

Mean length of pod among the genotypes studied ranged between 6.70 cm (RRBG-11-39) and 9.7 cm (RRBG-23-03) while the overall pod length was 7.85 cm.

4.2.5 Number of pods per cluster

The range of mean number of pods per cluster was between 2.16 (LRB-447) and 5.12 (Chandrapur local) while the grand mean number of pods per cluster was 3.38.

4.2.6 Number of seeds per pod

Highest value of seeds per pod was 10.02 (RRBG-11-36) and lowest value was 6.10 (LRB-447) while, average was 7.97.

4.2.7 Number of branches per plant

Mean number of primary branches per plant among the genotypes studied ranged from 2.10 (LRB-481) to 5.95 (RRBG-11-34). The mean number of branches per plant was 4.2.

4.2.8 Seed yield per plant

The mean seed yield per plant among the genotypes studied ranged between 1.73g (LRB-487) and 16.24 g (RRBG-11-37). The overall mean seed yield per plant was 7.08 grams.

4.2.9 1000 seed weight

The mean of 1000 seed weight among the genotypes studied, ranged from 35.90 g (RRBG-11-07) to 70.00 g (LRB-467). The overall mean for 1000 seed weight was 49.83 grams.

4.2.10 Seed yield per plot

The mean of seed yield per plot was 0.56 kg per plot. Minimum value of yield was 0.14 kg per plot (LRB-487) and the highest value was 1.28 kg per plot (RRBG-11-37).

4.2.11 Seed yield per hectare

Mean yield of seed per hectare was 15.43 quintals and range was 3.83 q. (LRB-487) to 35.56 quintal (RRBG-11-37).

4.3 Parameters of Genetic variability

The ranges of each character are given in Table-4.3.

4.3.1 Estimates of components of variation

The estimates of genotypic, phenotypic and environmental variances for different characters studied are presented in table 4.3. The magnitude of genotypic variance was highest for plant height at maturity (1766) followed by days to maturity (1127.25) and days to 50% flowering (904.99). Phenotypic variances however, ranged between 0.13 (seed yield per plot) and 1775.56 (plant height at maturity).

The estimates of environmental variance were of higher magnitude for the traits *viz.*, plant height at maturity (9.55), followed days to maturity (3.129) while low estimates were observed for seed yield per plot (0.001) followed by and pod length (0.11).

Table 4.3 Component of genetic variation in genotype.

Sr. No.	Character	Range	(6^{2}g)	(6^{2}e)	(6^{2}p)	Heritability (b.s.) (%)	GCV %	PCV %	GA	G.A. as % of mean
1.	Days to 50% flowering	55.50-121.50	905	1.997	907.00	99.78	34.08	34.12	61.9	70.13
2.	Days to maturity	101.50-179.00	1127	3.129	1130.13	99.72	24.83	24.86	69.07	51.07
3.	Plant height at maturity (cm)	55.50 - 177 .00	1766	9.550	1775.55	99.46	36.28	36.38	86.34	74.53
4.	Length of pod (cm)	6.70-9.66	0.51	0.011	0.52	97.91	9.14	9.24	1.46	18.62
5.	pods / cluster	2.16-5.12	0.60	0.016	0.61	97.56	22.91	23.20	1.58	46.58
6.	seeds / pod	6.08-10.02	1.47	0.043	1.51	97.15	15.20	15.42	2.46	30.86
7.	No. of branches / plant	2.10-5.95	0.81	0.040	0.85	95.88	21.50	21.96	1.82	43.37
8.	Seed yield / plant (g)	1.73-16.24	21.48	0.410	21.89	98.12	65.42	66.04	9.46	133.49
9.	1000 seed weight (g)	35.90-70.00	54.31	0.100	54.41	99.81	14.78	14.79	15.17	30.42
10.	Seed yield / plot (kg)	0.14-1.28	0.19	0.000	0.13	98.46	64.32	64.60	0.74	131.94
11.	Seed yield / ha. (q)	3.83-35.56	98.41	0.650	99.05	99.35	64.28	64.49	20.37	131.99

4.3.2 Genotypic and phenotypic coefficients of variation (GCV & PCV)

The estimates of genotypic and phenotypic coefficients of variation are presented in table 4.3. The highest genotypic co-efficient of variation was exhibited by the characters seed yield per plant (65.42) followed by seed yield per plot (64.32) while remaining characters exhibited low estimates of genotypic co-efficient of variation. Pod length showed lowest value (9.14).

The high estimate of phenotypic coefficients of variation was observed in the case of seed yield per plant (66.04) followed by seed yield per plot (64.60), while low estimates exhibited by traits namely pod length (9.24) and moderate value for 1000 seed weight which was 14.79.

4.3.3 Heritability

The estimates of heritability in broad sense are presented in table 4.3. The high estimates of heritability in broad sense was exhibited by 1000 seed weight (99.81 %) followed by days to 50% flowering (99.78).

All character had shown very high heritability.

4.3.4 Genetic advance

Plant height at maturity showed highest genetic advance over all other character (86.34) while the character seed yield showed minimum value (0.74). Genetic advance as per cent of mean showed moderate value for length of pod. Remaining all characters showed high genetic advance as per cent of mean.

4.4 Correlations

Table 4.4 represents the correlation coefficients between the characters at both genotypic as well as phenotypic levels.

The significant associations between any two traits or yield components are described below.

4.4.1 Association between seed yield per plant and its Components

With the yield component, all components showed significant and positive correlation with yield per plant except 1000 seed weight (-0.5953) which was significant but negatively correlated.

While in phenotypic correlation, here also all character showed significant positive correlation with grain yield per plant except 1000 seed weight (-0.5896) which was significant but negatively correlated.

Highest genotypic correlation value recorded for correlation of days to maturity (0.9213) followed by days to 50% flowering (0.9211), plant height at maturity (0.9077), pods per cluster (0.8841), seeds per pod (0.8550), branches per plant (0.7006), and length of pod (0.5803) which was least correlated.

Highest phenotypic correlation value recorded for correlation of days to 50% flowering (0.9126) followed by days to maturity (0.9124), plant height at maturity (0.8967), pods per cluster (0.8655), seeds per pod (0.8305), branches per plant (0.6865), and length of pod (0.5665) which was least correlated.

Table 4.4 : Genotypic (Above diagonal) and phenotypic (below diagonal) correlation of 11 character.

Characters	Branches/plant	Seeds/ pod	Pods per cluster	Length of pod (cm)	Plant height at maturity	Days to 50% flowering	Days to maturity	1000 seed weight	Seed Yield / plant (g)	Seed yield / plot (kg)	Seed yield / ha. (q)
Branches per plant	1.0000	0.6490**	0.6901**	0.3351*	0.7484**	0.7799**	0.7671**	-0.4041**	0.7006**	0.7063**	0.7052**
Seeds/ pod	0.6154**	1.0000	0.8464**	0.7691**	0.8604**	0.8774**	0.8631**	-0.5024**	0.8550**	0.8609**	0.8567**
Pods per cluster	0.6705**	0.8270**	1.0000	0.6011**	0.8325**	0.8874**	0.8867**	-0.5600**	0.8841**	0.8883**	0.8823**
Length of pod (cm)	0.3203*	0.7613**	0.5928**	1.0000	0.5272**	0.4988**	0.4930**	-0.2839*	0.5803**	0.5907**	0.5893**
Plant height at maturity	0.7269**	0.8481**	0.8214**	0.5209**	1.0000	0.9558**	0.9552**	-0.5684**	0.9077**	0.9094**	0.9096**
Days to 50% flowering	0.7632**	0.8639**	0.8768**	0.4939**	0.9523**	1.0000	0.9959**	-0.6080**	0.9211**	0.9240**	0.9224**
Days to maturity	0.7489**	0.8495**	0.8738**	0.4879**	0.9510**	0.9933**	1.0000	-0.6078**	0.9213**	0.9241**	0.9225**
1000 seed weight	-0.3950**	-0.4949**	-0.5504**	-0.2798*	-0.5668**	-0.6060**	-0.6064**	1.0000	-0.5953**	-0.5957**	-0.5928**
Seed Yield per plant (g)	0.6865**	0.8305**	0.8655**	0.5665**	0.8967**	0.9126**	0.9124**	-0.5896	1.0000	0.9999**	0.9999**
Seed yield per plot (kg)	0.6879**	0.8444**	0.8734**	0.5809**	0.9036**	0.9195**	0.9191**	-0.5935**	0.9957**	1.0000	0.9999**
Seed yield per ha. (q)	0.6904**	0.8401**	0.8691**	0.5794**	0.9042**	0.9188**	0.9186**	-0.5907**	0.9964**	0.9989**	1.0000

* and ** means significance level at 5% and 1% respectively.

4.4.2 Association between remaining 8 yield contributing character

The inter relationship between component characters at genotypic and phenotypic levels are presented below.

Days to 50% flowering showed significant positive correlation with all characters except with 1000 seed weight (-0.6080) which was significantly negatively correlated at genotypic level. Correlation between yield per plant, yield per plot and yield per hectare were nearly one within themselves at genotypic level.

Days to 50% flowering showed higher value than any other genetic correlation with days to maturity (0.9959) and followed by plant height (0.9552), pods per cluster (0.8874), seeds per pod (0.8774), branches per plant (0.7799), and length of pod (0.4988). Same in phenotypic level showed highly significant correlation with all character but 1000 seed weight (-0.6060) was also highly significant but negatively correlated.

Days to maturity showed significant positive correlation at genotypic as well as phenotypic level except for 1000 seed weight which was significantly negatively correlated. Other all characters were highly significant and positively correlated. Highest value was for day to 50 per cent flowering (0.9959) and least value was for length of pod (0.4933) at genotypic level.

Plant height at maturity showed positive correlation with all characters except 1000 seed weight at genotypic as well as phenotypic levels. Which was highest correlated with days to 50% flowering (0.9558) and least value was recorded for length of pod (0.5272). Plant height at maturity showed significantly negatively correlated with 1000 seed weight (-0.5684).

Length of pod, pods per cluster and branches per plant all three characters were showed positive significant correlation with each other. Here was also negative correlation with 1000 seed weight.

1000 seed weight was significantly but negatively correlated with all characters at genotypic as well as phenotypic level.

4.5 Divergence

4.5.1 Clustering pattern of the strain

The clustering pattern obtained on the basis of magnitude of D^2 values studied was presented in table-4.5a. Fifty four rice bean genotypes were grouped into ten clusters. Cluster IV consisted maximum number of genotypes i.e. 22 followed by cluster I (11 genotypes), cluster II (7genotypes), cluster III (6 genotypes) and cluster VIII (3 genotypes). Cluster V, VI, VII, IX and X were contained only one genotype.

4.5.2 Intra and inter-cluster distance

The intra and inter cluster D^2 and D value were worked out by D^2 statistics. The D^2 value of cluster elements was used as measures of intra and inters cluster distance. They are presented in table 4.5 b.

Maximum intra cluster distance was observed in cluster IV (D=16.74) followed by cluster VIII, III, II, and I having intra cluster distance 15.76, 12.93, 11.21 and 10.87 respectively. While the cluster V, VI, VII, IX and X had no intra cluster distance.

Table 4.5 a : Distribution of 54 genotypes into different clusters.

Cluster Number	No. of genotype included	Genotypes
I	11	LRB-448 (29), RBL-1(49), LRB-487(48), LRB-460 (35), LRB-472(41), LRB-481(45), Chandrapur local (54), LRB-484 (47), LRB-319 (26), LRB-470 (40), Bhandara Local (53)
II	7	LRB-325 (27), LRB-477 (42), LRB-447(28), LRB-455 (30), RBL-6 (50), LRB-463 (36), LRB-482 (46)
III	6	LRB-458 (33), LRB-467 (39), LRB-465(38), LRB-456 (31), LRB-480 (44), LRB-478 (43)
IV	22	RRBG-11-18 (10), RRBG-11-37-1-2 (22), RRBG-11-03 (2), RRBG-11-40 (24), RRBG-11-04 (3), RRBG-11-30 (16), RRBG-11-14 (8), RRBG-11-20(11), RRBG-11-25 (14), RRBG-11-27 (15), RBL-50 (52),RRBG-11-36(20), RRBG-11-32 (17), RBL-35 (51), RRBG-11-16 (9), RRBG-11-05 (4), RRBG-11-40-1-3 (25), RRBG-11-35 (19), RRBG-11-11 (6), RRBG-11-37 (21), RRBG-11-34 (18), RRBG-11-39 (23).
V	1	RRBG-11-13 (7)
VI	1	LRB-457 (32)
VII	1	RRBG-11-02 (1)
VIII	3	RRBG-11-23 (12), RRBG-11-23-3 (13), RRBG-11-07 (5)
IX	1	LRB-464 (37)
X	1	LRB-459 (34)

*No. in the bracket denotes the serial number of genotypes.

In inter cluster distances, highest distance was in between cluster VIII and cluster IX (D=103.71) followed by cluster VIII and cluster III (D=89.7), cluster IV and IX (D=86.28) and IX and X (D=79.31).

Cluster I had the largest distance from cluster VIII (D=73.93), followed by cluster IV (D=61.1). Least distance was for cluster VI (D=15.93).

Cluster II had longest distance from cluster VIII (D=63.39) followed by cluster IX (D=61.46), and closest from cluster X (D= 21.03) and cluster I (24.18).

Cluster III had longest from cluster VIII (D=89.70) followed by cluster IV (D=73.68) while nearest was cluster IX (20.75).

Cluster IV was closest to cluster V and it was followed by cluster VII (21.78). While longest was cluster IX (86.28) and cluster VI (63.26).

Cluster V found maximum distance from cluster IX (D=72.79) followed by cluster III (62.70) and cluster X (62.67). Nearest was cluster VII (11.19).

Cluster VI recorded maximum distance from cluster VIII (74.92). Least distance was measured with cluster I (15.93).

Cluster VII most distantly away from cluster IX (74.50) while most likely attached cluster was cluster V (11.19).

Cluster VIII showed highest distance from cluster IX (103.71) followed by cluster III (89.70), cluster VI (74.92) and cluster I (73.93). Nearest was cluster IV (26.95).

Cluster IX was longest from VIII cluster (103.71) followed by IV cluster (86.28). Nearest cluster found was cluster III (20.75).

Table 4.5 b : Average intra and inter-cluster D^2 and D values in 10 cluster of 54 genotype of Rice bean

Cluster Distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	10.87 (118.15)	24.18 (584.67)	23.98 (575.04)	61.10 (3733.21)	54.64 (2985.53)	15.93 (253.76)	54.85 (3008.52)	73.93 (5465.64)	40.30 (1624.09)	41.14 (1692.50)
Cluster II		11.21 (125.66)	44.38 (1969.58)	56.47 (3188.86)	56.56 (3199.04)	28.11 (790.17)	55.91 (3125.92)	63.39 (4018.19)	61.46 (3777.33)	21.03 (442.26)
Cluster III			12.93 (167.18)	73.68 (5428.74)	62.70 (3931.29)	25.18 (634.03)	63.66 (4052.59)	89.70 (8046.09)	20.75 (430.56)	61.91 (3832.85)
Cluster IV				16.74 (280.22)	21.46 (460.53)	63.26 (4001.82)	21.78 (474.36)	26.95 (726.30)	86.28 (7444.23)	56.92 (3239.89)
Cluster V					0 (0.0)	55.92 (3127.04)	11.19 (125.21)	40.29 (1623.28)	72.79 (5298.38)	62.67 (3927.53)
Cluster VI						0 (0.0)	58.59 (3432.78)	74.92 (5613.01)	39.08 (1527.25)	45.42 (2062.98)
Cluster VII							0 (0.0)	41.40 (1713.96)	74.50 (5550.25)	60.89 (3707.59)
Cluster VIII								15.76 (248.38)	103.71 (10755.76)	58.33 (3402.39)
Cluster IX									0 (0.0)	79.31 (6290.08)
Cluster X										0 (0.0)

** Figures in brackets denote the D^2 values.

Cluster X was highest distance from cluster IX (79.31), while it was least distance for cluster II which was 21.03.

4.6 Cluster mean performance

Cluster mean performances for 11 characters studied are given in table 4.6. It revealed that a wide range of variability for most of the characters. The variability range is described in detailed as below.

4.6.1 Days to 50 per cent flowering (nos.)

Cluster VI showed earliest flowering (56) followed by cluster III (57.33) while cluster VII (121.5) was required maximum days to 50% flowering followed by cluster V (118.5).

4.6.2 Days to maturity

Cluster VII and cluster V, took maximum days to maturity i.e., 174 and 172 respectively. While earliest maturity was recorded by cluster VI and cluster III (102 days each) followed by close value for cluster I (102.14) and cluster II (102.21). Also nearly same value (102.50) was shown by cluster IX and cluster X.

4.6.3 Plant height at maturity

Taller plant was found in cluster VIII (163.93 cm) and V (159.6 cm each). Cluster IV also shown maximum height (154.85 cm). While dwarf plant was in cluster X (55.5 cm).

4.6.4 Length of pod

Cluster VI showed maximum length of pod (9.25 cm) followed by cluster VIII (8.95 cm), cluster V (8.55 cm) and cluster IX (8.15 cm). While cluster X yield minimum length (6.85 cm) among all the clusters.

4.6.5 Pods per cluster

Cluster V shown maximum pods per cluster (4.2) followed by cluster IV and cluster VIII (4.08 each). Cluster I (2.57) and cluster II (2.67) had shown minimum pods per cluster.

4.6.6 Seeds per pod

Maximum number of seeds recorded in cluster VIII and cluster V (9.55 and 9.30 respectively) followed by cluster IV (9.01). Minimum number of seeds per pod was found in cluster X (6.05), cluster II (6.80), cluster I (6.90) and cluster III (6.93).

4.6.7 Branches per plant

Genotype of higher magnitude for branches per plant were grouped in cluster IV (4.98) followed by cluster X (4.60). Minimum branches per plant were grouped in cluster II (3.21) and cluster VI (3.30).

4.6.8 Seed yield per plant

While considering the seed yield per plant, cluster VIII showed highest value (12.98 g) followed by cluster V (11.50 g). Low value for this character was observed in cluster II (2.49 g) followed by cluster I (2.86).

4.6.9 1000 seed weight

1000 seed weight recorded maximum weight in cluster IX (70.00 g) followed by cluster III (62.49 g). Lowest limit for this character was found in cluster VIII (37.62 g).

Table 4.6 : Mean performance of clusters for 11 characters

Cluster Means	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Pods per cluster	Seeds per pod	Branches per plant	Seed yield per plant (g)	1000 seed weight (g)	Seed yield / plot (kg)	Seed yield /ha. (q)
Cluster I	58.95	102.14	78.47	7.37	2.57	6.90	3.55	2.86	54.50	0.23	6.39
Cluster Ii	58.57	102.21	72.21	7.44	2.67	6.80	3.21	2.49	46.54	0.20	5.59
Cluster III	57.33	102.00	78.57	7.43	2.72	6.93	3.63	3.03	62.49	0.24	6.67
Cluster IV	117.89	168.05	154.85	8.13	4.08	9.01	4.98	11.23	45.86	0.88	24.29
Cluster V	118.50	172.00	159.60	8.55	4.20	9.30	4.40	11.50	52.75	0.87	24.15
Cluster VI	56.00	102.00	92.80	9.25	3.45	8.20	3.30	3.10	55.25	0.25	7.05
Cluster VII	121.50	174.00	144.80	7.35	3.65	7.80	4.40	8.95	52.45	0.71	19.65
Cluster VIII	117.67	167.17	163.93	8.95	4.08	9.55	4.53	12.98	37.62	1.02	28.32
Cluster IX	62.00	102.50	63.70	8.15	2.90	7.25	3.70	3.05	70.00	0.26	7.25
Cluster X	59.50	102.50	55.50	6.85	3.15	6.05	4.60	3.00	40.00	0.24	6.50

4.6.10 Grain yield per plot

Cluster VIII was only cluster showing grain yield per plot (1.02 kg) more than 1 kg per plot followed by cluster IV (0.88 kg). Very less yield were obtained from cluster II, cluster I, cluster X, cluster III, cluster VI and cluster IX having yield 0.20 kg, 0.23 kg, 0.24 kg, 0.24 kg, 0.25 kg, and 0.26 kg per plot respectively.

4.6.11 Grain yield per hectare

Range of variation for this character was very high. Maximum yield (28.32 q) was obtained from cluster VIII followed by cluster IV (24.29 q) and cluster V (24.15 q). Minimum yield were obtained from cluster II (5.59 q).

4.7 Per cent contribution of characters in divergence.

Total 54 genotypes of rice bean were studied for 11 characters for genetic divergence. Characters were showed a very wide range of contribution for genetic diversity, as enlisted in table 4.7

Out of these, 1000 seed weight (55.35%) contributed highest for genetic divergence. It was followed by days to maturity (27.67%), length of pod (5.24%), plant height at maturity (3.77%) and days to 50 per cent flowering (3.00).

While other character contributed very less in genetic diversity *viz.*, seed yield per plant (1.26%), seed yield per ha. (1.19).

Seeds per pods (0.49%) contributed least in genetic diversity followed by pods per cluster and seed yield per pod (0.56% each).

Table 4.7 : Per cent contribution of 11 characters for divergence in Rice bean.

Sr. No.	**Source**	**Contribution %**
1.	Days to 50% flowering	3.00%
2.	Days to maturity	27.67%
3.	Plant height (cm)	3.77%
4.	Length of pod (cm)	5.24%
5.	Pods/ cluster	0.56%
6.	Seeds/pod	0.49%
7.	Branches/plant	0.91%
8.	Seed yield /plant (g)	1.26%
9.	1000 seed weight	55.35%
10.	Seed yield /plot (kg)	0.56%
11.	Seed yield /ha (quintals)	1.19%
	Total	100.00 %

5. DISCUSSION

Plant breeding deals with the management of genetic variability. Variability and genetic diversity are the basic factors required for the success of any breeding programme and selection of elite genotype. Assessment of genetic divergence is done to identify diverse parents that can be used in breeding programme. Many statistical methods are available to assess the available variability. Genotypic and phenotypic coefficient of variation allows to evaluate the extent of variability present in the material under study, where as heritability suggest the relative role of genetic factors in expression of phenotypes (Falconer, 1960). It also acts as an index of inheritance of particular character to its offspring. However, knowledge of heritability alone does not help in selecting genotype for breeding programme. Heritability along with genetic advance will help to fix the possible genetic control for any particular character. All the variability parameters help to select the breeding method, whereas the D^2 statistics suggested by Mahalanobis (1936) and clustering (Rao, 1952) guides to select the genetically divers genotype for hybridization programme.

In the present investigation, entitled “Genetic diversity in rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi)” attempts were made to study the variability for 11 different morphological characters among the 54 genotypes the correlation between the different variables on seed yield and genetic diversity among all genotypes.

The results on various aspects are discussed in this chapter, under the following subheadings.

1. Variability, GCV and PCV.
2. Heritability and genetic advance.
3. Correlation.
4. Genetic divergence.

5.1 Variability, Genotypic coefficient of variation and Phe notypic coefficient of variation.

Considerable amount of variability was observed in respect of days to 50% flowering ranged (55.50 to 121.50 days), days to maturity (101.50 to 179.00 days), Plant height at maturity (55.50 to 177.00 cm), pod length (6.70 to 9.66 cm), number of pods per cluster (2.16 to 5.12 cm), number of seeds per pod (6.08 to 10.02), number of branches per plant (2.10 to 5.95), seed yield per plant (1.73 to 16.24 g), 1000 seed weight (35.90 to 70.00 g) seed yield per plot (0.14 to 1.28 kg) and Seed yield per hectare (3.83 to 35.56 q/ha). This indicated an ample scope for exploration of above traits as high amount of variation was observed. Chaudhari (1997) reported wide range of variation for most of the yield component except for pod length, branches per plant, 100 seed weight.

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), it was observed that PCV estimate were slightly higher than GCV for all characters indicating the small influence of environment on these traits.

Very high GCV and PCV were found for seed yield per plant (65.42 GCV and 66.04 PCV), seed yield per plot (64.32

GCV and 64.60 PCV) and seed yield per hectare (64.28 GCV and 64.49 PCV). Which was higher than R.K. Gill, Singh and Brar (2008) they found medium range of GCV for this character, while Gadekar and Dhumale found higher range.

Days to 50% flowering (34.08 GCV and 34.12 PCV), days to maturity (24.83 GCV and 24.86 PCV), plant height at maturity (36.28 GCV and 36.38 PCV) , number of branches per plant (21.50 GCV and 21.96 PCV), number of pods per cluster (22.91 GCV and 23.20 PCV) showed high value of GCV and PCV while, number of seeds per pod (15.20 GCV and 15.42 PCV) and 1000 seed weight (14.78 GCV and 14.79 PCV) have medium GCV and PCV and low value was found for length of pod (9.14 GCV and 9.24 PCV).

These results are in conformation with Gill *et al.* (2008) showed low value of GCV and PCV for days to 50% flowering, days to maturity, plant height at maturity, number of branches per plant, seeds per pod, pod length and 100 seed weight. Gadekar and Dhumale showed GCV and PCV high for branches per plant, number of seeds per pod, medium for days to 50 per cent flowering, length of pod, while medium GCV and high PCV for plant height and 100 seed weight. High influence of environment was recorded by them. Jadhav *et al.* (1996) reported high GCV and PCV for plant height, branches per plant, pods per cluster, seeds per pod, grain yield per plant. Chaudhari *et al.* (1997) reported moderate estimates of GCV for grain yield per plant and high PCV for it.

In some characters like number of pods per cluster, seed yield per plant, showed the large difference in GCV and PCV which indicate that these characters are highly influenced by environmental factors in their expression while in case other characters the estimate of GCV and PCV were nearly equal indicating that the variability existing in these character was due to genetic factors and had less influence of environmental factors in their expression.

5.2 Heritability and Genetic advance.

Heritability decides the resemblance of progeny with their parents (Falconer, 1960) while genetic advance provides the knowledge about expected gain for a particular characters after selection. The heritability estimates is better indicator of heritable portion of variation (Burton and Dewane, 1953). In general, in self-pollinated crops, characters with high heritability possess high genetic advance, but when phenotypic variation in population is low, genetic advance also tends to low and vice-versa. This showed that variation and heritability are very much important for any breeding programme.

When heritability is moderate to high with larger magnitude of expected genetic advance for a particular character, it is said to be governed by additive gene action but if the results are opposite and either of the condition like high heritability with low genetic advance or low heritability with low genetic advance is observed for any given character, then presence of non-additive gene action may be suspected.

In the present investigation, all the characters expressed high estimates of heritability in broad sense indicating the scope for selection of these traits.

Das and Dana (1985) reported low heritability for plant height and number of branches per plant and high for days to flower and pods per plant. While, Gadekar and Dhumale (1990) observed high estimates of heritability and genetic advance for branches per plant grains per pod and seeds per pod. Jadhav *et al.* (1996) observed high heritability for grain yield per plant. Chaudhari *et al.* (1997) observed high heritability for grain yield per plant and plant height.

Genetic advance for length of pod, number of pods per cluster, number of seeds per pod, number of branches per plant, seed yield per plant and seed yield per plot were low but when expressed as percentage means it was fairly high. In case of these characters showed high heritability coupled with low genetic advance. The plant height at maturity showed highest genetic advance where as seed yield per plot had lowest genetic advance.

Johnson *et al.* (1955) reported that heritability estimates along with genetic advance will be more useful than heritability alone in predicting the resultant effect for selecting the best individuals.

Thus considering the estimates of genetic parameters like GCV, heritability and genetic advance together, it is evident that days to 50% flowering, days to maturity, plant height at maturity, number of pods per cluster, 1000 seed weight and seed yield per hectare are the important characters selection for these traits could be more effective for improvement in rice bean.

5.3 Correlation

The information about inter relationship between the yield and yield component facilitates the choice of suitable breeding method to be applied and selecting the parents for improving the crop. The phenotypic and genotypic correlation has their own importance in breeding programme. The phenotypic correlation coefficient helps in determining selection index, where as genotypic correlation coefficient provides a close measure of association between characters and gives an indication of characters, which may be useful for overall improvement of crop. They may also help to identify characters that have little or no importance in selection programme.

In the present investigation, it was observed that the genotypic correlation coefficient were higher in magnitude than their corresponding phenotypic correlation coefficient for all the character. Seed yield per plant showed positive correlation with days to maturity, days to 50% flowering, plant height at maturity, number of pods per cluster, number of seeds per pod, number of branches per plant and length of pod. While negative but significant correlation with 1000 seed weight. All genotypic and phenotypic correlation with each other found highly significant except 1000 seed weight showed negative but significant correlation with all character.

Saste S.V. (2004) revealed that seed yield had significant positive correlation with number of pods per plant, number of branches per plant, pod length, number of clusters per plant, 100 seed weight, number of pods per cluster, number of seeds per plant. Days to 50% flowering and days to maturity shows negative but significant correlation. Solanke A.U. (2001) recorded seed yield per plant exhibited positive significant correlation with plant height, number of branches per plant, number of clusters per plant and number of pods per plant at both genotypic and phenotypic correlation. Chaudhari (2000) reported that plant height, number of branches per plant and pod length showed significant positive association with grain yield while grain protein content showed significant negative correlation. Gadekar *et al.* (1990) reported that grain yield per plant was positively and significantly correlated with plant height, grains per pod, pods per plant, length of pod, cluster per plant and pods per cluster.

The yield components *viz.*, number of branches per plant, number of pods per plant, pod length and 100 seed weight were found to be significant positively inter correlated among themselves, indicating that simultaneous election for these traits might bring an improvement in seed yield. The importance of this association was also stressed by Gadekar *et al.* (1990) and Baisakh (1992).

5.4 Genetic Divergence

Selection of elite genotypes with high performance for yield and yield contributing component with suitable genetic divergence among them is the most important and difficult job for starting any hybridization programme. It would be possible to identify desirable genotypes from the genetic variability estimated, but it is difficult to expect any extra ordinary results from their progeny unless we have knowledge about divergence between them.

Mahalanobis (1936) developed the concept of D^2 statistics, which act as important tool for plant breeders. The degree of divergence between biological population at genotypic level and relative contribution of different components to the total divergence at both intra and inter cluster levels can be evaluated by this method. Rao (1952) first time suggested the application of this technique for the assessment of genetic diversity in plant breeding.

5.4.1 Clusters formation, Intra and inter-cluster distance and mean performance

The basic concept behind the formation of clusters is to get intra and inter cluster distance. This acts as index for selection of parents with diverse origin. The intra and inter cluster values are means derived from D values of cluster elements. The crossing between the genotypes in different clusters with high inter cluster D values will prove to be more correct approach to get desirable results.

The cluster IV comprised most of the genotypes i.e. 22 while cluster I had 11 genotypes, cluster II had 7 genotype, cluster III had 6 genotype, cluster VIII had 3 genotype. Cluster V, cluster VI, cluster VII, cluster IX and cluster X were monogenotypic. The genotypes included in the monogenotypic clusters possess wide variation from rest of the genotypes as well as from each other indication the genetic diversity in their constitution. In present investigation grouping of genotypes into 10 clusters itself indicated wide genetic diversity among the genotypes.

In the present investigation D values between all possible pairs of 54 genotypes ranged from 11.19 to 103.71. Means cluster had a wide range of diversity. Maximum inter cluster distance was observed between cluster VIII and IX (D = 103.71) suggesting that genotypes included in cluster VIII might have entirely different genetical architecture from the genotypes included in the cluster IX. The cluster distance between cluster III and cluster VIII was 89.70 followed by cluster IV and cluster IX was 86.28 and cluster IX and cluster X was 79.31. The less inter cluster distance between these clusters revealed that the genetic constitution of the genotypes in one cluster had close proximity with the genotypes in other cluster of the pair.

Wide range of diversity was also reported, R. K. Gill *et al.* (2008) distributed 50 genotypes into VIII cluster in which one cluster contain 24 genotypes. Thaware *et al.* (1997) grouped 60 genotypes in thirteen clusters. While Chaudhari (1997) evaluated 60 genotypes into seventeen clusters, however Mandal and Dana (1998) distributed 27 geographically diverse strains into seven cluster. Jadhav and patil (1996) grouped 50 genotypes into fifteen clusters where as Sharma and Hore (1994) grouped 28 genotypes into six clusters. Eight clusters were recorded by Kumar *et al.* (1996) while evaluating 30 induced mutant genotypes of rice bean.

Maximum intra-cluster distance recorded in cluster IV (D=16.74) while no intra-cluster distance in cluster V, VI, VII, IX, X. Lowest intra-cluster distance indicating might have genetical similarities with one another and appeared to have evolved from the common gene pool.

Considering the mean performance of clusters, for the eleven characters, it was observed that the cluster VIII had the highest seed yield per plant, seed yield per plot and seed yield per hectare, number of seeds per pod and plant height at maturity. Maximum length of pod was showed by cluster VI, while number of pod per cluster was recorded by V cluster. Cluster IV showed highest branches per plant and highest 1000 seed weight recorded for cluster III.

5.4.2 Relative contribution of different character towards divergence

The variance of cluster means provide information on the relative importance of different characters towards divergence.

In the present study, the variance of cluster means were high for 1000 seed weight (55.35%) followed by days to maturity (27.67%), indicating that these characters were responsible for genetic divergence in the material under study. While least contribution made by number of seeds per pods, number of pods per cluster, number of branches per plant and seed yield per plot.

Chaudhari (1997) showed major responsible character was plant height. Salunke A.U. (2001) recorded character for divergence were plant spread, pod length and plant height while least contributed characters were pods per cluster and days to maturity.

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

In self pollinated crops, genetic makeup of the plant remains constant, it is important to have divergent parent with good performance for yield as well as other quantitative traits for hybridization, to obtain a desirable segregant through selection in the subsequent generation. Hays and Johnson (1939) and East and Hays (1942) suggested the greater heterosis from crosses between diverse parents than those between closely related ones. Timothy (1963) found genetic divergence as one of the criteria for selecting parents for hybridization, which may produce transgressive segregants in the later generation.

The use of multivariate analysis was advocated by Bhatt (1970) for the selection of parents. The crosses from these parents may show improvement in the yielding ability of the progeny. He also stated that statistical distance of all possible cluster combination may be considered arbitrarily as a guideline and suggested that crosses belonging to different clusters showing an inter cluster distance equals to mean statistical or more, night be attempted.

Arunachalam and Bandopadhyay (1984) device a method, which assert parent divergence into four divergence classes (DC) vi DC_1, DC_2, DC_3 and DC_4. To take into account the magnitude of variation in parental divergence, the mean (M) and standard deviation (S) of the intra and inter cluster divergence were calculated. They had conducted two experiments in groundnut and one in rape seed and concluded that the chance for the occurrence of a high frequency of heterotic crosses with high heterosis value were more when the parents were chosen whose divergence lies between interval M-S and M+S (DC_3 and DC_2) as compared to the crosses between parents whose divergence fall outside of this interval.

In the present investigation attempts were made to classify the cluster combination into four divergent classes as per the method suggested by Arunchalam and Bandopadhyay (1984). The statistical distances (D value) showed in fig. 1 represents the index of genetic diversity among clusters. The mean (M) calculated for 45 inter cluster and 10 intra cluster was 51.79 with a standard deviation (S) 21.63. The minimum (X) and maximum (Y) values among these distances were 11.19 and 103.71 respectively. Thus divergence of classes are presented in table 5.1

As per the Arunchalam and Bandopadhyay (1984) the crosses between the divergence class DC2 and DC3 will be more heterotic and promising than others. However, in current investigation all 10 clusters were included in DC_2 and DC_3. It means we have to conduct crossing programme with large number of crosses, which is not possible and also it will be difficult to handle, to reduce the risk from the point of heterosis, high yielding genotypes from the selected clusters should be used. However, while choosing genotypes from clusters, other practical considerations like yield, quality, resistance to disease should be taken into account. The genotypes, which deserve to be considered as potent for crossing, are given in table 5.2 on the basis of their high *per se* performance for the yield and yield components.

Table 5.1 : Distribution of different cluster combination into four divergence classes based on D values between them.

	DC_4		DC_3		DC_2		DC_1	
X		M-S		M		M+S		Y
10.87		30.15		51.79		73.42		103.71

(I,II), (I,III), (I,VI), (II,VI), (II,X) , (III,VI), (III,IX), (IV,V), (IV,VII),(IV,VIII), (V,VII).	(I,IX), (I,X), (II,III), (V,VIII), (VI,IX), (VI,X), (VII,VIII).	(I,IV), (I,V), (I,VII), (II,IV), (II,V), (II,VII), (II,VIII), (II,IX), (III,V), (III,VII), (III,X), (IV,VI), (IV,X), (V,VI), (V,IX), (V,X), (VI,VII),(VII,X), (VIII,X).	(I,VIII), (III,IV), (III,VIII), (IV,IX), (VI,VIII), (VII,IX), (VIII,IX), (IX,X).

Table 5.2 - Potent parents for hybridization.

Sr. No.	Name of genotype	Clus-ter	Characteristics
1.	RRBG-11-03	IV	Higher number of seeds per pod, yield, branches per plant and length of pod.
2.	RRBG-11-13	V	Pods per cluster, seeds per pod and moderate 1000 seed weight and yield.
3.	RRBG-11-16	IV	More pods per cluster, seeds per pod and yield.
4.	RRBG-11-23	VIII	Higher pods per cluster, seeds per pod, yield and moderate branches and seed weight.
5.	RRBG-11-23-03	VIII	Plant height, seeds per pod and yield is higher.
6.	RRBG-11-27	IV	Seeds per pod, branches per plant and yield more with less height.
7.	RRBG-11-36	IV	Less maturity days and height, more length of pod, seeds per pod and yield.
8.	RRBG-11-37	IV	Highest yield among all, length of pod and seeds per plant.
9.	LRB-459	X	Higher length of pod and seeds per pod and moderate pods per cluster with less days to maturity.
10.	LRB-467	III	Highest seed weight among all, less days to 50% flowering and maturity, and moderate length of pod.

6. SUMMARY AND CONCLUSION

The present investigation “Genetic diversity in Rice bean (*Vigna umbellata* (Thumb) Ohwi and Ohashi)” was undertaken with following objectives.

1. To measure genetic diversity in quantitative characters.
2. To study the nature and extent of genetic diversity.

Fifty four genotypes of rice bean were evaluated in randomized block design with two replications during *kharif* 2012. The observations were recorded on yield and yield contributing characters *viz.*, days to 50 per cent flowering (nos.) days to maturity (nos.), plant height (cm), length of pod (cm), number of pods per cluster (nos.), number of seeds per pod (nos.), number of branches per plant (nos.), seed yield per plant (g), 1000 seed weight (g), seed yield per plot (g) and seed yield per hectare (q).

Wide range of variation was observed for all the 11 characters considered for the study. The analysis of variance exhibited significant differences among the genotypes for all the eleven characters indicating the presence of substantial degree of variability.

Phenotypic coefficient of variation (PCV) was found to be more than (genotypic coefficient of variation (GCV) for all eleven characters indicating the role of environment for expression of the traits. The seed yield per plant exhibited the highest GCV and PCV (65.42 GCV and 66.04 PCV respectively) followed by seed yield per plot and seed yield per hectare. The character length of pod had least GCV and PCV.

The characters *viz.*, days to 50 per cent flowering (nos.) days to maturity (nos.), plant height (cm), length of pod (cm), number of pods per cluster (nos.), number of seeds per pod (nos.), number of branches per plant (nos.), seed yield per plant (g), 1000 seed weight (g), seed yield per plot (g) and seed yield per hectare (q) expressed high estimate of heritability in broad scene indicating the scope for selection of these traits. 1000 seed weight showed highest heritability followed by days to 50% flowering, days to maturity and seed yield per hectare. Very high broad sense heritability observed for all characters with high genetic advance as per cent of mean suggesting the role of additive gene effects for these characters.

In this investigation plant yield character significantly and positively correlated with all character except 1000 seed weight with which it was significant but negatively correlated.

In the present investigation, D values between all possible pairs of 54 genotypes ranged between 11.19 and 103.71. the genotypes were grouped into ten clusters. Cluster IV was largest with 22 genotypes followed by cluster I (11 genotypes), cluster II (7 genotypes) and III (6 genotypes). Cluster VIII contain 3 genotype while remaining all clusters were monogenotypic.

Wide range of inter cluster distance indicated between cluster VIII and cluster IX (103.71) and cluster VIII and cluster III (89.70) suggest that the genotypes present in one cluster differ entirely from those present in another cluster. The minimum inter cluster distance was observed between cluster V and VII cluster.

Maximum intra cluster distance as observed for cluster IV, suggesting that the genotypes present in these clusters might have different genetical architecture and might had originated from different genetic pool. No intra cluster distance observed in cluster V, cluster VI, cluster VII, cluster IX and cluster X.

The variances of cluster means revealed that 1000 seed weight and days to maturity contribute the maximum genetic divergence in present study whereas number of seeds per pod and number of pods per cluster contribute least genetic divergence.

The cluster combinations were classified into four divergence classes, following the method suggested by Arunachlam and Bandopadhyay (1984). Crosses were suggested between clusters in a pair from inter cluster D values, which fall in divergence classes DC2 and DC3 i.e. having intermediate inter cluster distance between them, which would give higher chances of producing high frequency and magnitude of heterosis in future when they will be crossed. The following parents are suggested for tentative breeding programme based on divergence studies.

1. RRBG-11-03
2. RRBG-11-13
3. RRBH-11-16
4. RRBG-11-23
5. RRBG-11-23-03
6. RRBG-11-27
7. RRBG-11-36
8. RRBG-11-37
9. LRB-459
10. LRB-467

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8. VITA

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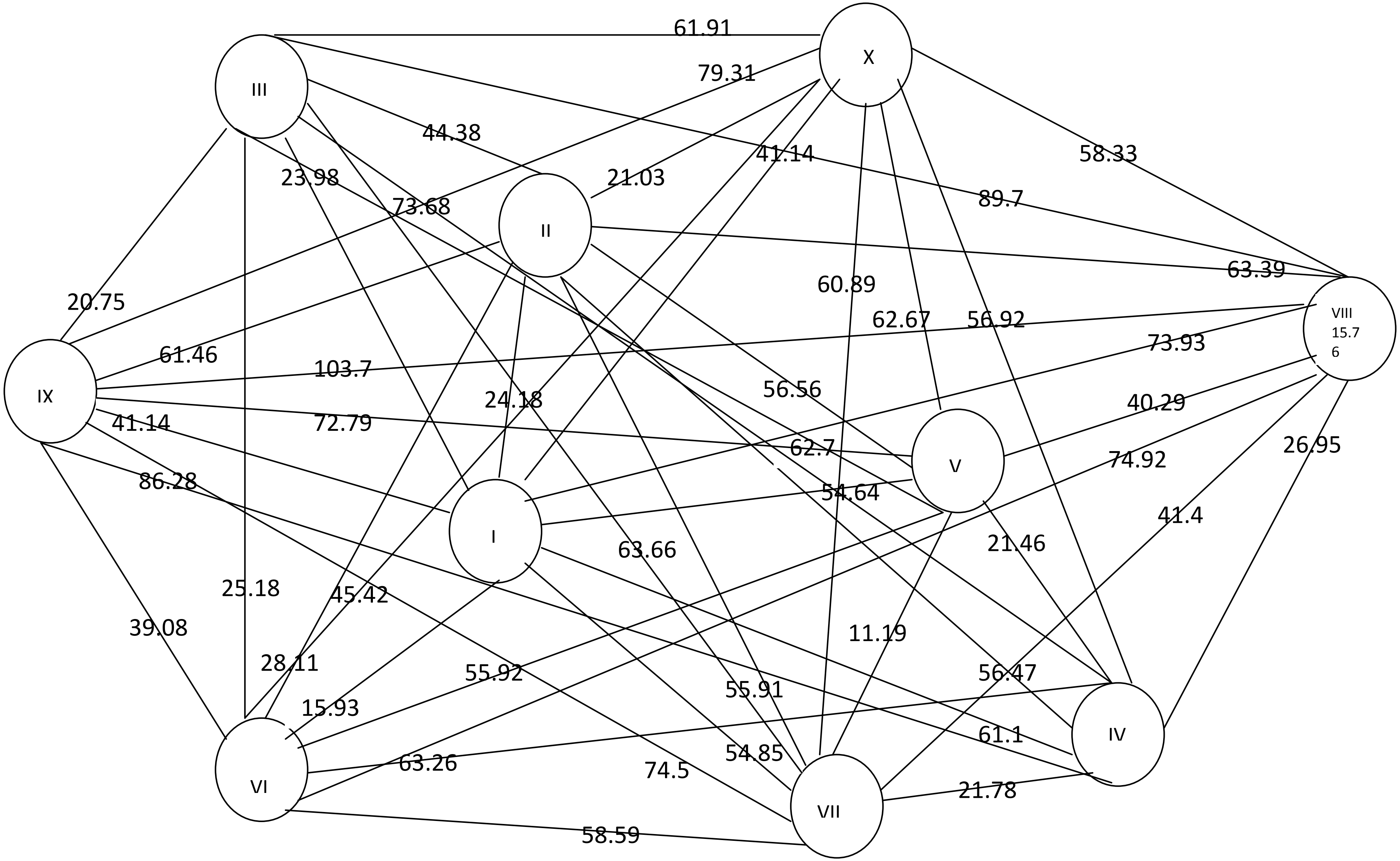

Fig. 1 :CLUSTER DIAGRAM (NOT IN SCALE)

GENETIC DIVERSITY IN RICE BEAN (*Vigna umbelllata (*Thumb) Ohwi and Ohashi)

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ABSTRACT

Genetic divergence using D^2 statistic of 54 rice bean (*Vigna umbellate)* cultivars of different ecogeographic origins revealed existence of considerable diversity. The diversity among the cultivars measured by intercluster distance, was adequate for improvement of rice bean by hybridization and selection. The cultivars included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in rice bean.

Key words: Rice bean, *Vigna umbellate,* genetic diversity.

Rice bean (*Vigna umbelllata (*Thumb) Ohwi and Ohashi) an under utilized legume is native of south and South East Asia (1). In India rice bean is distributed mainly in the tribal regions of North Eastern Hills, Western and Eastern Ghats in Peninsular India (2). Rice bean possibly has the highest yielding capacity among the Asiatic chickpeas, and if a sizeable consumer demand build up, it could become a very useful pulse crop (3). The genetic divergence analysis using D^2 statistic (4) seems to be a powerful tool for quantifying the degree of divergence.

Rice bean being an under-utilized crop information on quantum of genetic divergence is lacking, hence the present investigation was carried out to measure the genetic diversity to identify suitable parents for hybridization for its improvement.

MATERIALS AND METHOD

The experimental material consisting 54 cultivar was evaluated in randomized block design with two replication during *Kharif*, 2012 at underutilized crop project field, department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri. Each genotype was represented by four row, of 3.0 meter length in each replications. The sowing on medium soil was done on 28th July, 2012. The row to row spacing was 30 cm while plant to plant spacing was 15 cm. All the agronomic practices were followed to raise the crop. Data were recorded on 5 randomly selected competitive plants from each plot for the characters such as days to 50 per cent flowering, days to maturity, plant height, length of pod, number of pods per cluster, number of seeds per pod, number of branches per plant, seed yield per plant, 1000 seed weight, seed yield per plot and seed yield per hectare. Replication wise data for each character were subjected for analyses of variances and covariances. Multivariate analysis was done utilising Mahalanois D^2 statistic and cultivars were grouped into different clusters following Tocher's method as described by Rao (5).

RESULTS AND DISCUSSION

The analysis of variance showed a wide range of variation and significant differences among the genotypes for all the characters studied. Significant treatment means sum of squares for all characters studied. High GCV and PCV found for seed yield per plant, plant height at maturity, days to 50 per cent flowering, days to maturity, number of pods per cluster and for number of branches per plant, while it is moderate for number of seeds per pod and for 1000 seed yield. Least GCV and PCV recorded for length of pod. The character shows high broad sense heritability with high genetic advance, it means that character governed by additive gene action.

Table 1. Component of genetic variation in genotype.

Sr. No.	Character	Range	(6^{2}g)	Heritability (b.s.) (%)	GCV %	PCV %	GA	G.A. as % of mean
1.	Days to 50% flowering	55.50-121.50	905	99.78	34.08	34.12	61.9	70.13
2.	Days to maturity	101.50-179.00	1127	99.72	24.83	24.86	69.07	51.07
3.	Plant height at maturity (cm)	55.50 - 177 .00	1766	99.46	36.28	36.38	86.34	74.53
4.	Length of pod (cm)	6.70-9.66	0.51	97.91	9.14	9.24	1.46	18.62
5.	pods / cluster	2.16-5.12	0.60	97.56	22.91	23.20	1.58	46.58
6.	seeds / pod	6.08-10.02	1.47	97.15	15.20	15.42	2.46	30.86
7.	No. of branches / plant	2.10-5.95	0.81	95.88	21.50	21.96	1.82	43.37
8.	Seed yield / plant (g)	1.73-16.24	21.48	98.12	65.42	66.04	9.46	133.49
9.	1000 seed weight (g)	35.90-70.00	54.31	99.81	14.78	14.79	15.17	30.42
10.	Seed yield / plot (kg)	0.14-1.28	0.19	98.46	64.32	64.60	0.74	131.94
11.	Seed yield / ha. (q)	3.83-35.56	98.41	99.35	64.28	64.49	20.37	131.99

The cultivars were grouped into 10 clusters. The cluster IV was the largest containing 22 cultivars followed by cluster I with 11cultivars. Cluster II, cluster III and cluster VIII contain 7,6 and 3 cultivars respectively whereas cluster V, VI, VII, IX and X were unique.

In intra and inter cluster D^2 values among 54 genotype, cluster V and VII shows minimum inter cluster values while cluster VII and IX shows maximum inter cluster distance. Five cluster are monogenotypic. In these clusters, Maximum, inter cluster indicated that the cultivars included in these clusters had maximum divergence. Hence, intermating between the cultivars included in these different clusters may give high heterotic response and thus better sergeants.

Table 2: Distribution of 54 genotypes into different clusters.

Cluster Number	No. Of genotype included	Genotypes
I	11	LRB-448 (29), RBL-1(49), LRB-487(48), LRB-460 (35), LRB-472(41), LRB-481(45), Chandrapur local (54), LRB-484 (47), LRB-319 (26), LRB-470 (40), Bhandara Local (53)
II	7	LRB-325 (27), LRB-477 (42), LRB-447(28), LRB-455 (30), RBL-6 (50), LRB-463 (36), LRB-482 (46)
III	6	LRB-458 (33), LRB-467 (39), LRB-465(38), LRB-456 (31), LRB-480 (44), LRB-478 (43)
IV	22	RRBG-11-18 (10), RRBG-11-37-1-2 (22), RRBG-11-03 (2), RRBG-11-40 (24), RRBG-11-04 (3), RRBG-11-30 (16), RRBG-11-14 (8), RRBG-11-20(11), RRBG-11-25 (14), RRBG-11-27 (15), RBL-50 (52),RRBG-11-36(20), RRBG-11-32 (17), RBL-35 (51), RRBG-11-16 (9), RRBG-11-05 (4), RRBG-11-40-1-3 (25), RRBG-11-35 (19), RRBG-11-11 (6), RRBG-11-37 (21), RRBG-11-34 (18), RRBG-11-39 (23).
V	1	RRBG-11-13 (7)
VI	1	LRB-457 (32)
VII	1	RRBG-11-02 (1)
VIII	3	RRBG-11-23 (12), RRBG-11-23-3 (13), RRBG-11-07 (5)
IX	1	LRB-464 (37)
X	1	LRB-459 (34)

Table 3 : Average intra and inter-cluster D^2 and D values in 10 cluster of 54 genotype of Rice bean.

Cluster Distances	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	10.87 (118.15)	24.18 (584.67)	23.98 (575.04)	61.10 (3733.21)	54.64 (2985.53)	15.93 (253.76)	54.85 (3008.52)	73.93 (5465.64)	40.30 (1624.09)	41.14 (1692.50)
Cluster II		11.21 (125.66)	44.38 (1969.58)	56.47 (3188.86)	56.56 (3199.04)	28.11 (790.17)	55.91 (3125.92)	63.39 (4018.19)	61.46 (3777.33)	21.03 (442.26)
Cluster III			12.93 (167.18)	73.68 (5428.74)	62.70 (3931.29)	25.18 (634.03)	63.66 (4052.59)	89.70 (8046.09)	20.75 (430.56)	61.91 (3832.85)
Cluster IV				16.74 (280.22)	21.46 (460.53)	63.26 (4001.82)	21.78 (474.36)	26.95 (726.30)	86.28 (7444.23)	56.92 (3239.89)

Cluster V					0 (0.0)	55.92 (3127.04)	11.19 (125.21)	40.29 (1623.28)	72.79 (5298.38)	62.67 (3927.53)
Cluster VI						0 (0.0)	58.59 (3432.78)	74.92 (5613.01)	39.08 (1527.25)	45.42 (2062.98)
Cluster VII							0 (0.0)	41.40 (1713.96)	74.50 (5550.25)	60.89 (3707.59)
Cluster VIII								15.76 (248.38)	103.71 (10755.76)	58.33 (3402.39)
Cluster IX									0 (0.0)	79.31 (6290.08)
Cluster X										0 (0.0)

** Figures in brackets denote the D^2 values.

Table 4 : Mean performance of clusters for 11 characters

Cluster Means	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of pod (cm)	Pods per cluster	Seeds per pod	Branches per plant	Seed yield per plant (g)	1000 seed weight (g)	Seed yield / plot (kg)	Seed yield /ha. (q)
Cluster I	58.95	102.14	78.47	7.37	2.57	6.90	3.55	2.86	54.50	0.23	6.39
Cluster II	58.57	102.21	72.21	7.44	2.67	6.80	3.21	2.49	46.54	0.20	5.59
Cluster III	57.33	102.00	78.57	7.43	2.72	6.93	3.63	3.03	62.49	0.24	6.67
Cluster IV	117.89	168.05	154.85	8.13	4.08	9.01	4.98	11.23	45.86	0.88	24.29
Cluster V	118.50	172.00	159.60	8.55	4.20	9.30	4.40	11.50	52.75	0.87	24.15
Cluster VI	56.00	102.00	92.80	9.25	3.45	8.20	3.30	3.10	55.25	0.25	7.05
Cluster VII	121.50	174.00	144.80	7.35	3.65	7.80	4.40	8.95	52.45	0.71	19.65
Cluster VIII	117.67	167.17	163.93	8.95	4.08	9.55	4.53	12.98	37.62	1.02	28.32
Cluster IX	62.00	102.50	63.70	8.15	2.90	7.25	3.70	3.05	70.00	0.26	7.25
Cluster X	59.50	102.50	55.50	6.85	3.15	6.05	4.60	3.00	40.00	0.24	6.50

An examination of cluster mean values revealed that the genotypes in cluster VII took maximum days for flowering and for maturity, while minimum days for both character recorded by cluster VI. Mean plant height was maximum for cluster

VIII and minimum for cluster X. Cluster VI possessed maximum length of pod. pods per cluster was recorded maximum in cluster V. Seeds per pod and yield per plant, per plot, per hectare were highest in cluster VIII. The suggested parents for crossing programme should belongs to diverse clusters characterized by large intercluster distances (6). Such genotypes have genes with different magnitude of effects and the chances to obtain recombinants outside the range of parents are greater enough. Therefore in present study, the hybridization between the cluster III, IV, V, VII and X might useful. The genotypes RRBG-11-03, RRBG-11-23 were found with more yield, plant height, branches per plant and seeds per pod. The hybridization between RBG-11-03, RRBG-11-13, RRBG-11-16, RRBG-11-23, RRBG-11-23-03, RRBG-11-27, RRBG-11-36, RRBG-11-37, LRB-459 and LRB-467 in future breeding programme for higher yield and for seed weight.

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