

Studies on Genetic Variability, Character Associations and Genetic Divergence in Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm

Thesis

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CERTIFICATE

This is to certify that the thesis entitled "**Studies on Genetic Variability, Character Associations and Genetic Divergence in Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm**" submitted in partial fulfilment of the requirements for the degree of **Master of Science in Agriculture** with major in **Seed Science and Technology** of the College of Post-Graduate Studies, V.C.S.G Uttarakhand University of Horticulture and Forestry, Bharsar, is a record of *bona fide* research carried out by **Ms. Meghana Singh, Id.No. UUHf/12148** under my supervision and no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been acknowledged.


(Arun Bhatt)
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CERTIFICATE

We, the undersigned, members of the Advisory Committee of Ms. **Meghana Singh**, Id. No. UUHF/12148, a candidate for the degree of **Master of Science in Agriculture** with major in **Seed Science and Technology**, agree that the thesis entitled "**Studies on Genetic Variability, Character Associations and Genetic Divergence in Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm**" may be submitted in partial fulfilment of the requirements for the degree.



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“Delight thyself also in the lord: and he shall give thee the desires of thine heart; Commit thy way unto the lord: trust also in him, and he shall bring it to pass”

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Meghana Singh
(Author)

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VITÆ

The authoress was born on 7th August, 1990 at Pauri, Pauri Garhwal, Uttarakhand. She passed her High School Examination in 2006 from Bhagat Ram Modern School, Pauri and Intermediate Examination in 2009 from Messmore Inter College, Pauri. She did B.Sc from H. N. B. Garhwal Central University in 2012. She joined V. C. S. G. Uttarakhand University of Horticulture and Forestry in 2012 for M.Sc (Ag.) with major in Seed Science and Technology.

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INTRODUCTION

Legume is widely recognized to be a symbol of sound agriculture economy, being a major source of protein for vegetarian human diet and with unique capacity to improve the soil fertility through nitrogen fixation. The capacity to fixation atmospheric nitrogen relationship with rhizobia has made the legumes essential component of sustainable agriculture. Pulse contain a high percentage of quality protein nearly three times as much as cereals. Apart from traditional tropical pulses example chickpea, mung bean, lentil, pigeon pea, urd bean and pea (**Chandel and Singh, 1984**).

Rice bean variously known as climbing mountain bean, mambi bean, oriental bean, and haricot bean is a native of South and South East Asia (Ohwi, 1965) and locally known as Naurangi or Rayansh. Rice bean is a self pollinated crop but there is some evidence of natural cross pollination (**Sastrapradja and Sustarnu, 1977**). Rice bean (*Vigna umbellata*, (Thunb.) **Ohwi and Ohashi**) is a diploid ($2n=24$) and less known pulse native to south and south East Asia (**Ohwi Jisabura, 1965**). This underutilized and under exploited crop has recently gained attention as an additional grain legume/pulses crop and possess immense potential due to its high nutritional quality, high grain yield ability and multi-purpose usage such as food, animal feed, cover crop and as soil enriched, it is more tolerant to pest and disease and in storage it is less infected by storage pest (**Chatterjee and Dana, 1977**).

Rice bean is widely cultivated in India, China, Korea, Japan, Malayasia, Myanmar, Indonesia, Philippines, Bangladesh, Srilanka and Nepal (**Purseglove 1974, Rachie and Roberts, 1974**). In India rice bean is an important underutilized crop and its distribution is mainly confined to tribal region, North-Eastern region and Western and Eastern Ghats in Peninsular region, often in hilly tracts (**Arora, 1986**). In North Eastern region rice bean is predominantly grown under shifting cultivars as well as rainfed mixed farming system in Assam, Arunachal Pradesh, Mizoram, Nagaland, North Bengal and Sikkim. The distribution pattern indicates its diverse adaptations ranging from warm humid sub-tropical to temperate climate (**Bhag Mal, 1994**). Rice bean is a multipurpose grain legume crop mainly for food, fodder and green manure specifically by the resources poor farmers in the marginal areas of South Asia and South East Asia. It is mainly cultivated in the tropical and sub-tropical climatic

region (**Gautam *et al.*, 2007**). The potential productivity of rice bean has been found superior over other pulse crops, such as green gram and black gram. In mid altitude, particularly Himalayan region, beyond 1500m above mean sea level, other pulse crops like black gram and green gram cannot be grown successfully. However, under these conditions, rice bean gives reasonably good seed yield because of its better cold tolerance ability and better adaptation to acidic soil condition (**Dutta *et al.*, 2000**).

The rice bean is a multipurpose crop with a good potential to be used as food, fodder and green manure. Immature pods and leaves of rice bean are used as vegetable. The nutritional quality of rice bean appears to be the best among all traditional pulses (**Arora, 1986, Chandel *et al.*, 1988**). The nutritional quality of rice bean is excellent due to the presence of high amount of protein and appreciable quantities of limiting amino acids such tryptophan and methionine which rank it as one of the best among the pulses (**NAS, 1975**). The seed contain vitamins such as thiamine, riboflavin, niacin, and ascorbic acid (**Joshi *et al.*, 2006**). Because of its high nutritional quality and other associated benefits, rice bean qualifies for intensive research and development efforts for increased and sustained production. So far, crop improvement efforts have been limited and as such negligible information exists on germplasm evaluation of rice bean.

Normally, it is sown in late-may to end June. Rice bean is susceptible to frost, but tolerate high temperature is best grown where temperature averages 18-30 and rainfall as 1,000-1,500mm per annum. The crop has been and reported to be generally resistance to many diseases common to leguminous crops (**Chandel *et al.*, 1988**). It is often as intercrop or mixed crop with maize (*Zea mays*), sorghum (*Sorghum bicolor*) or cowpea (*Vigna unguiculata*). Rice bean is best adapted to drought-prone sloping areas and flat rain fed conditions. It is grown preferably in marginal lands. Preliminary studies have shown that rice bean can be grown in different types of soil including grey, black, yellow or cream colored soils. However, red soil, which is moderate in fertility status, is considered best for rice bean cultivation (**Khanal and Poudal, 2008**). Based on indigenous knowledge of farmers, rice bean cultivation on highly fertile soil only promotes vegetative growth rather than an increment in yield.

It is normally ready to harvest in 120-150 days after sowing. The higher the altitude, the longer is the crop duration. The early varieties are ready for harvest along with maize, but medium and late varieties require an additional 3-4 weeks. It can be harvested when

approximately 75% of the pods turn brown. To obtain a good yield, it is advisable to harvest the pods in 2-3 or more pickings as per need. To save seed loss from pod shattering, it is worth collecting pods during morning and late afternoon. The common practice by the locals is to harvest the whole plant when majority of the pods are dry and then sun-dry the plants on the threshing floor for 3-4 days. After this, the pods along with the whole plant are beaten with sticks to collect seeds. Rice bean is a crop with multiple use value. Several food items are prepared locally from rice bean. The seeds, which are primary products, are usually taken as a soup or as a pulse (*Dal*) with rice. The grains from young pods are used as vegetables. Rice bean foliage is highly nutritious animal fodder. Some farmers include this crop in their cropping system to increase soil fertility. Rice bean is also used as a cover crop in hills as it is deterrent against soil erosion. Farmers prefer rice bean varieties that have high potential grain yield. Also, they equally consider fodder yield while selecting a rice bean variety because livestock is an integral part of the Indian farming system.

Genetic diversity among rice bean germplasm is important because it provides a gene pool which has developed natural resistance to pest and other environmental stresses. The availability of diverse resources is a prerequisite for genetic improvement of a crop including rice bean. The extent of variation in presently cultivated varieties is relatively high. The purpose of studying variability is to select promising germplasm in rice bean. The productivity of rice bean is very low due to lack of high yielding varieties, which is the major hindrance of the crop getting unique production. It is necessary to identify high yielding varieties. Besides the availability of genetic resources, their characterization is essential for the effective utilization in crop improvement programme. To date, it is little known, little researched and little exploited. The genetic reconstruction of a plant type is required for developing high yielding varieties by incorporating and improving the yield components. Hence, the knowledge on genetic parameters within the available genotypes is a prerequisite for effective selection and development of superior varieties.

Genetic variability plays an important role in a crop for best selecting of genotypes for making rapid improvement in yield and other desirable characters as well as to select the potential parent for hybridization programmes. This crop had a greater genetic variation with regard to fruit yield and its components. Heritability is an index for calculating the relative

influence of environment on expression of genotypes. It becomes very difficult to judge how much of the variability is heritable and how much is non-heritable (**Singh and Kumar, 2005**). Heritability percentages in broad sense are estimated for the various characters of vegetative growth, seed yield and its components for effective selection. Genetic advance under selection measures the role of genetic progress as the deviation between the mean genotypic value of the selected families and the mean genotypic value of the base population due to selection. The correlation coefficients are worked out to describe the degree of association between independent and dependent variables.

Path coefficient analysis measures the direct influence of one variable upon another and permits the separation of correlation coefficients into components of direct and indirect effects. This gives clear picture of direct and indirect effects of the various traits on grain yield of plant. Acknowledge on genetic diversity, its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. Mahalanobis D^2 techniques appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. A great extent of diversity present in various quantitative traits among the genotypes of rice bean suggested good scope for improvement in economic traits through conventional breeding. Assessment of available genetic variability for important economic traits to develop high yielding varieties is an important function in crop breeding.

The information on studies on genetic variability and diversity on rice bean is available in the temperate region, poor adaptability to sub optimal low temperature in rain-fed condition at high altitudes and lack of promising high yielding cultivars are major constraints for bringing up rice bean cultivation in hill regions of Uttarakhand at commercial scale.

The object of breeding mostly confined to evaluate different genotypes of rice bean under high hills, low temperature and rain-fed condition of Himalayas from a set of germplasm collected from different places at hills and plains of India. Moreover, information on extent of genetic variability among available genetic resources, the nature and extent of association between various yield attributes and relative importance and direct and indirect influence of each of the component traits on yield could prove helpful in formulating an effective breeding strategy for randomized the productivity of rice bean at specific region of

Uttarakhand. The present investigation, therefore, includes 28 genotypes of rice bean (*Vigna umbellata*) for studying the following objectives:

- To examine the genetic variability and evaluate the lines for various characters in rice bean germplasm.
- To estimate heritability and genetic advance for yield and its component characters.
- To compute correlation coefficients among different characters.
- To find out direct and indirect effect of various characters on grain yield by path coefficient analysis.
- To estimate the genetic divergence in different genotypes in rice bean.

REVIEW OF LITERATURE

Rice bean is a promising multipurpose but an underutilized and under exploited crop with a good potential to be as food, fodder, green manure and a cover crop. Its high nutrition and other benefits do indicate that this crop qualifies for intensive research and development efforts for sustained production. So far crop improvement efforts have been limited and as such no more information exists on the germplasm and varieties evaluation of the rice bean crop. The literature relevant to the present investigation on rice bean germplasm is limited, thus an attempt has been made to include work done in other related crops under the following sub headings:

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

2.1 Genetic Variability

Variability that exists among the population forms the main basis for selection in any crop improvement programme. Genetic variability, the basis of selection in any crop improvement is the primary consideration of many investigators. Genetic variability is the real measure for variability concealed in a population, while the phenotypic variability is a measure of variability due to genotype, environment and their interaction.

The genetic coefficient of variation alone gives the real picture of variability. The extent of genetic variability existing in a crop is of great importance, since greater the genetic diversity, wider is the scope for selection. **Frankel (1974)** also emphasized the importance of variability in plant population in designing the most effective breeding programme.

Samal *et al.* (1995) reported high variability for days to 50% flowering, followed by 100 seed weight and plant height in beans.

Pande *et al.* (1996) reported that high variability was present in pod yield per plant followed by plant height, pod weight, pods per plant and pod length, while there was least variation with days to maturity in french bean.

Kapila *et al.* (1997) analysed 54 strains of *Phaseolus vulgaris* collected from Western Himalayas and found significant variability for seed yield per plant, biological yield per plant, pods per plant, 100 seed weight, plant height and seeds per pod.

Singh *et al.* (1998) observed significant differences for days to flowering, days to maturity, plant height and branches per plant in 15 rice bean.

Arya *et al.* (1999) studied the variability in 25 indigenous and exotic genotypes of french bean. The highest variance was observed for pod yield per plant, followed by pods per plant and 100 seed weight.

Singh *et al.* (2001) studied the genetic variability in 100 genotypes of rice bean for 9 characters with days of flowering, days of maturity, plant height, pods per plant, pod length, branches per plant, seeds per plant, seeds per pod, 100 seed weight and seed yield per plant. The analysis of variance revealed that significant difference was observed among the genotypes for all the characters.

Sirohi and Kumar (2006) observed high variability in mung bean for pods per plant (18.36 to 49.67), branches per plant (3.51 to 7.99) and where as plant height (61.83 to 70.67), 100 seed weight (2.50 to 3.74) were found to have moderate magnitude of variability and very low magnitude of variability was obtained for days to 50 % flowering (50.00 to 56.33) and number of seed per pod (9.37 to 11.03).

Gohil *et al.* (2006) observed high genotypic coefficient of variation for number of pods per plant followed by seed yield per plant in 55 diverse germplasm of pea.

Thirty seven genotypes of *Vigna mungo* and three *Vigna radiate* resembling to *Vigna mungo* for seed characters were studied to determine the extent of genetic variation based on morphological characters (**Ghafoor *et al.*, 2006**). The highest genetic variation was observed for plant height, days to flowering, days to maturity, number of pods per plant, pod length, seed per pod and grain yield per plant.

Singh and Singh (2006) studied 31 advance line including 6 varieties of pea (*Pisum sativum*) for genetic variability and character association for seed yield per plant and related attributes. The maximum variability was observed for seed yield per plant followed by pods per plant, plant height, branches per plant, and 100 seed height.

Changkija and Rungsung (2009) found that highest range of variability in seed yield per plant followed by 100 seed weight and pods per plant.

Konda et al. (2009) studied 40 genotypes of black gram for genetic variability of seed yield and its component traits. High estimates of variation were observed for plant height and 100 seed weight. Moderate variation was observed for days to 50% flowering and grain yield per plant. On other hand low values of variation were seen for seed per pod, pod length, days to maturity and pods per plant.

Vaghela et al. (2009) studied in 55 diverse genotypes of kabuli chickpea (*Cicer arietinum* L.) which revealed significant difference for all the characters with wide range of variation. Estimates of genotypic and phenotypic coefficient of variation were high for seed yield per plant and number of pods per plant.

Lakshmana et al. (2010) estimated the genetic parameters for 12 traits in rice bean genotypes and observed wide range for per cent germination (1.58 to 96.53), days to 50% flowering (47.00 to 63.69), plant height at harvest (45.27 to 55.99 cm), number of branches per plant (3.20 to 4.20), number of pods per plant (23 to 47), pod length (7.13 to 9.20 cm), number of seeds per pod (5.67 to 9.33), seed yield per plant (11.59 to 15.18) and 100 seed weight (7.20 to 8.36).

Narasimhulu et al. (2013) evaluated genetic variability in 40 mungbean genotypes for different quantitative characters and observed high GCV and PCV for number of branches per plant, pods per plant, biological yield per plant and harvest index, respectively.

Ramya et al. (2014) studied genetic variability parameters in M2 generation in 5 set of 500 well matured seeds of black gram. High estimates of PCV and GCV was observed for primary branches per plant, number of clusters per plant, number of pods per plant and single plant yield.

Degefa *et al.* (2014) studied the magnitude of genetic variability among 13 mung bean accessions for growth and grain yield characters. The phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating that there was environmental influence on these traits.

2.2 Heritability and Genetic advances

Information on heritability estimates and genetic advance is a pre requisite for planning a sound breeding programme, which is used to predict the genetic gain to be obtained by selection for morphological traits. Heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their off springs.

Genetic advance is another measure of genetic gain under selection. It is defined as the improvement in the mean genotypic value of selected plants over the parental population. The success of genetic advance depends on genetic variability, heritability and selection intensity. When heritability estimation is used in conjunction with genetic advance, the utility of heritability is increased. **Johnson *et al.* (1995)** suggested that heritability and genetic advance when calculated together are more useful in predicting the resultant effect of selection. The studies made on these aspects are reviewed here under.

Chakraborty and Mukherjee (2001) reported high heritability, coupled with high genetic advance for 100 grain weight, grain yield per plant, number of pods per plant and days to 50% flowering while high heritability with low genetic advance was observed for days to maturity and plant height.

Kumar *et al.* (2002) reported high heritability for green fodder yield per plant, number of days to 50% flowering; plant height and dry fodder yield per plant in the study involved 5 cultivars of cow pea.

Heritability in broad sense and expected genetic advance for seed yield and its component trait were studied in 55 diverse germplasm of pea (**Gohil *et al.*, 2006**).

Singh and Singh (2006) studied 31 advance line including 6 varieties of pea (*Pisum sativum*) and found that high heritability for all characters except days to flowers and pod length in broad sense.

Yucel *et al.* (2006) studied heritability between yield and yield components in 15 kabuli chickpea (*Cicer arietinum* L.). Broad-sense heritability ranged from 5.47% (days to flowering) to 51.66% (seed number per plant). Heritability for seed number, 1000 seed weight, and number of full pods were greater than those for the other traits.

Changkija and Rungsung (2009) conducted experiment on rice bean and found that 100 seed weight showed the highest % of heritability while highest genetic advance was recorded for seed yield per plant followed by seed weight.

Idahosa *et al.* (2010) studied heritability and genetic advance of 8 cowpea genotypes for grain yield and its components as well as other vegetative characters. High broad-sense heritability percentage was observed in all characters except for pod weight character which indicated low estimate of 25.5%. The expected genetic advance as percentage of population mean (GA%) was relatively high for pod length, pod weight, seeds per pod and 100-seed weight characters in the two locations.

Nwosu *et al.* (2013) studied on heritability and genetic advance in 5 genotypes of cow pea (*Vigna unguiculata* L. Walp) cultivated in two agro ecological environments and observed that high heritability and genetic advance as per cent of mean by clusters per plant, pods per plant, peduncle length, pod length, dry pod weight, 100 seed weight, seeds per pod, number of seeds per plant and seed yield per plant.

Narasimhulu *et al.* (2013) revealed high of genetic advance as percent of mean for 100 seed weight and harvest index in mung bean. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, pods per plant, pods per cluster, biological yield per plant, harvest index and seed yield per plant.

Ajayi *et al.* (2014) evaluated 10 genotypes of cowpea to estimates broad sense heritability, and genetic advance as percent of mean with 20 quantitative traits and found that high broad sense heritability values for all traits studied except for plant height shows that these traits are less influenced by environmental effects.

Ramya *et al.* (2014) found high heritability per cent and high genetic advance percentage of mean for number of primary branches and seed yield per plant in blackgram.

Degefa *et al.* (2014) assessed the magnitude of heritability in broad sense and genetic advance among 13 mung bean accessions for growth and grain yield characters. The combined results showed high heritability and genetic advance for seeds per plant and seed yield indicating that these characters were under the control of additive genetic effects. High genetic advance expected as percent of mean coupled with high heritability was observed for number of primary branches, number of seeds per plant and number of secondary branches, pods per plant and 100 seed weight for combined analysis.

2.3 Correlation Coefficient

The efficiency of selection can be improved by estimating the relative degree of association between pairs of characters. On the basis of significant correlation coefficients between yield and other economic traits, the selection procedure to improve the yield is simplified because the latter is complex in inheritance. The phenotypic correlation indicate the extent of observed relationship between two characters and these include both heredity and the environmental influences, while genotypic correlation coefficient provides a real association between two characters and are highly useful in selection (**Johnson *et al.*, 1955**).

Dhedhi *et al.* (1997) found that pod length, seeds per pod and 100 seed weight had negative and low association with seed yield in pigeon pea. Days to flowering and maturity displayed significant and positive association with pod length, seeds per pod and 100 seed weight.

Sharma and Mishra (1997) revealed that days to 50% flowering, plant height, pods per peduncle and seed yield had a high positive phenotypic correlation with pods per peduncle, number of seeds per pod and harvest index in cow pea.

Chaudhari *et al.* (2000) evaluated correlation coefficient in 60 genotypes of rice bean for seed yield and its component. Correlation studies indicates that grain yield per plant was significantly and positively associated with plant height, number of branches per plant, pods per cluster, pods per plant and length at both genotypic and phenotypic levels indicating that these characters were principle yield components of rice bean.

Hasan *et al.* (2003) studied correlation in 25 local and exotic genotypes of mash bean (*Vigna mungo*) for important trait towards grain yield and found that all the characters had

positively and highly significant associated with grain yield except harvest index which shows highly significant but negative correlation with grain yield.

Yucel *et al.* (2006) studied correlation between yield and its components in 15 kabuli chickpea (*Cicer arietinum* L.) and observed that positive and significant ($P < 0.05$) relationships were determined between seed yield per plant and plant height, first pod height, secondary branch, total pod, and number of full pods and seeds per plant.

Eswari and Rao (2006) studies that selection based on days to 50% flowering, days to maturity, pods per plant, seed per pod and 100 seed weight along with a medium plant height and plant could be useful for improve the yield in green gram.

Joshi *et al.* (2008) worked out for 12 characters in 60 genotypes of lentil and found that number of pods per plant, 100 seed weight and pod length had significant positive association with grain yield per plant. Days to 75% flowering showed significant positive association with number of pods per plant and number of seeds per plants, while negative association with pod length and grain yield per plant.

Tabasum *et al.* (2010) evaluated 10 genotypes of mung bean and observed that primary and secondary branches per plant, pod length and 100 seed weight exhibited negative and non significant genotypic and phenotypic correlations with seed yield while cluster per plant, pods per plant, total plant weight and harvest index showed positive and significant genotypic and phenotypic correlations with seed yield.

Shivade *et al.* (2011) evaluated 36 genotypes of black gram for 15 quantitative characters and found that plant height, number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, length of pod, number of seeds per pod and dry matter per plant had strong positive association with seed yield per plant at both the phenotypic and genotypic level.

Ali *et al.*, (2011) studied correlation in chickpea (*Cicer arietinum* L and found that biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and 100-seed weight were positive and significant at genotypic level but

positive and highly significant at phenotypic level. Whereas, number of days taken to flowering, number of days taken to maturity, primary branches per plant, secondary branches per plant was positively correlated with the grain yield per plant at genotypic and phenotypic levels. Plant height was negative and non-significantly correlated with grain yield per plant at both genotypic and phenotypic levels.

Gaikwad *et al.* (2011) evaluated 40 different genotypes of chickpea (*Cicer arietinum* L.) and observed that seed yield per plant exhibited highly significant positive association with, number of pods per plant, secondary branches per plant and 100seed weight.

Ahmad *et al.* (2012) evaluated 4 irradiated mung bean genotypes to estimate the phenotypic correlation for emergence rate with plant height at first pod maturity, plant height at 90% pod maturity, pods per plant, grains per pod was negative and non significant while it was positive with cluster per plant and 100-seed weight.

Naveed *et al.* (2012) studied correlation and found that biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and 100-seed weight were positive and significant correlated at genotypic level but positive and highly significant correlated at phenotypic level.

Narasimhulu *et al.* (2013) estimated correlation in mung bean which revealed that seed yield had positive and significant correlation with number of pods per plant, clusters per plant, number of pods per cluster and biological yield per plant.

Jivani *et al.* (2013) estimated correlation in chick pea for seed yield per plant and its 10 component characters. The seed yield per plant had significant and positive correlation with number of pods per plant, biological yield per plant and harvest index at both genotypic and phenotypic levels. Among the component traits, biological yield per plant had significant and positive association with plant height, number of pods per plant and 100-seed weight.

Ajayi *et al.* (2014) estimated high positive genotypic and phenotypic correlations between numbers of pods per plant, number of seeds per pod, number of seeds per plant and seed weight indicates that selection for these will result in increase in yield of 10 genotypes of cowpea.

Punia *et al.* (2014) studied correlation among 133 accessions of urd bean collected from different agro-ecological zones for 8 quantitative traits and found seed yield per plant had strong positive correlation with number of pods per plant and number of branches per plant and strong negative correlation with days to 50% flowering and days to maturity.

Bharti *et al.* (2014) evaluated 100 germplasm lines and four checks of black gram with 11 quantitative characters. A very strong positive association of grain yield per plant was observed with number of clusters per plant, number of pods per cluster, number of seeds per pod, biological yield per plant and harvest index. Thus, the characters showing highly significant positive correlation among yield and its components suggested that selection would be highly effective and efficient in improving these traits, while days to maturity showed negative correlation with grain yield.

Shanko *et al.* (2014) exhibited that seed yield had positive and significant environmental correlation with number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, number of pods per plant, number of seeds per pod and plant height.

Kumar *et al.* (2014) observed highly significant and positive correlated at phenotypic and genotypic for seed yield with number of branches, number of clusters, number of pods per plant, number of seeds per plant pod weight, total biomass and also highly significantly and positively correlated among themselves.

Guar *et al.* (2014) estimated genotypic, phenotypic and environmental correlations in all possible character combinations for 28 genotypes of urd bean and found that the magnitude of genotype was higher than phenotypic coefficient against the environmental correlation for days to maturity, pod length, seeds per pod, seeds per plant and significant produce in terms of biological yield. At genotypic level pods per plant (0.0247), seeds per pod (0.0053), biological yield (0.9431) and harvest index (0.1018) had positive direct effect on seed yield.

2.4 Path coefficient analysis

The studies on correlation coefficient merely indicate the nature of association between two characters which alone does not provide exact idea about the relative effect of

each component characters towards the major economic product under experiment. A component character may have no direct effect on concerned economic trait but it may influence through other related components. Hence the knowledge of direct and indirect effects of different characters on desired traits is essential for selection to improve the population.

The details of the technique of path coefficient analysis for partitioning the correlation coefficient analysis into direct and indirect was first documented by **Wright (1921)** and was further illustrated as a means of analyzing correlation coefficient by **Dewey and Lu (1959)**.

Hasan *et al.* (2003) studied path coefficient analysis in 25 local and exotic genotypes of mashbean for important traits contributing towards grain yield and found that harvest index had maximum direct effect on grain yield followed by biological yield per plant.

Yucel *et al.* (2006) evaluated 15 kabuli chickpea (*Cicer arietinum* L.) and found that path coefficient analysis based on seed yield per plant revealed that all the other traits, except days to flowering, first pod height, and total pod number, exhibited high positive direct effects.

Tabasum *et al.* (2010) estimated the path analysis and found that the positive direct effects were exerted through secondary branches, pods per plant, pod length, 100 seed weight, total plant weight and harvest index while primary branches, plant height, clusters per plant and pods per cluster had negative direct effects in 10 genotypes of mung bean.

Shivade *et al.* (2011) studied 36 genotypes of black gram and found that days to first flowering, number of clusters per plant, number of pods per cluster, length of pod, 100-seed weight, dry matter per plant, harvest index, number of seeds per pod and number of branches per plant had positive direct effect on seed yield per plant at genotypic level.

Sharma and Saini (2011) evaluated path analysis indicated that number of pods per plant and branches per plant could be useful as selection indices for development of high yielding genotypes of chick pea.

Gaikwad *et al.* (2011) studied path coefficient analysis which indicated the highest and positive direct effect for number of pods per plant and 100-seed weight in chick pea.

Manggoel *et al.* (2012) studied path analysis in 10 cowpea accessions and observed high positive direct effects of number of peduncles per plant, flowers per plant and 100 seed weight on grain yield.

Naveed *et al.* (2012) estimated high direct effects for number of days taken to flowering and maturity, biomass per plant and 100-seed weight on grain yield per plant in chickpea.

Dash (2013) studied path coefficient analysis for 10 characters in 36 micro mutants of forage rice bean variety and found that leaves per plant and days to flowering had high positive direct effect on fodder yield while branches per plant and branch length had moderate direct effect.

Rao *et al.* (2013) observed direct and indirect effects in 50 pigeon pea genotypes and found that days to maturity, number of primary branches per plant, number of pod per plant and it had significant positive association with seed yield.

Jivani *et al.* (2013) evaluated 105 diverse genotypes of chickpea to estimate path coefficient analysis for seed yield per plant and its 10 component characters and found that the maximum positive direct effect for harvest index, followed by biological yield per plant, number of pods per plant, and 100-seed weight towards seed yield.

Punia *et al.* (2014) studied path coefficient analysis in 133 accessions of urdbean collected from different agro-ecological zones for 8 quantitative traits and found that number of pods per plant and number of branches per plant had major direct and indirect effect on yield contributing traits in urd bean.

Bharti *et al.* (2014) evaluated path analysis in 100 germplasm lines and four checks of black gram with 11 quantitative characters and found that biological yield per plant followed by harvest index, had direct positive contributors towards seed yield, while number of clusters per plant, number of pods per cluster and seeds per pod via biological yield per plant contributed indirectly towards grain yield.

2.5 Genetic divergence

In genetic studies, the study of genetic divergence is used to differentiate well defined population and to choose suitable parents for obtaining heterotic hybrids and cross combinations that are likely to provide better recombinants with desired agronomic values in later generations. The theoretical background of Mahalanobis D^2 statistics or generalized distance among group constellation has been critically discussed in a series of communications (**Rao, 1952 and Anderson, 1958**). The D^2 statistics was found to be an effective tool among the various techniques available for genetics differentiation among population (**Rao, 1960; Cassie, 1963 and Sabal, 1965**).

Mahalanobis D^2 statistic technique, which is based on multivariate analysis of quantitative traits, is a powerful tool for measuring genetic divergence. The degree of genetic diversity is worked out between any two populations over all the characters taken under study. Genetically divergent population falls into different groups on clustering thus enabling selection parents. The geographic distributions of genotypes are compared with genetic diversity, very often these exhibits parallelism.

This generalized distance method has been extensively used in various crop plants for elucidating information on the available genetic diversity. The outcome of various studies, conducted by using Mahalanobis D^2 analysis is briefly reviewed here under in rice bean and in some of the other pulses.

Rao (1996) reported that days to early flower, pods per plant and 100 seed weight had higher contribution towards genetic divergence.

Bakiyarani *et al.* (2000) concluded that genetic divergence for physiological traits like single plant yield, harvest index and earliness in flowering together accounted for 80% of the total genetic divergence in cowpea. Diversity envisages and works as a conserving force for productive utilization of available germplasm, particularly for wild species whose population are highly reduced in number and serves as a source of material for reintroduction and a major repository of genetic material for future.

Das *et al.* (2001) evaluated genetic divergence among 65 soy bean (*Glycine max*) genotypes from 18 diverse origins. Significant variability among genotypes was observed for

all of the 11 traits studied, *i.e.* days to 50% flowering, days to maturity, plant height, mean internodal length, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, oil content and seed yield per plant. Variance of cluster means revealed that pods per plant and plant height had the maximum contribution towards divergence.

Two hundred germplasm lines, along with 6 commercial varieties of mung bean (*Vigna radiata* L., Wilczek) were evaluated over 4 diverse environments for seed yield and its components *i.e.* days to 50% flowering, days to maturity, days from flowering to maturity, plant height, primary branches per plant, pods length, seeds per pod, 100 seed weight and seed yield per plant (**Raje and Rao, 2001**). The genetic diversity was found to be unrelated to geographical diversity. On the basis of this analysis, genetically diverse genotypes with desirable combination of particular characters were identified and crossing programme was suggested.

Borah and Khan (2002) observed genetic divergence in 60 cultivar of fodder cowpea. These cultivars were grouped into 10 clusters. Dry matter yield, green fodder yield and plant height showed high per cent contribution towards total genetic divergence.

Ushakumari et al. (2002) reported that high contribution towards total genetic divergence was recorded for plant height (22.69%), seeds per pod (17.63%), number of branches (16.82%), number of pods per cluster (15.27%) and pod length (13.47%) in cowpea.

Venkatesan (2004) assessed genetic diversity in 20 genotypes of cowpea (*Vigna unguiculata* L. Walp) for days to first flower, plant height, branches per plant, cluster per plant, pods per plant, pod yield per plant, pod length, seed per pod, 100 seed weight and seed yield per plant. The result indicated considerable diversity among the genotypes.

Singhal et al. (2010) conducted experiment on genetic divergence in horse gram (*Macrotyloma uniflorum* L.) and found analysis of variance for all the characters under study, was highly significant differences among genotypes. The mean performance was reported for per cent (70.77), days to 50% flowering (58.77), primary branches per plant (4.03) and pods per plant (25.04).

Nagalaxmi *et al.* (2010) evaluated genetic diversity in 66 genotypes of cowpea, by using Mahalanobis's D^2 analysis. These genotypes were grouped into 23 clusters. Cluster II showed minimum intra cluster distance was observed in the cluster II. The inter-cluster distance found to maximum between the clusters XXII and XXIII and minimum between clusters II and V. The results indicated that grain yield per plant contributed maximum towards total genetic divergence followed by 100 seed weight and days to 50% flowering.

Gokulakrishna *et al.* (2012) found that seed yield per plant followed by pod length, 100 seed weight and number of primary branches per plant had maximum contribution toward total genetic divergence in mung bean.

Singh *et al.* (2012) studied genetic divergence in 75 genotypes of black gram. These genotypes were grouped into seven clusters. Cluster V consisted maximum accessions (21) followed by cluster VI (19) and VII (13) and cluster I consisted only 1 accession. The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the accessions. Plant height, seed yield per plant, number of seeds per plant, number of seeds per pod and 1000-seed weight were major traits causing genetic divergence among accessions. Cluster II had highest mean value for number of pods per plant, 1000-seed weight and seed yield per plant, cluster IV had highest value for number of seeds per plant and number of seeds per pod.

Vavilapalli *et al.* (2014) evaluated genetic divergence among 22 cowpea genotypes were grouped in 6 clusters by using Mahalanobis D^2 and found that clusters I was the largest, containing eleven genotypes followed by the clusters III (5 genotypes) and cluster II with three genotypes. The inter cluster distance was maximum between cluster III and VI followed by cluster III and V. Based on inter cluster distance and per se performance of genotypes, the entries *viz.*, VU 1, VU 2, VU6, VU 8 and VU 21 were selected, which could be intercrossed to recover good recombinants and desirable segregants. The pod yield per plant contributed maximum divergence (66.23%) which was followed by pod weight (20.78%) and plant height (8.23%).

MATERIALS AND METHODS

The present investigation was carried out during *Kharif* 2014 at Research Block of Crop Improvement, College of Forestry, Ranichauri, Tehri Garhwal, Uttarakhand. The details of materials used and procedures followed during the course of investigation are described in this chapter in followings headings:

3.1 Site of Experiment

3.1.1 Location

The experimental site, College of Forestry, Ranichauri is located at 10 km away from Chamba (Reshikesh-Gangotri road) at an altitude of about 2100 m above mean sea level, lying between 30° 15' N latitude and 78° 30' E longitudes under mid hill zones of Uttarakhand. The field evaluations of the genotypes were carried out in the experimental block of Department of Crop Improvement.

3.1.2 Climate

The Campus falls under humid temperate type climate with an annual rainfall of. The mean monthly metrological data on temperature, relative humidity, rainfall and sunshine during the period of experiment is presented in Appendix-I. During cropping period the mean maximum temperature varied between 11.8°C to 12.1°C and the mean minimum temperature ranged between 3.2°C to 3.3°C. Bright sunshine varied from 3.7 to 8.9 hrs.

3.1.4 The Soil

The soil of the experimental block of Crop Improvement Department was silty clay loam in texture having slightly acidic ph (5.5 to 6.8), low in available nitrogen (200 to 220 kg/ha) and available phosphorous (8.5 to 10.5 kg/ha) and also low in available potash (150 to 160 kg/ha). The depth of soil extends up to 1.0 meter.

3.1.5 Cropping history of the experimental field

The experimental field, which is situated in the Crop Improvement Block, had moderate to good fertility level. Wheat was cultivated in the experimental field during the previous cropping season.

3.2 Experimental Material

The experimental materials for the present investigation comprised of 28 diverse entries of rice bean obtained from the Department of Crop Improvement, College of Forestry, Ranichauri.

Table 3.2: Details of Rice bean entries used in the studies carried out for the Experiment

Sl. No.	Entries	Sl. No.	Entries
1	IC 419489	15	IC 137189
2	IC 394537	16	IC 369282
3	IC 524549	17	IC 538983
4	IC 524076	18	IC 524082
5	IC 394201	19	IC 421875
6	IC 524070	20	LRB 319
7	IC 524085	21	LRB 322
8	IC 524084	22	LRB 456
9	IC 524075	23	LRB 458
10	IC 524074	24	LRB 471
11	IC 524522	25	LRB 472
12	IC 411730	26	PRR 1 ©
13	IC 538870	27	PRR 2 ©
14	IC 419806	28	BRS 1 ©

3.2.2 Experimental Design and Layout

The experiment was conducted in the Randomized Complete Block Design (RBD) during *kharif* season under rainfed condition. There were 25 entries along with the three check was planted during the first week of June, 2014.

The details of experimental lay-out are given below:

Crop	:	Rice bean
Entry	:	25
Check	:	03
Design	:	RCBD
Replication	:	03
Spacing	:	30 × 15 cm
Number of rows per plot	:	Single
Date of sowing	:	03-06-2014

3.3 Cultural Operations

3.3.1 Seed bed preparation

Seed bed was prepared by ploughing with power tiller thrice upto a depth of 20 cm. There after manual labelling was done. Breaking of soil clods were carried out prior to sowing in order to prepare a fine tilth and to ensure optimum moisture conservation.

3.3.2 Fertilizer application

The crop was fertilized with 20kg nitrogen, 40kg of phosphorous and 20kg of potash. All fertilizers were applied at the time of sowing under rainfed condition.

3.3.3 Seed sowing

The seeds were sown on 03 June, 2014, at about 4-6 cm depth by opening furrow with *kutla*. Each furrow was manually dribbled with seed and covered with soil immediately.

The recommended row to row distance 30 cm and 15 cm between plants was maintained after germination by thinning of extra plant population after 20 days of germination.

3.3.4 Crop management

The crop was raised under rainfed condition. The distribution of rainfall was fairly good throughout the crop season except late arrival of monsoon which delayed the germination of the crop. Two hand weeding were done at 30 and 50 days after sowing, to keep the experimental plot free from weeds.

3.3.5 Harvesting and threshing

At maturity, crop was cut from the ground level with the help of sickles and tied into bundles and tagged. The bundles were allowed to dry under the sun for 8-10 days. Manual threshing of bundles of individual plot was done.

3.4 Observations recorded

3.4.1. Days of flowering

The number of days required to 50% flowering was recorded in each genotype in all three replication.

3.4.2. Days to maturity

Number of days taken for crop maturity was taken as the number of days from sowing to the maturity of crop.

3.4.3. Plant height (cm)

Plant height was recorded at the time of maturity stage. Heights of five randomly selected plants were measured by scale from the ground level to tip of the top most ear head. The average was expressed as plant height in cm.

3.4.4 Stem thickness (mm)

The stem thickness of stem was measured with the help of vernier caliper of five randomly selected plants in each entry in three replications.

3.4.5 Leaflet size (cm)

Leaf length of five randomly selected plants was recorded and averaged.

3.4.5 Number of primary branches

Observation of number of primary branches was recorded at fully maturation stage of the crop. Five plants were selected from each replication and count the branches. The average was expressed as number of branches per plant.

3.4.7 Number of pods per plant

To record the number of pods per plant, five plants were selected randomly from every plot from the marked row at harvest. Their pods were counted and averaged to express the number of pods per plant.

3.4.8 Number of seeds per pod

Number of seeds of five randomly selected pods were counted and averaged.

3.4.9 Pod length (cm)

Pod length was measured from the basal to end of the tip of the pod and was averaged for five randomly selected pods.

3.4.10 100 seed weight (g)

After threshing and recording the net plot yield, a random sample of fully grown 100 seeds was counted and weighed to record the test weight.

3.4.11 Seed yield per plant (g)

To record the number of seeds per plant, the pods of five randomly selected plants were harvested, threshed and seeds were weighed and averaged to express the seed yield per plant.

3.5 Statistical analysis

3.5.1 Analysis of variance

The statistical analysis for all the characters studied was done by the method recommended by **Cochran and Cox (1992)** for Randomized Complete Block Design:

Source of variation	Degree of freedom	Sum of square	Mean sum of square	Variance ratio (F Value)
Replication (r)	r-1	S _r	S _r /r-1= MS _r	MS _r /Mse
Treatment (t)	t-1	S _t	S _t /t-1= MS _t	MS _t /Mse
Error (e)	(r-1) (t-1)	S _e	S _e /(r-1)(t-1)= MSe	

Where,

r = Number of replication.

t = Number of treatments/genotypes

The standard error, critical difference and coefficient of variation

Were calculated as follow:

$$\text{SE of mean (SE}_{\text{m}} \pm) = \sqrt{\text{MSE}/t}$$

$$\text{SE of mean difference (SE}_{\text{d}} \pm) = \sqrt{2\text{MSE}/t}$$

$$\text{Critical difference (C.D)} = \sqrt{2\text{MSE}/r} \times \text{'t' value at error d.f.}$$

Where,

t = Table value of 't' distribution at error d.f and 5% and 1% level of probability

$$\text{Coefficient of variation (C.V.\%)} = \frac{\text{Standard deviation}}{\text{Grand Mean}} \times 100$$

Where,

$$\text{Standard deviation} = \sqrt{\text{MSE}}$$

$$\text{CD}_{(0.05)} = \text{SE (d)} \times \text{table value of } t_{(0.05)} \text{ at error degree of freedom.}$$

Where

SE (m) $\pm$ = Standard error of mean

SE (d) $\pm$ = Standard error of difference

CD _(0.05) = Critical difference at 5% level of significance

All the characters, which showed significant differences among genotypes, were further subjected to analysis for the following parameters:

3.5.2 Parameters of variability

3.5.3 Heritability

3.5.4 Genetic advance

3.5.5 Correlation coefficients

3.5.6 Path coefficient analysis

3.5.7 Genetic divergence analysis

3.5.2 Variability

Variability for different characters was estimated as suggested by **Burton and de vane (1953)**. The coefficient of variability at genotypic (GCV), phenotypic (PCV), and environmental (ECV) levels were estimated as follows:

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$ECV = \frac{\text{Environmental standard deviation}}{\text{Mean}} \times 100$$

3.5.3 Heritability

Heritability in broad sense was calculated as per formula given by **Burton and De vane (1953)** and **Allard (1960)**.

$$\text{Heritability (h}^2 \text{ \%)} = \frac{\text{Genotypic variance (Vg)}}{\text{Phenotypic variance (Vp)}} \times 100$$

3.5.4 Genetic advance

The expected genetic advance resulting from selection of five per cent superior individuals were worked out by **Burton and De vane (1953)** and **Johnson *et al.* (1955)**.

$$\text{Genetic advance} = h^2 \times \sqrt{V_p} \times K$$

Where

h^2 = Heritability in broad sense

$\sqrt{V_p}$ = Phenotypic variance deviation

K = Selection differential at 5% selection intensity

The value of K = 2.06 (Allard, 1960).

For categorizing the magnitude of different parameters the limits used, are given below

PCV and GCV > 20 % - High

10 – 20 % - Moderate

< 10 % - Low

Heritability (h^2) > 75 % - High

50% – 75% – Moderate

< 50 % - Low

3.4.5 Correlation Coefficient:

The following formula used for calculating the phenotypic correlation coefficient as suggested by **Robinson *et al.* (1951)**.

(a) Genotypic correlation coefficient:

$$r_{xy}(g) = \frac{Cov.xy(g)}{\sqrt{var.x(g) \times Var.y(g)}}$$

Where,

$r_{xy}(g)$ = genotypic correlation coefficient between traits 'x' and 'y'

$Cov.xy(g)$ = genotypic covariance for the two traits 'x' and 'y'

var .x (g) = genotypic variance for the trait 'x'

var .y (g) = genotypic variance for the trait 'y'

(b) Phenotypic correlation coefficient:

$$r_{xy}(g) = \frac{Cov.xy(g)}{\sqrt{var.x(p) \times Var.y(p)}}$$

Where,

$r_{xy}(p)$ = phenotypic correlation coefficient between traits 'x' and 'y'

$Cov.xy(p)$ = phenotypic covariance for the two traits 'x' and 'y'

var .x (p) = phenotypic variance for the trait 'x'

var .y (p) = phenotypic variance for the trait 'y'

3.5.6 Path-coefficient analysis

The following formula was used for calculating path coefficient analysis was carried out by **Dewy and Lu (1959)**

$$r_{iy} = P_{iy} + \sum r_{ij} P_{jy}$$

Residual factor was calculated as follow:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum P_{jy} r_{iy}$$

r_{iy} = Correlation coefficient between i_{th} and y character.

P_{iy} = Direct effect of i_{th} character on y.

3.5.7 Genetic divergence analysis:

The genetic divergence among 28 genotypes of rice bean was worked out using Mahalanobis' D^2 statistic (**Rao, 1952**). The various steps of the analysis are as follow:

- i. A set of uncorrelated linear combination (Y's) was obtained by the pivotal condensation of the matrix (Rao, 1952) of a set of correlated variables (X's).
- ii. Using the relationship between Y's and X's the mean different genotypes for different characters (X_1 to X_{18}) were transformed into the mean values of a set of uncorrelated linear combination (Y_1 to Y_{18}).
- iii. The D^2 between i^{th} and j^{th} genotypes for K characters was calculated as:

$$D^2_{ij} = \sum (Y_{it} - Y_{jt})^2$$

The K components were calculated separately and added to get D^2_{ij}

- iv. The K components of D^2_{ij} for each combination were ranked in descending order of magnitude.
- v. These ranks were added up for each component over all the combination of i and j and the rank totals were obtained.
- vi. Testing D^2_{ij} as the generalized statistical distance between i^{th} and j^{th} population, the population were grouped into number of clusters on the basis of D^2 values. Any two genotypes belonging to the same cluster had the smallest possible intra-cluster distance (Tocher's method).
- vii. Percent contribution of each character towards genetic divergence was calculated as below:

$$\text{Percentage contribution of character } x = \frac{N}{C} \times 100$$

Where,

N = Number of genotypes combination which was ranked first for character x.

C = All possible combination of genotypes involved in D^2 analysis.

3.5.7.1 Group constellation

Varieties were grouped into a number of clusters. D^2 being treated as the square of generalized distance, according to the method described by Tocher (Rao, 1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should, at least on an average, show a smaller D^2 value than those belonging to two different clusters. In other words, if variety V_1 and V_2 are close together and variety V_3 is distant from both shown by this generalized distance, V_1 and V_2 form one cluster.

The average D^2 values of all possible genotypes combinations in one cluster with those in the other were computed and its square root was used to represent the 'statistical distance' between two clusters.

3.5.7.2 Intra-and cluster genetic distances

For the measure of intra cluster D^2 values, the following formula was used

$$\text{Intra-and inter cluster } D^2 = \frac{\sum D_i^2}{N}$$

$$N = n(n-1)/2$$

Where

$\sum D_i^2$ is the sum of D^2 values between all possible combinations (N) within and between clusters, respectively.

n= number of populations included in a cluster

Intra-and inter cluster genetic distances (d) were computed square root of average intra-and inter cluster D^2 values *i.e.*,

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

3.6.7.3 Contribution of different characters to divergence

The relative contribution of different characters to the total D^2 between each pair of genotypes was give a score of 1 to P (P being the number of characters) based on the

magnitude of D^2 value due to each character. A rank of 1 represented the highest contribution and P the lowest of characters 'X'.

Contribution of each character was calculated using the following formula

$$\text{Percentage contribution of character} = \frac{N(X)}{n(n-1)/2} \times 100$$

Where

$N(X)$ = Number of genotypic combinations which are ranked first for character 'X' out of the total genotypic combinations of $n(n-1)/2$.

n = number of genotypes

Another modified formula was also used to calculate the percentage contribution of a character towards divergence as given below:

$$\frac{B-A_i}{\sum(B-A_i)} \times 100$$

Where

A_i = Total rank of i^{th} characters

B = Constant value which is higher than the highest value of the A_i

RESULTS AND DISCUSSION

The present investigation entitled “**Studies on genetic variability, character associations and genetic divergence in rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm**” was carried out on 28 genotypes of rice bean at Research Block, Department of Crop Improvement, V. C. S. G. Uttarakhand University of Horticulture and Forestry, Ranichauri, Tehri-Garhwal. The results obtained for various morphological parameters are being presented under the following heads:

- 4.1 Mean performance for quantitative traits
- 4.2 Analysis of variance
- 4.3 Genetic variability
- 4.4 Heritability and genetic advance
- 4.5 Correlation coefficients analysis
- 4.6 Path coefficient analysis
- 4.7 Genetic divergence

4.1 Mean performance for quantitative traits

The means performance of 28 genotypes for 11 characters is presented in Table 4.1.

4.1.1 Days to 50% flowering

The days to 50% flowering varied from 81.00 days (IC-419489 and LRB 458) to 101.66 days (IC-524522) with a general mean of 90.51 days. Out of 28 genotypes, 15 were significantly earlier for days to 50% flowering than the general mean and the best line among them were PRR-1 (82.33 days), LRB 456 (83.33 days), IC-137189 (86.00 days), LRB 319 (86.00 days), LRB 472 (86.66 days), IC-524075 (87.66 days) and IC-524074 (87.66 days) which were statistically at par with earliest days to 50% flowering IC-419489 and LRB 458.

A range of high variability in days to 50% flowering is desirable for selecting the genotypes for earliness. A wide range of variability in days to 50% flowering has also been reported by Ghafoor *et al.* (2006) in mung bean, Lakshmana *et al.* (2013) in rice bean and Ramya *et al.* (2014) from 28.00 days to 40.00 days in black gram.

4.1.2 Days to maturity

The days to maturity ranged from 147.33 days (PRR-1) to 167.66 days (IC-538983) with general mean of 158.15 days. Twelve, out of 28 genotypes matured significantly earlier than the general mean. The best lines for early maturity were PRR-2 (149.33 days), LRB 456 (151.66 days) and LRB 458 (152.66 days) which were statistically at par with genotypes PRR-1.

Variation in days to maturity character showed higher value might be due to their different genetic constitution. Result of present findings are in line with that of Singh *et al.* (2001) while working on rice bean, Ghafoor *et al.* (2006) in mung bean and Ramya *et al.* (2014) ranged from 68.66 days to 75.00 days in black gram.

4.1.3 Plant height (cm)

The general mean for plant height was 74.45 cm which ranged from 60.60 cm (LRB 322) to 89.26 cm (IC-394537). Out of 28 genotypes, eleven exhibited significantly shorter plant height than the general mean and best lines among them for short stature were namely, IC-419806 (61.53 cm) and IC-524549 (63.40 cm) which were statistically at par with genotype LRB 322.

Plant height is usually a good index of plant vigour which may contribute towards productivity. The plant growth habit can also serve as a guide to determine the suitable planting distance for a crop and the optimum plant population per unit area for harvesting maximum yields. Variation in plant height is attributed to inherent genetic difference of the crop. Variability in plant height has also been reported by Singh *et al.* (2001), Konda *et al.* (2009), Narashimulu *et al.* (2013) in mung bean and Ramya *et al.* (2014) in black gram.

4.1.4 Stem thickness (mm)

The general mean for stem thickness was 4.64 mm which ranged from 2.71 mm (LRB 471) to 6.28 mm (IC-394537). Out of 28 entries, fifteen were significantly higher thickness than the general mean. The best lines for higher stem thickness were IC-524082 (5.56 mm), IC-524522 (5.69 mm), IC-421875 (5.70 mm), IC-137189 (5.84 mm), IC-369282 (5.91 mm), IC-524074 (6.00 mm) and IC-538870 (6.07 mm) which were statistically at par with genotype IC-394537.

Stem thickness is a character expressing vigour of the genotype. This trait is also important in the view of selecting the population resistance lodging. A wide range of variability

among the genotypes included in this investigation could offer better opportunity of population improvement for this character through selection breeding. Eswari and Rao (2006) have also observed a wide range of variability in stem thickness of green gram genotypes.

4.1.5 Pod length (cm)

The lowest and highest means for pod length were recorded for IC-538983 (5.38 cm) and PRR-1 (9.00 cm), respectively. The general mean for pod length was recorded 6.62cm. Out of 28 genotypes, ten showed significantly longer pod than the general mean and the best genotypes among them were LRB 322 (8.52mm) and LRB 456 (8.26mm) which were statistically at par with the genotype PRR-1.

Pod length is principal yield contributing character in rice bean. The pod length mainly governed by genetic constitution of the genotype but environmental effect is also supposed to play crucial role in increasing the length of pod. Pod length of black gram genotypes have also been expressed by Singh *et al.* (2001), Ghafoor *et al.* (2006), Konda *et al.* (2009), Lakshmana *et al.* (2010) Meshram *et al.* (2013) and Ramya *et al.* (2014).

4.1.6 Number of pods per plant

The general mean for number of pods per plant was 22.27 with a range of 17.68 (IC-524522) to 33.90 (PRR-2). Out of 28 genotypes, nine possessed significantly higher number of pods per plant than the general mean and the best line among them was PRR-1 (32.84), which was statistically at par with the genotype PRR-2.

The high magnitude of variability for number of pods per plant in present study might be due to their different genetic makeup of germplasm. Similar results have also been reported by Borah *et al.* (2001) in rice bean, Narasimhulu *et al.* (2013) from 8.78 to 34.39 in mung bean, Meshram *et al.* (2013) (15.60 to 35.40) and Ramya *et al.* (2014) ranged from 4.00 to 45.00 in black gram.

4.1.7 Leaflet size (cm)

The lowest and highest means for leaflet size were observed for IC-419806 (5.71 cm) to LRB 458 and LRB 471 (7.22 cm), respectively. The general mean for leaflet size was 6.36 cm. Out of 28 genotypes, eleven showed significantly higher than the general mean and the best

five genotypes among them namely, LRB 319 (7.11 cm), LRB 472 (7.07 cm), PRR-1 (6.99 cm), BRS 1 (6.91 cm) and LRB 456 (6.72 cm), these genotypes were statistically at par with the best genotypes LRB 458 and LRB 471.

Variation was found among the genotypes for leaflet size indicating less influence of environment on the phenotypic expression of this character and might be mostly governed by genetic factors. Similar result was also reported by Kumar *et al.* (2002) in cowpea.

4.1.8 Number of primary branches

The general mean for number of primary branches was 3.02. The IC-524070 showed lowest mean (2.50) for number of primary branches per plant while highest mean was recorded in case of PRR-2(4.16). Out of 28 genotypes, twelve possessed significantly higher number of primary branches per plant than general mean and the best entries among them were IC-394537 (3.53) and IC-419489 (3.43) which were statistically at par with PRR-1.

These results confirm the findings of Singhal *et al.* (2010) in horse gram and Ramya *et al.* (2014) ranged from 3.00 to 6.00 in black gram.

4.1.9 Number of seeds per pod

The lowest and highest mean performance for number of seeds per pod was observed for IC-137189 (4.83) to PRR-1 (8.80), respectively. Out of 28 entries, nine were significantly better than the general mean. None of genotype was statistically at par and general mean for number of seeds per pod was 6.05.

Similar results have also been reported by Borah *et al.* (2001) and Lakshmana *et al.* (2010) in rice bean, Narashimulu *et al.* (2013) (8.00 to 12.40) in mung bean, Meshram *et al.* (2013) (4.13 to 7.33) and Ramya *et al.* (2014) ranged from 3.00 to 5.00 in black gram.

4.1.10 100 seed weight (g)

The 100 seed weight ranged from 5.43g (IC-524076) to 10.05g (BRS-1) with general mean of 7.00g. Out of 28 genotypes, fifteen had significantly higher 100 seed weight than the general mean. None of them were statistically at par. Narashimulu *et al.* (2013) had also reported a wide range of variability in 100 seed weight from 3.37 g to 5.44 g in mung bean, whereas

Meshram *et al.* (2013) (3.38 to 4.53 g) and Ramya *et al.* (2014) ranged from 2.58 to 5.68 g in black gram.

4.1.11 Seed yield per plant (g)

The general mean for seed yield per plant was recorded 7.98g. The highest mean (10.27g) was recorded in PRR-2 while lowest mean (6.25g) was recorded in IC-524084. Out 28 genotypes, ten exhibited significantly higher seed yield per plant than the general mean and the best lines among them were PRR-1 (10.21g), LRB 471 (10.18g), LRB 456 (9.99g), LRB 458 (9.92g) and LRB 472 (9.39g) was statistically at par with the best genotype, PRR-2.

Seed yield is the major determinant variable for selecting a particular crop/variety for its commercialization and income generation capability. The above results indicated a wide range or variability in seed yield for per plant across the genotypes and check varieties. Such a pronounced level of variability could be used to improve the population of grain amaranth. Narashimulu *et al.* (2013) had also reported a wide range of variability in seed yield from 4.07 gm to 8.95 g in mung bean, whereas Meshram *et al.* (2013) (2.86 to 5.62 g) and Ramya *et al.* (2014) ranged from 1.18 to 11.75 g in black gram.

On the basis of results as discussed above, it may be summarized that the genotype LRB-322 (60.60) was promising for plant height whereas the genotype LRB 458 and IC-419489 for earliest flowering (81.00 days). Maximum number of pods per plant, number primary branches per plant and seed yield per plant was noticed in PRR 2 © (33.90, 4.16 and 10.27 g, respectively). The check variety PRR 1 was promising for days to maturity, pod length (9.00 cm) and number of seeds per pod (8.80) whereas the genotype LRB 458 and LRB 471 was promising for leaflet size (7.22 cm) and BRS 1 for 100 seed weight (10.05 g). It may be concluded that the genotype LRB 322 could be utilized for improving plant height either by direct selection or hybrid breeding programme with objective to breeding for earliness the popular genotypes PRR 1 could be a better parent whereas characters represented in terms of number of pods per plant, number primary branches and seed yield per plant simultaneously be improved by use of PRR 2. Therefore, the genotypes PRR 1, PRR 2, LRB 322, LRB 458 and BRS-1 could be used in breeding programme for development of high yielding variety as a

parent for improvement of grain yield, pod length, number of seed per pod and 100 seed weight respectively.

4.2 Analysis of Variance

The results of analysis of variance for Randomized Complete Block Design for different characters of twenty-five rice bean germplasm including three checks have been presented in Appendix-II. The mean squares due to genotypes were highly significant for all the characters under study. It indicated that the germplasm tested were highly variable. Substantial variations in rice bean have been also reported in previous workers (Singh *et al.* 2001, Vaghela *et al.* 2009 and Narasimhulu *et al.* 2013).

4.3 Genetic variability

Computation of genotypic, phenotypic and environmental variances, genotypic coefficient of variance (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were statistically worked out to understand the nature and extent of variability in expression of different characters prevailed in population and that led to facilitate selection for various traits for identifying desired genotyped suitable for hills. The genetic variability of different field parameters were presented in Table 4.2

Genetic variability is the base of all improvement programme. Selection can lead to improvement in crop plant only when sufficient genetic variability is present in the population. Larger variability ensures better chances of producing desired genotypes. Variation at environment and phenotypic level is not helpful in effective selection, hence genetic variability and additive genetic variability is adopted by breeders as per the precise information about the variability present in population for different economic traits.

The data presented in Table 4.2 revealed that phenotypic variance for all the traits had higher values corresponding to their genotypic counterpart although the differences were not much high in all the cases.

Genotypic and phenotypic variance were highest for plant height (46.25 cm and 60.58 cm) followed by days to 50% flowering (29.69 and 49.45), number of pods per plant (16.82 to 22.98) and days to maturity (16.24 to 29.33). The characters like seed yield per plant

(1.31g to 1.66g) followed by stem thickness (0.98 mm to 1.26 mm) and 100 seed weight (0.96g to 1.12g) had medium genotypic and phenotypic variances. Rest of characters had low values at genotypic and phenotypic variance. The variance is expressed as deviation from mean value. Therefore, it could never be assigned as high and low.

High genotypic and phenotypic variances have also been reported by Ali *et al.* (2011) for days to 50% flowering and number pods per plant in chickpea, Manggoel *et al.* (2012) for days to 50% flowering and number pods per plant in cowpea, Nwosu *et al.* (2013) for plant height and seed yield per plant in cowpea, Ajayi *et al.* (2014) for days to 50% flowering and number pods per plant in cowpea, Degafa *et al.* (2014) for number of pods per plant and days to maturity in mung bean. Corresponding to present findings, low genotypic and phenotypic variances have been reported by Yucel *et al.* (2006) for days to flowering and Ali *et al.* (2011) for number of primary branches in chickpea while Manggoel *et al.* (2012) for number of primary branches, Nwosu *et al.* (2013) for pod length and Ajayi *et al.* (2014) for number of seeds per pod in cowpea. Therefore, selection based on phenotypic performance of genotypes could be effective mechanism in improvement of population for desirable traits with high level of reproducibility in subsequent generations.

The magnitude of phenotypic coefficient variation (PCV) were greater than their corresponding genotypic coefficient variation (GCV) in respect of all quantitative traits indicating that the apparent variation is not only due to genotypes but also due to influence of environment although the difference between GCV and PCV were narrow. A maximum genotypic and phenotypic coefficient of variation was observed for stem thickness (GCV=21.34%, PCV=24.13%) while high phenotypic coefficients of variation (PCV) were recorded for number of pods per plant (21.52%). Moderate estimates (<20% - >10%) of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for pod length (GCV=14.65%, PCV=16.33%), number of seeds per pod (GCV=12.71%, PCV=16.29%), 100 seed weight (GCV=14.02%, PCV=15.14%) and seed yield per plant (GCV=14.31%, PCV=16.13%), whereas moderate estimate at genotypic coefficient of variation only by number of pods per plant (18.41%) and phenotypic coefficient of variation were recorded only by number of primary branches (18.45%). The low estimates (<10%) of GCV and PCV were recorded for days to 50% flowering (GCV=6.02%,

PCV=7.77%), days to maturity (GCV=2.55%, PCV=3.42%) and leaflet size (GCV=6.41%, PCV=8.09%) whereas, low estimate at genotypic coefficients of variation were recorded for plant height (9.13%) and number of primary branches (8.26%).

High value of PCV and GCV were noticed only by stem thickness and moderate estimates of PCV and GCV were observed for pod length, number of seeds per pod, 100 seed weight and seed yield per plant indicating the presence of high variability in germplasm for selection. Hence, these characters can be relied upon and simple selection can be practiced for further improvement.

Genetic variability is the basis for any heritable improvement in the crop plants. The magnitude of phenotypic coefficient of variation was high as compared to the genotypic coefficient of variation for all the characters studied indicating the important role of environmental variation in expression of different traits in rice bean. The result of present investigation were within agreement to the finding of Tabasum *et al.* (2010) for number of pods in mung bean, Manggoel *et al.* (2012) for 100 seed weight in cowpea, Nwosu *et al.* (2013) for number of pods per plant in cowpea, Meshram *et al.* (2013) for 100 seed weight in cowpea, Narashimulu *et al.* (2013) and Degafa *et al.* (2014) for seed yield per plant, number of pods per plant and number of primary branches in mung bean, Ramya *et al.* (2014) and Ajayi *et al.* (2014) for number of pods per plant and 100 seed weight in cowpea.

4.4 Heritability and Genetic Advance

Effectiveness of a particular breeding procedure for different traits is mainly influenced by heritability which is useful in determining the expression of phenotype related to the genotypic contribution of the trait. Johnson *et al.* (1955) stated that heritability values together with the genetic advance aided in predicting the expected progress through selection.

The estimates made with regards to heritability (broad sense) and genetic advance in per cent of mean for all the eleven characters are presented in Table 4.2. The heritability in broad sense ranged from 20.05% in case of number of primary branches to 100 seed weight 85.74% for 100 seed weight. High heritability was recorded for 100 seed weight (85.74%), pod length (80.50%), seed yield per plant (78.70%), stem thickness (78.19%) and plant height (76.34%). Moderate estimates of heritability was observed for number of pods per

plant (73.19%), leaflet size (62.90%), number of seeds per pod (60.84%), days to 50% flowering (60.04%) and days to maturity (55.37%) while, low heritability was noticed only by number of primary branches (20.05%). High heritability for different traits indicated that large proportion of phenotypic variance was attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression.

Similar results have also been reported by Vaghela *et al.* (2009) was found for days to 50% flowering and 100 seed weight in chickpea. Tabasum *et al.* (2010) 100 seed weight and number of seeds per pod in mung bean, Idahosa *et al.* (2010) for plant height in cowpea, Ali *et al.* (2011) for plant height in chickpea, Meshram *et al.* (2013) for 100 seed weight and number of seeds per pod in mung bean, Manggoel *et al.* (2013) and Nwosu *et al.* (2013) for 100 seed weight, days to 50% flowering and number of pods per plant in cowpea, Meshram *et al.* (2013) for days to maturity and number of seeds per pod in mung bean, Ajayi *et al.* (2014) 100 seed weight and number of pods per plant in cowpea, Ramya *et al.* (2014) in black gram; Degafa *et al.* (2014) for days to maturity in mung bean.

Further, the heritability estimate itself may not be solely and useful index of genetic potentiality of a character. Thus, high heritability estimates coupled with high genetic advance indicate that traits are governed mainly due to additive genetic effects therefore selection may effective for these traits.

Genetic advance (GA) is improvement over the base population that can potentially be made from selection for a characteristic. It is a function of the heritability of the traits, the amount of phenotypic variation and the selection differential (the average phenotypic value of the selected individuals expressed as deviation from population mean) that breeder uses (Johnson *et al.*, 1995). A higher value of genetic advance and heritability estimates was obtained due to additive gene effects (Panse, 1957). Genetic advance was worked out to assess the response to selection likely to occur in selection of breeding programme (Sharma *et al.*, 2000 and Das *et al.*, 2010).

The estimates of genetic advance in per cent of mean were very high for stem thickness (38.87%), number of pods per plant (32.45%), pod length (27.08%), 100 seed weight (26.74%), seed yield per plant (26.15%) and number of seeds per pod (20.42%)

exhibited high genetic advance (>20%). Plant height (16.44%) and leaflet size (10.48%) recorded moderate genetic advance (>10% - <20%), whereas days to 50% flowering (9.61%) number of primary branches (7.62%) and days to maturity (3.9%) showed low genetic advance (<10%). High genetic advance has also been reported by Narasimhulu *et al.* (2013) in mung bean.

In the present investigation moderate estimates of heritability coupled with high genetic advance in per cent of mean were observed for number of pods per plant and number of seeds per pod whereas, high estimates of heritability coupled with high genetic advance were observed for stem thickness, pod length, 100 seed weight and seed yield per plant. Therefore, direct selection for these characters would be effective as heritability and genetic advance might be due to additive gene interaction. Similar result were also reported by Changkija and Rungsung (2009) in rice bean, and Ali *et al.* (2011) in chickpea, Tabasum *et al.* (2010) in mung bean and Meshram *et al.* (2013) in black gram. Plant height and leaflet size show moderate heritability coupled with genetic advance in per cent of mean which indicated possibility of obtaining reasonable response to selection in these traits owing to their high transmissibility but moderate to high variability. The remaining characters *viz.* days to 50% flowering, days to maturity and number of primary branches showed low genetic advance which indicated that selection may not be effective in improving these traits due to non-additive gene action which may be epistasis and dominance effect.

4.5 Correlations Coefficient

The yield is a complex polygenic character. Genetic improvement in yield depends on the knowledge and extent of its association with various component characters. An understanding of the association among the different pairs of component characters and their relative association with yield is necessary for improvement in the desired traits. In the present investigation also the phenotypic and genotypic correlation coefficients were worked out.

The estimates of correlation coefficients among different pairs of characters at phenotypic and genotypic (Table 4.3 and 4.4) showed a close resemblance to each other. A detail of the results of inter character association is given below:

A perusal of Table 4.4 showed that seed yield per plant was highly significant and positive phenotypic correlation with number of pods per plant (0.734) followed by pod length (0.632), leaflet size (0.609), number of seeds per pod (0.591), number of primary branches (0.296) and plant height (0.294) while it showed negative and highly significant phenotypic correlation with stem thickness (-0.557), days to maturity (-0.490) and days to 50% flowering (-0.402). Number of pods per plant showed highly significant positive phenotypic correlation with pod length (0.644) but it showed negative and highly significant correlation with stem thickness (-0.577) followed by days to maturity (-0.480) and days to 50% flowering (-0.301). Number of seeds per pod possessed highly significant and positive phenotypic correlation with pod length (0.616) followed by number pods per plant (0.529), leaflet size (0.384) and number of primary branches (0.338) while it was highly significant and negative phenotypic correlation with stem thickness (-0.390) and days to maturity (-0.339) and significant and negative association with days to 50% flowering (-0.224). Leaflet size exhibited highly significant and positive phenotypic correlation with number of pods per plant (0.529) followed by pod length (0.497) and plant height (0.316) but it had highly significant and negative phenotypic correlation with stem thickness (-0.488) while, days to 50% flowering (-0.273) and days to maturity (-0.248) showed significant and negative phenotypic correlation with leaflet size. Days to maturity recorded highly significant and positive phenotypic correlation with days to 50% flowering (0.343) whereas, number of primary branches showed highly significant and positive phenotypic correlation with number of pods per plant (0.323). Pod length showed highly significant and positive phenotypic correlation with plant height (0.305) while, it had negative and highly significant phenotypic correlation with stem thickness (-0.444), days to 50% flowering (-0.390) and days to maturity (-0.327). The estimates of phenotypic correlation coefficient for rest of the characters pairs were non-significant.

The estimates of genotypic correlation coefficient between different characters showed close parallelism in direction with their corresponding phenotypic correlation (Table 4.4). The genotypic correlations were slightly higher in magnitude than corresponding correlation at phenotypic level.

The grain yield in almost all the crops is referred to as super character which results from multiplicative interactions of several other characters that are termed as yield

components. Thus, genetic architecture of grain yield in rice bean as well as other crops is based on balance or overall net affected produced by various yield components directly or indirectly with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient breeding strategy for evolving high yielding variety. In this respect, the correlation coefficient which provides symmetrical measurement of degree of association between two variables or characters, help us in understanding the nature and magnitude of association among yield and yield components.

Grain yield per plant was significantly and positively correlated at phenotypic levels with number of pods per plant, number of seeds per pod, leaflet size, number of primary branches and days to maturity. It indicated that for improvement of seed yield per plant in rice bean selection should be practiced keeping in the view number of seeds per pod, number of primary branches, leaflet size, number of pods per plant and days to maturity. Similar results on correlation have been also reported by Chaudhari *et al.* (2000), Jadhav *et al.* (2001) and Changkija and Rungsung (2009) in rice bean that grain yield per plant was significantly and positively associated with number of pods per plant and number of seeds per pod at phenotypic level indicating that these characters were principle yield components. Tabasum *et al.* (2010) observed in mung bean that seed yield had positive and significant correlation with number of pods per plant and number of seeds per pod, Shivade *et al.* (2011) observed that grain yield per plant had strong significant and positive association with number of pods per plant and number of seeds per pod in black gram, Gaikwad *et al.* (2011) and Ali *et al.* (2011) reported that grain yield per plant exhibited highly significant and positive association with number of pods per plant and number of seeds per pod in chickpea, Ahmed *et al.* (2012) and Narasimhmulu *et al.* (2013) observed in mung bean that seed yield had positive and significant correlation with number of pods per plant and number of seeds per pod and Jivani *et al.* (2013) reported that grain yield per plant exhibited highly significant and positive association with number of pods per plant and number of seeds per pod in chickpea, Shanko *et al.* (2014) exhibited that seed yield had positive and significant correlation with number of primary branches and number of seeds per pod in cowpea, Bharti *et al.* (2014) and Kumar *et al.* (2014)

observed that grain yield per plant had strong significant and positive association with number of pods per plant and number of seeds per pod in black gram.

4.5 Path Coefficient Analysis

Correlation study only provides information on the relationship and does not give an idea on the cause of this relation and sometimes information obtained is misleading with respect to identification of yield components. Path analysis is one which provides information on the cause of such association (Wright, 1921 and Dewey and Lu, 1959).

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct or indirect effects of yield components on seed yield to provide clear picture of character associations for formulating efficient selection strategy. Path analysis differs from simple correlations in that it points out the causes and their relative importance, whereas the latter measures simply the mutual association ignoring the causation. The results of various causes influencing seed yield per plant (effect) are shown in Table 4.5 and 4.6 at the phenotypic and genotypic levels, respectively.

4.5.1 Phenotypic path coefficient analysis

The direct and indirect effects of different characters on seed yield per plant at phenotypic level are presented in Table 4.5. The highest positive direct effect on seed yield per plant were exerted by number of pods per plant (0.318) followed by leaflet size (0.190), number of seeds per pod (0.182) and plant height (0.102) while highest negative direct effect on seed yield were exerted by stem thickness (-0.143), days to 50% flowering (-0.127) and days to maturity (-0.107). Number of pods per plant (0.205) and number of seeds per pod (0.112) exhibited high order positive indirect effect on seed yield per plant via pod length. Number of pods per plant (0.168) exhibited considerable positive indirect effect on seed yield via number of seeds per pod and leaflet size. The number of pods per plant (0.102) also made positive indirect effect on seed yield via number of primary branches. Leaflet size (0.101) made substantial positive indirect effect on seed yield via number of pods per plant. Number of pods per plant (-0.183) were exhibited highest negative indirect effect on seed yield via stem thickness. Number of pods per plant (-0.153) also exhibited negative indirect effect on yield via days to maturity. The rest of the estimates of indirect effects obtained in

path analysis at phenotypic level were negligible. The estimate of residual factor obtained in phenotypic path analysis was 0.5429.

4.5.2 Genotypic path coefficient analysis

The direct and indirect effects of different characters on seed yield per plant at genotypic level are presented in Table 4.6. The highest positive direct effect on seed yield per plant at genotypic level was recorded by number of pods per plant (0.834) followed by number of seeds per pod (0.358), leaflet size (0.241), plant height (0.180), days to maturity (0.164) and stem thickness (0.103). In contrast, high order negative direct effects on seed yield were exerted by pod length (-0.369) and 100 seed weight (-0.209). The direct effects of remaining characters were too low to be considered important. Number of pods per plant (0.786) followed by leaflet size (0.130) exhibited highest positive indirect effect on seed yield while high order negative indirect effect on seed yield were exhibited by pod length (-0.314) and days to maturity (-0.127) via number of seeds per pod. High order of positive indirect contribution shown by number of pods per plant (0.708) followed by leaflet size (0.241), number of seeds per pod (0.194) and days to 50% flowering (0.100) while pod length (-0.270) exerted substantial negative indirect effects on grain yield via leaflet size. Number of pods per plant (0.658) followed by number of seeds per pod (0.305), leaflet size (0.176) and days to 50% flowering (0.134) exerted substantial positive indirect effects on grain yield via pod length. Number of pods per plant (0.648) followed by number of seeds per pod (0.338) exhibited positive indirect effects on seed yield while pod length (-0.229) and days to maturity (-0.123) exerted negative indirect effects on seed yield via number primary branches. Number of seeds per pod (0.337) followed by leaflet size (0.204) and days to 50% flowering (0.117) exerted positive indirect effects on seed yield while negative indirect effects on grain yield via number of pods per plant were exhibited by pod length (-0.291) and days to maturity (-0.108). Pod length (0.239) exhibited high order positive indirect contribution towards seed yield per plant via days to 50% flowering whereas, number of pods per plant (-0.470), number of seed per pod (-0.143) and leaflet size (-0.116) exerted substantial negative indirect effect on seed yield via days to 50% flowering. High order positive indirect effect on seed yield per plant were exerted by pod length (0.201) via days to maturity, while negative indirect effects on grain yield were exerted by number of pods per plant (-0.551), number of seeds per pod (-

0.278) and days to 50% flowering (-0.105) via days to maturity. Pod length (0.199) exhibited positive indirect effects on grain yield while high order negative indirect effects on grain yield were exerted by number of pods per plant (-0.638), number of seeds per pod (-0.179) and leaflet size (-0.164) via stem thickness. Number of pods per plant (0.184), leaflet size (0.118) and number of seeds per pod (0.113) also made substantial positive indirect effects on grain yield while pod length (-0.157) were exhibited negative indirect effects on seed yield via plant height. Number of pods per plant (0.109) also exerted positive indirect effects on seed yield via 100 seed weight. The rest of the estimates of indirect effects at genotypic level were too low to be considered important.

Evaluation of entire genotypic and phenotypic path analysis revealed that the characters, viz. number of pods per plant, leaflet size, number of seeds per pod and plant height exhibited high positive direct effect on yield. These traits also had significant correlation with seed yield per plant both at genotypic and phenotypic levels. Hence, the relative information of these characters might be considered during the time of selection procedure for improving the seed yield in rice bean. The residual effect of both genotypic and phenotypic path coefficients suggested that more number of characters should be in-include to account the entire variability of rice bean crop in mid hills of Uttarakhand.

Similar results have been also reported by Tabasum *et al.* (2010) reported in mung bean, Sharma and Saini (2011), Gaikwad *et al.* (2011), Naveed *et al.* (2012) in chickpea and Manggoel *et al.* (2012) observed in cowpea, Jivani *et al.* (2013) in chickpea, Rao *et al.* (2013) reported in pigeon pea, Dash (2013) reported in rice bean, Shanko *et al.* (2014) in cowpea and Punia *et al.* (2014) reported in urd bean.

4.6 Genetic Divergence

The germplasm is the reservoir of the genetic variability which is exploited to meet the changing needs for developing improved varieties of a crop. It is important that considerable variability for various traits exists in the germplasm for profitable exploitation following recombination breeding or selection. Since it is not practically feasible to evolved large number of lines in hybridization programme executed for generating superior segregation for developing improved varieties, breeder has to choose or select and limited number of germplasm collections

for exploitation in breeding programme. The existence of optimum genetic divergence between the parents is an important pre requisite for success of any crop improvement programme based on recombination breeding because crosses between genetically diverse parents have been found to be provided superior for transgressive segregation in the segregating generations. Thus genetically diverse parent when crossed can bring together diversity of gene recombination either to exploit heterosis for developing hybrid varieties or to obtained superior recombinants for developing pureline varieties. Thus assessment of genetic diversity in the germplasm collection is an essential requirement for any breeding programme.

The studies of genetic divergence among the 28 genotypes of rice bean germplasm were performed by employing Mahalanobis D^2 statistic as described by Rao (1952). Genetic divergence among the 28 genotypes of rice bean germplasm could be studied under following subheadings:

4.6.1 Composition of clusters

4.6.2 Intra-and Inter cluster genetic distance ($\sqrt{D^2}$)

4.6.3 Cluster means and

4.6.4 Contribution of different characters to total divergence

4.6.1 Composition of clusters

The twenty eight genotypes of rice bean were grouped into six different non-overlapping clusters as presented in Table 4.7. The cluster V was largest group containing 9 genotypes (IC 394201, IC 524084, IC 524076, IC 538870, IC 421875, IC 137189, IC 524075, IC 419806, IC 524549), followed by cluster VI consisting of 8 genotypes (IC 524085, IC 411730, IC 524522, IC 369282, IC 524082, IC 524074, IC 538983, IC 524070) and cluster III represented by 5 genotypes (LRB 456, LRB 458, PRR 2 ©, LRB 471, PRR 1) whereas cluster II possessed 3 genotypes (LRB 319, LRB 472, LRB 322) and cluster I consisted of 2 genotypes (IC 419489, IC 394537). The cluster IV was represented by only 1 genotype (BRS 1).

Thus, the clustering pattern did not necessary bear any relevance with the geographical origin of the test germplasm as indicated in the present study. Presence of substantial genetic

diversity among the germplasm lines screened in the present study indicated that these materials may serve as good source for selecting the diverse parents for hybridization programme aimed as isolating desirable segregates for developing high yielding varieties of finger millet.

An examination of the clustering pattern of 28 rice bean genotypes into six clusters revealed that the genotypes of heterogeneous origin were frequently present in same cluster. Although, the genotypes originated in same place or geographical region were also found be grouped together in same cluster, the instance of grouping of genotypes of different origin or geographical region in same cluster were observed in case of almost all the cluster. This indicated lack of any definite relationship or correlation between genetic diversity and geographical origin of the finger millet genotypes evaluated in the present study. Therefore, the selection of parental materials for hybridization programme simply based on geographical diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. The observation is in conformity with the results obtained by Nagalaxmi *et al.* (2010) and Vavilapalli *et al.* (2014) in cowpea; Singh *et al.* (2012) in black gram.

4.6.2 Intra-and Inter cluster genetic distance ($\sqrt{D^2}$)

The estimates of intra- and inter-cluster distance represented by D^2 values have been given in Table 4.8. The intra-cluster distances ranged from 19.453 (cluster VI) to 43.369 (cluster III). The maximum inter-cluster distance was observed between cluster IV and V (200.266), followed by cluster II and IV (156.869), cluster I and IV (154.054) and cluster III and IV (152.162). The inter-cluster distance between cluster III and VI and cluster IV and VI were also high. The clusters with higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these cluster may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny. The minimum estimates for inter-cluster distance was recorded between cluster V and VI (37.084). The clusters with lowest inter-cluster distances indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter cluster distance were likely to

throw promising recombinants in the segregating generations. Selection of genotypes belonging to clusters with maximum inter-cluster distance for hybridization had also been proposed by Vavilapalli *et al.* (2014) and Nagalaxmi *et al.* (2010) in cowpea; Singh *et al.* (2012) in black gram.

4.6.3 Cluster means

The intra-cluster group means for eleven characters given in Table 4.9, revealed marked differences between the clusters in respects of cluster means for different characters.

Cluster I, having 2 genotypes, showed highest cluster for stem thickness (5.577 mm) and number of primary branches (3.483) but exhibited lowest cluster mean for days to 50% flowering (83.000), number of pods per plant (19.533) and 100 seed weight (6.083g). Cluster II exhibited average cluster mean for all characters but had lowest cluster mean for plant height (66.222cm). The 5 entries of cluster III were responsible for highest cluster mean for pod length (7.993cm), number of pods per plant (30.075), leaflet size (6.937cm), number of seeds per pod (7.473) and seed yield per plant (10.115g) but also exhibited lowest cluster mean for days to maturity (152.333 days) and stem thickness (3.279mm). The cluster IV having monogenotypic, resulting highest cluster mean for days to maturity (160.33 days), plant height (88.967cm) and 100 seed weight (10.050g) but this cluster were characterized by low mean for number of primary branches (2.800). Cluster V having highest number of genotypes (9) and showed lowest mean for leaflet size (5.998cm), number of seeds per pod (5.652) and seed yield per plant (7.142g). Cluster VI having 8 genotypes, exhibited highest cluster mean for days to 50% flowering (94.167 days) and days to maturity (60.333 days) but it showed lowest cluster mean for pod length (5.868cm).

On the basis of above results it is evident that cluster III had maximum cluster means for most of desirable characters *viz.*, pod length, number of pods per plant, leaflet size, number of seeds per pod and seed yield per plant. Similar results have also been obtained by Das *et al.* (2001) in soybean, Bakiyarani *et al.* (2000) in cowpea and Rekha *et al.* (2011) in pigeon pea.

4.6.4 Contribution of different characters to total divergence

The per cent contribution of eleven characters towards total genetic divergence is listed in Table 4.10. The maximum contribution towards expression of genetic divergence was exhibited by 100 seed weight (27.78%) followed by pod length (17.20%), stem thickness (12.96%) and plant height (11.38%). Seed yield per plant (7.41%), number of seeds per pod

(6.35%), days to 50% flowering and leaflet size (5.03%) also played considerable role in conditioning the genetic divergence. Days to maturity (3.44%), number of pods per plant (2.12%) and number of primary branches (1.32%) exhibited low contribution towards total genetic divergence. These were considered to be the most important characters for the genetic diversity point of view. The observation is in conformity with the result obtained by Raje and Rao (2001) in mung bean, Ushakumari *et al.* (2002), Borah and Khan (2002), Venkatesan (2004), Nagalaxmi *et al.* (2010) in cowpea, Singhal *et al.* (2010) in horse gram, Gokulakrishna *et al.* (2012) in mung bean; and Vavilapalli *et al.* (2014) in cowpea

In present investigation, an assessment of the contribution of different characters indicated that 100 seed weight, pod length, stem thickness, and plant height had maximum contribution to genetic divergence as these traits appeared maximum times first rank *viz.*, 105, 65, 49 and 43, respectively.

Keeping in the view, inter-cluster distance and cluster means, it could be concluded that the information high inter cluster distances and cluster means could be useful for developing future hybridization programme in the seek of heterotic hybrids in rice bean.

SUMMARY AND CONCLUSION

The present investigation in rice bean was under taken to (i) examine the genetic variability and evaluate the lines for various characters in rice bean germplasm (ii) estimate heritability and genetic advance for yield and its component characters (iii) compute correlation coefficients among different characters (iv) find out direct and indirect effect of various characters on grain yield by path coefficient analysis and (v) estimate the genetic divergence in different genotypes in rice bean.

In the present study, twenty eight genotypes of rice bean germplasm collections, showing wide spectrum of variation for various characters, were evaluated under normal soil and rainfed conditions during *Kharif*, 2014. The experiment was conducted following Randomized Complete Block Design with three replications at Research Block, Department of Crop Improvement, V. C. S. G. Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri, Tehri-Garhwal, Uttarakhand. The characters studied were days to 50% flowering, days to maturity, plant height (cm), stem thickness (mm), pod length (cm), number of pods per plant, leaflet size (cm), number of primary branches, number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). The data on eleven quantitative characters from the experiment were utilized for estimation of coefficients of variation at genotypic and phenotypic levels, heritability in broad sense, genetic advance in per cent of mean, genotypic and phenotypic correlations, path coefficients and genetic divergence. The salient result of the study and conclusions drawn from them are summarized below:

1. The analysis of variance of the experiment indicated highly significant differences among the twenty eight genotypes of germplasm collections for all the characters under study.
2. The entry PRR-2, followed by PRR-1, LRB 471, LRB 456, LRB 458 and LRB 472 produced highest seed yield per plant. These six lines also possessed high mean performance for most of yield component along with longer pod length and large number of pods per plant. In addition to above six entries, LRB 322, IC-419489 and IC-394537 also exhibited high mean performance for seed yield and some of the yield

components. The lines mentioned above and some other lines having high mean performance for characters other than seed yield may be used as donor parents in hybridization programme for improving the characters for which they showed high mean performance.

3. Wide spectrum of variation was observed for yield and its components in rice bean germplasm. Genotypic and phenotypic variances were highest for plant height, days to 50% flowering, number of pods per plant and days to maturity. High magnitudes of genotypic and phenotypic coefficients of variation were noticed for stem thickness and number of pods per plant indicates higher variability among characters. Hence, these characters are more suitable for selection procedure.
4. A high estimate of heritability coupled with high genetic advance in per cent of mean was observed for stem thickness, pod length, 100 seed weight and seed yield per plant indicated possibility of obtaining reasonable response to selection in these owing to their high transmissibility but moderate to high variability.
5. The genotypic correlation was generally similar in nature and higher in magnitude than corresponding phenotypic correlation coefficients. A very strong positive correlation of seed yield per plant at genotypic and phenotypic level was observed with number of pods per plant, pod length, leaflet size, number of seeds per pod and number of primary branches.
6. Path-coefficient analysis was carried out at genotypic as well as phenotypic level, identified number of pods per plant as major positive direct contributors followed by number of seeds per pod, leaflet size and plant height to seed yield per plant. Number of pods per plant and number of seeds per pod exhibited high order positive indirect effect on seed yield per plant via pod length whereas, number of pods per plant followed by leaflet size exhibited highest positive indirect effect on seed yield. The characters identified above merit due consideration in formulating effective selection strategy in rice bean for developing high yielding varieties.
7. The twenty eight genotypes of rice bean were grouped into six distinct clusters. Major clusters in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating no parallelism between genetic and geographic diversity. Therefore, crosses between members of clusters separated by high inter-cluster distances are likely to

thrown desirable segregates. In this context, the cluster pairs exhibiting very high inter-cluster distances were cluster IV and V, cluster II and IV, cluster I and cluster IV, cluster III and IV.

8. The different clusters showed considerable difference in intra-cluster group mean for eleven characters. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter-cluster distances between them are likely to be more rewarding.
9. 100 seed weight, followed by pod length, stem thickness, plant height and seed yield per plant, played substantial contribution towards total genetic divergence, while remaining characters had low role in conditioning the genetic diversity. Thus, the crossing of genotypes belonging to clusters separated by high inter-cluster distances and differing markedly for characters having high contribution towards total divergence would be more fruitful for isolating superior segregants in segregating generations.
10. Considering the high inter-cluster distances, cluster means and means performance of genotypes, crossing of entries of cluster IV (BRS-1 (c)) with entries of cluster V (IC-394201, IC-524084, IC-524076, IC-538870, IC-421875, IC-137189, IC-524075, IC-419806 and IC-524549). Similarly, crossing of promising genotypes belonging cluster II (LRB 319, LRB 472 and LRB 322), cluster I (IC-419489 and IC-394537) and cluster III (LRB 456, LRB 458, PRR-2, LRB 471 and PRR-1) with high yielding genotypes of cluster IV (BRS-1) would also be fruitful for obtaining transgressive segregants for developing high yielding and better quality rice bean varieties.

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Table 4.2 Estimates of variance and genetic parameters of different characters in rice bean

S. No	Characters	General mean	Variance			Coefficient of variation (%)			Heritability h^2 (%)	Genetic advance in % of Mean
			Genotypic	Phenotypic	Environment	Genotypic	Phenotypic	Environment		
			σ^2_g	σ^2_p	σ^2_e	(GCV)	(PCV)	(ECV)		
1.	Days to 50% flowering	90.51	29.69	49.45	19.76	6.02	7.77	4.91	60.04	9.61
2.	Days to maturity	158.15	16.24	29.33	13.09	2.55	3.42	2.29	55.37	3.91
3.	Plant height (cm)	74.45	46.25	60.58	14.33	9.13	10.45	5.08	76.34	16.44
4.	Stem thickness (mm)	4.65	0.98	1.26	0.27	21.34	24.13	11.27	78.19	38.87
5.	Pod length (cm)	6.62	0.94	1.17	0.23	14.65	16.33	7.21	80.50	27.08
6.	No. of pods per plant	22.28	16.82	22.98	6.16	18.41	21.52	11.14	73.19	32.45
7.	Leaflet size (cm)	6.37	0.17	0.27	0.10	6.41	8.09	4.93	62.90	10.48
8.	No. of primary branches	3.02	0.06	0.31	0.25	8.26	18.45	16.49	20.05	7.62
9.	No. of seeds per pod	6.06	0.54	0.97	0.38	12.71	16.29	10.19	60.84	20.42
10.	100 seed weight	7.00	0.96	1.12	0.16	14.02	15.14	5.72	85.74	26.74
11.	Seed yield per plant (gm)	7.99	1.31	1.66	0.35	14.31	16.13	7.44	78.70	26.15

Table 4.1 Mean performance of different genotypes of rice bean for field parameters

Sl. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Stem thickness (mm)	Pod length (cm)	No. of pods per plant	Leaflet size (cm)	No. of primary branches	No. of seeds/pod	100seed weight (gm)	Seed yield/plant
1	IC 419489	81.00	157.66	77.23	4.87	7.29	20.67	5.96	3.43	6.26	6.41	8.15
2	IC 394537	85.00	155.66	89.26	6.28	7.27	18.39	6.50	3.53	5.90	5.66	8.09
3	IC 524549	99.00	158.00	63.40	4.41	5.94	18.88	5.82	3.20	5.80	6.55	7.14
4	IC 524076	88.66	156.00	67.30	4.04	6.38	19.34	6.17	2.76	5.70	5.43	7.80
5	IC 394201	98.33	162.00	71.53	3.73	6.11	19.46	5.88	3.13	5.90	5.73	6.84
6	IC 524070	92.33	165.66	78.16	4.14	6.13	18.40	6.19	2.50	4.93	7.24	6.88
7	IC 524085	92.00	155.00	77.26	5.05	5.43	18.66	6.11	2.96	5.93	7.64	7.22
8	IC 524084	99.33	160.33	78.03	4.94	5.98	19.63	6.18	2.86	5.03	5.73	6.25
9	IC 524075	87.66	159.66	66.96	5.09	5.65	18.68	5.95	2.73	5.90	7.29	6.79
10	IC 524074	87.66	164.00	74.83	6.00	5.94	18.97	6.00	2.73	5.26	7.53	7.12
11	IC 524522	101.66	160.66	73.30	5.69	5.87	17.68	6.00	2.83	6.00	7.41	7.26
12	IC 411730	95.00	155.00	77.60	5.01	6.05	19.89	6.35	2.80	5.56	6.99	6.98
13	IC 538870	99.33	158.66	73.06	6.07	6.33	20.67	6.15	3.20	5.90	6.68	7.41
14	IC 419806	88.33	157.33	61.53	5.25	5.71	20.04	5.71	2.76	6.00	7.53	6.54
15	IC 137189	86.00	158.33	75.16	5.84	6.19	21.52	6.09	2.80	4.83	5.78	7.51
16	IC 369282	94.00	160.33	75.10	5.91	5.83	20.95	6.41	2.86	6.30	8.31	7.77
17	IC 538983	97.33	167.66	70.16	4.91	5.38	21.31	6.18	3.30	5.86	7.38	7.52
18	IC 524082	93.33	154.33	79.16	5.56	6.28	21.23	6.35	2.66	5.66	8.32	7.89
19	IC 421875	90.66	160.33	71.66	5.70	6.14	20.81	6.00	3.30	5.80	6.72	7.96
20	LRB 319	86.00	160.33	68.13	3.71	7.19	25.15	7.11	2.56	5.76	7.43	7.85
21	LRB 322	84.00	161.00	60.60	4.01	8.52	25.39	6.40	3.20	6.73	7.06	8.33
22	LRB 456	83.33	151.66	77.13	3.60	8.26	27.72	6.72	2.63	7.00	6.72	9.99
23	LRB 458	81.00	152.66	75.46	3.40	7.23	28.05	7.22	3.03	6.90	7.29	9.92
24	LRB 471	95.00	160.66	81.56	2.71	8.12	27.85	7.22	3.06	7.43	5.64	10.18
25	LRB 472	86.66	158.33	69.93	3.32	5.82	24.46	7.07	2.90	5.00	6.31	9.39
26	PRR 1 ©	82.33	147.33	85.50	3.93	9.00	32.84	6.99	3.80	8.80	7.18	10.21
27	PRR 2 ©	89.33	149.33	76.63	2.74	7.33	33.90	6.52	4.16	7.23	7.94	10.27
28	BRS 1 ©	90.00	160.33	88.96	4.13	7.95	23.07	6.91	2.80	6.23	10.05	8.28
	Mean	90.51	158.15	74.45	4.64	6.62	22.27	6.36	3.02	6.05	7.00	7.98
	C.V	4.91	2.28	5.08	11.27	7.21	11.14	4.92	16.49	10.19	5.71	7.44
	S.E	2.56	2.08	2.18	0.30	0.27	1.43	0.18	0.28	0.35	0.23	0.34
	C.D. 5%	7.27	5.92	6.19	0.85	0.78	4.06	0.51	0.81	1.01	0.65	0.97
	Lowest	81.00	147.33	60.60	2.71	5.38	17.68	5.71	2.50	4.83	5.43	6.25
	Highest	101.66	167.66	89.26	6.28	9.00	33.90	7.22	4.16	8.80	10.05	10.27

Table 4.4 Estimates of genotypic correlation coefficients between different characters in rice bean

Characters	Days to maturity	Plant height (cm)	Stem thickness (mm)	Pod length (cm)	No. of pods per plant	Leaflet size (cm)	No. of primary branches	No. of seeds per pod	100 seed weight	Correlation with Seed yield (g)
Days to 50 % flowering	0.508	-0.089	0.268	-0.648	-0.564	-0.482	-0.279	-0.398	-0.033	-0.581
Days to maturity		-0.287	0.298	-0.545	-0.660	-0.395	-0.751	-0.776	-0.029	-0.640
Plant height (cm)			0.044	0.425	0.221	0.491	0.356	0.315	0.182	0.359
Stem thickness (mm)				-0.540	-0.764	-0.681	-0.223	-0.501	0.053	-0.677
Pod length (cm)					0.788	0.732	0.621	0.851	0.043	0.795
No.of pods per plant						0.848	0.776	0.942	0.130	0.987
Leaflet size (cm)							0.010	0.541	0.167	0.890
No. of primary branches								0.944	-0.178	0.720
No. of seeds per pod									0.176	0.835
100 seed weight										0.036

*Significant at 5% level ** Significant at 1% level

Table 4.3 Estimates of phenotypic correlation coefficients between different characters in rice bean

Characters	Days to maturity	Plant height (cm)	Stem thickness (mm)	Pod length (cm)	No. of pods per plant	Leaflet size (cm)	No. of primary branches	No. of seeds per pod	100 seed weight	Correlation with Seed yield (g)
Days to 50 % flowering	0.343**	-0.102	0.176	-0.390**	-0.301**	-0.273*	-0.021	-0.224*	-0.009	-0.402**
Days to maturity		-0.277*	0.190	-0.327**	-0.480**	-0.248*	-0.195	-0.339**	0.003	-0.490**
Plant height (cm)			0.022	0.305**	0.174	0.316**	0.091	0.164	0.118	0.294**
Stem thickness (mm)				-0.444**	-0.577**	-0.488**	-0.147	-0.390**	0.054	-0.557**
Pod length (cm)					0.644**	0.497**	0.177	0.616**	0.036	0.632**
No. of pods per plant						0.529**	0.323**	0.529**	0.149	0.734**
Leaflet size (cm)							0.106	0.384**	0.097	0.609**
No. of primary branches								0.338**	-0.058	0.296**
No. of seeds per pod									0.132	0.591**
100 seed weight										0.031

*Significant at 5% level ** Significant at 1% level

Table 4.6 Estimates of path coefficients between different characters in rice bean at genotypic level

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Stem thickness (mm)	Pod length (cm)	No. of pods per plant	Leaflet size (cm)	No. of primary branches	No. of seeds per pod	100 seed weight	Correlation with Seed yield (g)
Days to 50 % flowering	-0.207	-0.105	0.018	-0.055	0.134	0.117	0.100	0.057	0.082	0.006	-0.581
Days to maturity	0.083	0.164	-0.047	0.049	-0.089	-0.108	-0.065	-0.123	-0.127	-0.004	-0.640
Plant height (cm)	-0.016	-0.052	0.180	0.008	0.076	0.040	0.088	0.064	0.057	0.032	0.359
Stem thickness (mm)	0.027	0.030	0.004	0.103	-0.055	-0.078	-0.070	-0.023	-0.051	0.005	-0.677
Pod length (cm)	0.239	0.201	-0.157	0.199	-0.369	-0.291	-0.270	-0.229	-0.314	-0.016	0.795
No. of pods per plant	-0.470	-0.551	0.184	-0.638	0.658	0.834	0.708	0.648	0.786	0.109	0.987
Leaflet size (cm)	-0.116	-0.095	0.118	-0.164	0.176	0.204	0.241	0.002	0.130	0.040	0.890
No. of primary branches	0.014	0.039	-0.018	0.011	-0.032	-0.040	-0.000	-0.052	-0.049	0.009	0.720
No. of seeds per pod	-0.143	-0.278	0.113	-0.179	0.305	0.337	0.194	0.338	0.358	0.063	0.835
100 seed weight	0.006	0.006	-0.038	-0.011	-0.009	-0.027	-0.035	0.037	-0.036	-0.209	0.036

Table 4.5 Estimates of path coefficients between different characters in rice bean at phenotypic level

Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Stem thickness (mm)	Pod length (cm)	No. of pods per plant	Leaflet size (cm)	No. of primary branches	No. of seeds per pod	100 seed weight	Correlation with Seed yield (g)
Days to 50 % flowering	-0.127	-0.043	0.013	-0.022	0.049	0.038	0.034	0.002	0.028	0.001	-0.402
Days to maturity	-0.037	-0.107	0.029	-0.020	0.035	0.051	0.026	0.021	0.036	-0.000	-0.490
Plant height (cm)	-0.010	-0.028	0.102	0.002	0.031	0.017	0.032	0.009	0.016	0.012	0.294
Stem thickness (mm)	-0.025	-0.027	-0.003	-0.143	0.063	0.082	0.069	0.021	0.056	-0.007	-0.557
Pod length (cm)	-0.013	-0.011	0.010	-0.015	0.033	0.021	0.016	0.006	0.020	0.001	0.632
No. of pods per plant	-0.095	-0.153	0.055	-0.183	0.205	0.318	0.168	0.102	0.168	0.047	0.734
Leaflet size (cm)	-0.052	-0.047	0.060	-0.093	0.094	0.101	0.190	0.020	0.073	0.018	0.609
No. of primary branches	-0.001	-0.009	0.004	-0.007	0.008	0.015	0.005	0.047	0.016	-0.002	0.296
No. of seeds per pod	-0.041	-0.061	0.030	-0.071	0.112	0.096	0.070	0.061	0.182	0.024	0.591
100 seed weight	0.000	-0.000	-0.007	-0.003	-0.002	-0.009	-0.006	0.003	-0.008	-0.062	0.031

Residual effect = 0.5429

Appendix- II Analysis of variance for field parameters of rice bean

Mean sum of square			
Characters	Replication	Treatment	Error
Degree of freedom	2	27	54
Days to 50% flowering	9.869	108.826**	19.757
Days to maturity	13.583	61.814**	13.089
Plant height (cm)	29.111	153.069**	14.330
Stem thickness (mm)	0.133	3.225**	0.274
Pod length (cm)	0.650	3.052**	0.228
No. of pods per plant	3.115	56.624**	6.161
Leaflet size (cm)	0.243	0.598**	0.098
No. of primary branches	0.346	0.434**	0.248
No. of seeds per pod	0.647	2.159**	0.381
100 seed weight (gm)	0.517	3.049**	0.160
Seed yield per plant (gm)	0.136	4.272**	0.353

APPENDIX I: Metrological data during the experiment period

Month	Temperature (⁰ c)		Relative humidity (%)	Rainfall (mm)	Sunshine (hrs.)
	Maximum	Minimum			
June	12.0	3.2	71	15.1	8.9
July	12.1	3.2	95	398.5	3.7
August	12.1	3.3	94	406.0	5.6
September	11.9	3.3	95	80.2	5.8
October	11.9	3.2	83	7.3	7.1
November	11.8	3.2	76	0.0	8.4
December	11.8	3.2	66	17.7	6.5

Table 4.8 Inter and Intra cluster distance $\sqrt{D^2}$ values among 28 genotypes of rice bean

	I	II	III	IV	V	VI
I	28.341	83.171	95.813	154.054	63.07	65.629
II		40.668	75.476	156.869	69.53	75.605
III			43.369	152.162	144.097	139.387
IV				0.00	200.266	117.252
V					26.724	37.084
VI						19.453

Table 4.9 Intra cluster group means for various components of yield in rice bean

S. No.	Characters	Cluster Means					
		I	II	III	IV	V	VI
1.	Days to 50 % flowering	83.000	85.556	86.200	90.000	93.037	94.167
2.	Days to maturity	156.667	159.889	152.333	160.333	158.963	160.333
3.	Plant height (cm)	83.250	66.222	79.260	88.967	69.852	75.700
4.	Stem thickness (mm)	5.577	3.684	3.279	4.133	5.013	5.287
5.	Pod length (cm)	7.282	7.183	7.993	7.950	6.051	5.868
6.	No. of pods per plant	19.533	25.003	30.075	23.070	19.896	19.640
7.	Leaflet size (cm)	6.230	6.862	6.937	6.917	5.998	6.203
8.	No. of primary branches	3.483	2.889	3.340	2.800	2.974	2.833
9.	No. of seeds per pod	6.083	5.833	7.437	6.233	5.652	5.692
10.	100 seed weight (gm)	6.040	6.939	6.959	10.050	6.385	7.605
11.	Seed yield per plant (gm)	8.125	8.526	10.115	8.280	7.142	7.333

Table 4.7 Clustering pattern of 28 genotypes of rice bean on the basis of genetic divergence

No. of clusters	No. of genotypes	Genotypes
Cluster 1	2	IC 419489, IC 394537
Cluster 2	3	LRB 319, LRB 472, LRB 322
Cluster 3	5	LRB 456, LRB 458, PRR 2©, LRB 471, PRR 1©
Cluster 4	1	BRS 1©
Cluster 5	9	IC 394201, IC 524084, IC 524076, IC 538870, IC 421875, IC 137189, IC 524075, IC 419806, IC 524549
Cluster 6	8	IC 524085, IC 411730, IC 524522, IC 369282, IC 524082, IC 524074, IC 528983, IC 524070

Table 4.10 Contribution of different plant growth and seed yield characters to total divergence in rice bean

S. No.	Characters	Number of times appearing first in ranking	Percent contribution
1.	Days to 50 % flowering	19	5.03
2.	Days to maturity	13	3.44
3.	Plant height (cm)	43	11.38
4.	Stem thickness (mm)	49	12.96
5.	Pod length (cm)	65	17.20
6.	No. of pods per plant	8	2.12
7.	Leaflet size (cm)	19	5.03
8.	No. of primary branches	5	1.32
9.	No. of seeds per pod	24	6.35
10.	100 seed weight (gm)	105	27.78
11.	Seed yield per plant (gm)	28	7.41

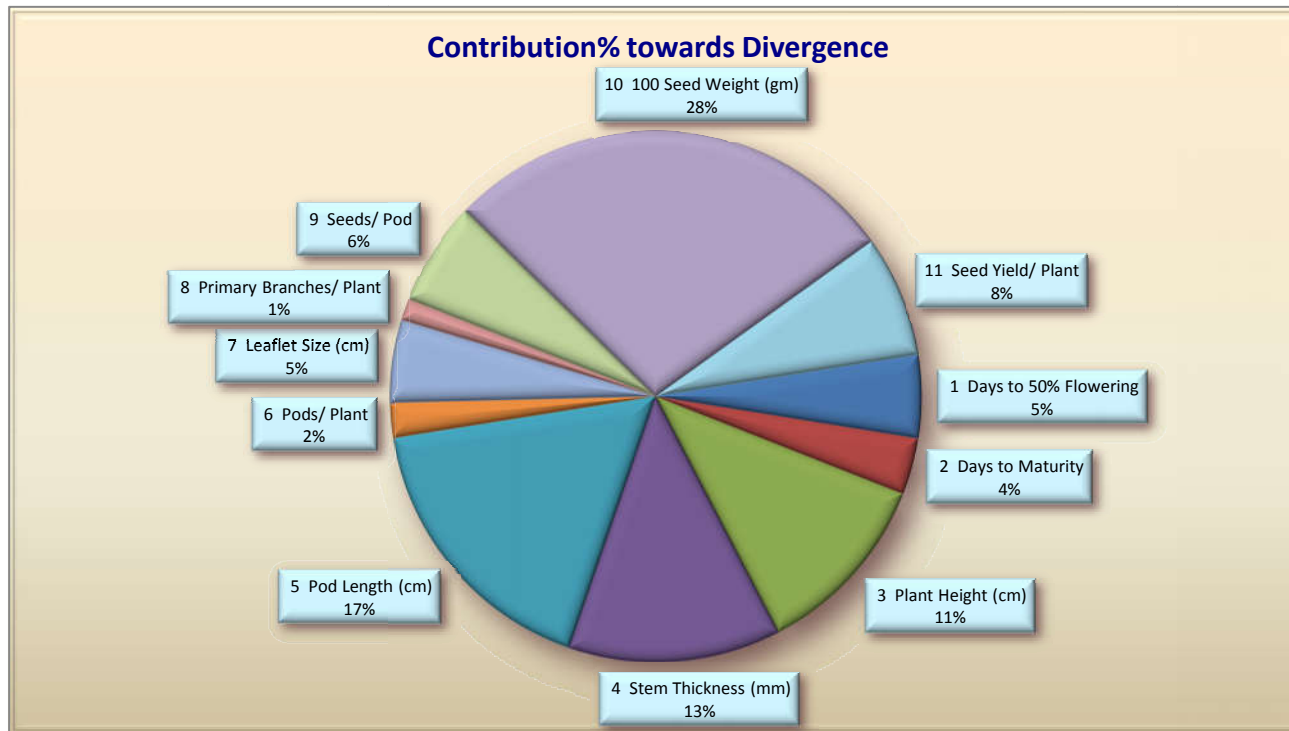


Fig.2 Contribution of each character to divergence of rice bean

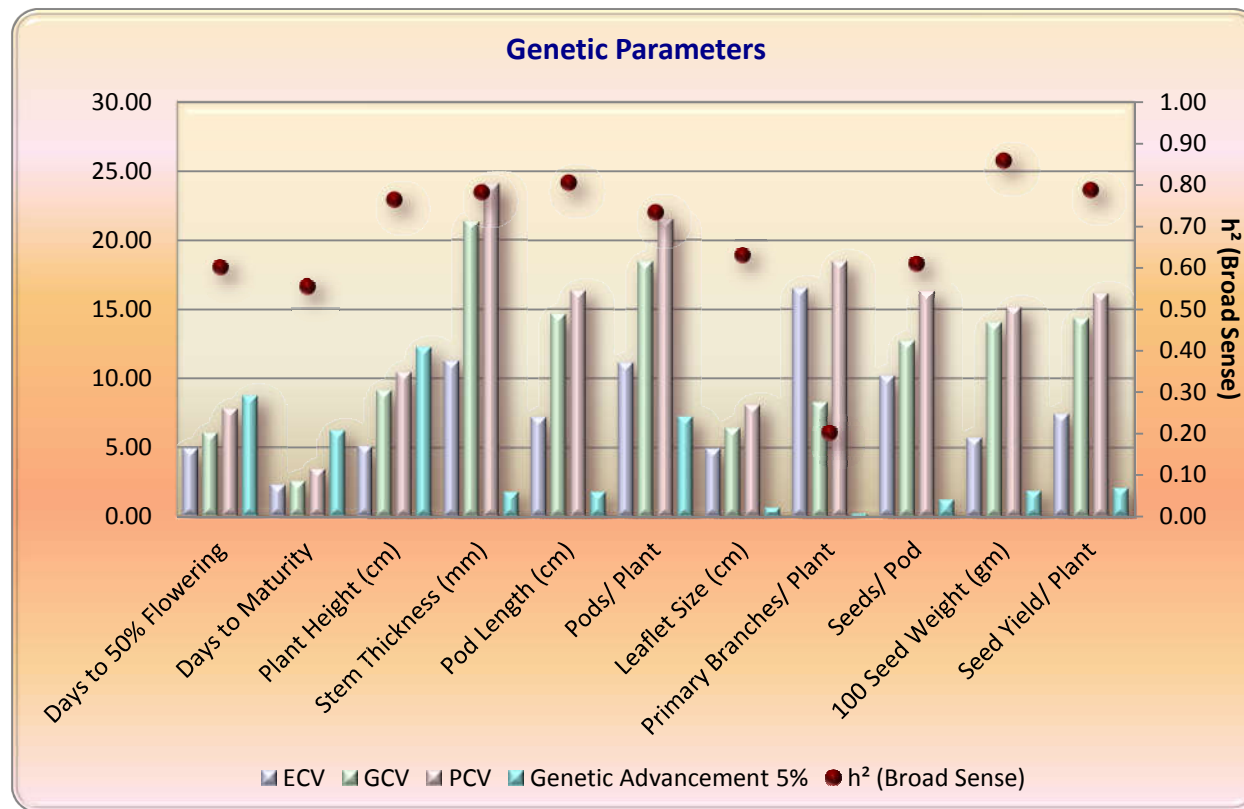


Fig. 1 Estimates of variance and genetic parameters of different characters in rice bean

ABSTRACT

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Advisor	: Dr. Arun Bhatt (Associate Professor, Crop Improvement)		

Topic: “Studies on Genetic Variability, Character Associations and Genetic Divergence in Rice bean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi] Germplasm”

The present investigation was conducted during *Kharif*, 2014 at Research Block, Department of Crop Improvement, V. C. S. G. Uttarakhand University of Horticulture and Forestry, College of Forestry, Ranichauri Campus, Tehri Garhwal, Uttarakhand. The 28 diverse genotypes of rice bean including three checks *viz.*, PRR-1, PRR-2 and BRS-1 were evaluated in Randomized Complete Block Design with three replications. The characters studied were days to 50 per cent flowering, days to maturity, plant height (cm), stem thickness (mm), pod length (cm), number of pods per plant, leaflet size (cm), number of primary branches, number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). The data was analyzed for estimation of mean, range, coefficients of variation, heritability and genetic advance, correlation coefficients, path coefficients and genetic divergence.

The genotype exhibiting high mean performance for seed yield along with high performance for some other yield components were PRR-2, PRR-1, LRB 471, LRB 456, LRB 458 and LRB 472. High magnitudes of phenotypic and genotypic coefficients of variation were noticed for stem thickness and number of pods per plant. High estimates of heritability coupled with high genetic advance as per cent of mean were observed for stem thickness, pod length, 100 seed weight and seed yield per plant. Seed yield per plant exhibited very strong positive association with number of pods per plant, pod length, leaflet size, number of seeds per pod and number of primary branches at phenotypic and genotypic levels. Path-coefficient analysis identified number of pods per plant and leaflet size as major direct contributors towards seed yield per plant at genotypic and phenotypic levels. The twenty eight genotypes of rice bean were grouped into six clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. The cluster pairs exhibiting very high inter-cluster distances were cluster IV and V, cluster II and IV, cluster I and cluster IV and cluster III and IV. Considering cluster mean and genetic distance the crossing of entry of clusters IV with entries of cluster V and those of cluster II, I and III with the entries of cluster IV would be fruitful for obtaining transgressive segregants for developing high yielding and better quality rice bean varieties.

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सारांश

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सलाहकार	: डा० अरुण भट्ट (सह-प्राध्यापक, फसल सुधार विभाग)		

शीर्षक: नौरंगी (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) के जननद्रव्यों में आनुवंशिक विभिन्नता, चरित्र संघ और आनुवंशिक विचलन पर अध्ययन

वर्तमान अध्ययन नौरंगी के अट्ठाईस विविध जननद्रव्यों का शोध प्रक्षेत्र, फसल सुधार विभाग, वानिकी महाविद्यालय, रानीचौरी (वीर चन्द्र सिंह गढ़वाली उत्तराखण्ड औद्यानिकी एवं वानिकी विश्वविद्यालय) खरीफ 2014 में किया गया। नौरंगी के कुल अट्ठाईस जननद्रव्यों के साथ तीन स्थानीय प्रचलित जाँच प्रजातियों क्रमशः पी०आर०आर०-1, पी०आर०आर०-2 तथा बी०आर०एस०-1 को परीक्षण हेतु रेन्डोमाइज्ड कम्पलीट ब्लॉक डिजाइन में तीन अनुकरणों में असिंचित स्थिति में बोया गया। आनुवंशिक के विभिन्न अभिलाक्षणिक गुणों के लिए पचास प्रतिशत पुष्पन में लगे दिवस, पकने की अवधि, पौधों की लम्बाई (सेमी०), तने की मोटाई (मि०मि०), फली की लम्बाई (सेमी०), प्रति पौधा फलियों की संख्या, मध्य पत्ती की लम्बाई (सेमी०), प्राथमिक शाखाओं की संख्या, प्रति फली बीजों की संख्या, 100 बीजों का वजन (ग्रा०) एवं प्रति पौधा बीज उत्पादन (ग्रा०) का अध्ययन किया गया। आकड़ों का विश्लेषण माध्य, सीमा, प्रारूप विभिन्नता, आनुवंशिकता और आनुवंशिक वृद्धि, सहसंबंध गुणांक, पथ गुणांक तथा आनुवंशिक विचलन के आकलन हेतु किया गया।

जननद्रव्यों पी०आर०आर०-1, पी०आर०आर०-2, एल०आर०बी०-471, एल०आर०बी०-456, एल०आर०बी०-458 तथा एल०आर०बी०-472 ने बीज पैदावार के उच्च प्रदर्शन के साथ-साथ कुछ अन्य उपज घटकों के लिए भी उच्च माध्य प्रदर्शन किया। तने की मोटाई एवं प्रति पौधा फलियों की संख्या सस्य सूचकांक कायिक एवं आनुवंशिक प्रारूप विभिन्नता के लिए उच्च पाये गये। उच्च आनुवंशिकता के साथ युग्मित उच्च आनुवंशिक वृद्धि प्रतिशत जैसे तने की मोटाई, फली की लम्बाई, 100 बीजों का वजन एवं प्रति पौधा बीज उत्पादन की संख्या में पाया गया। प्रति पौधा फली संख्या, फली लम्बाई, मध्य पत्ती की लम्बाई, प्रति फली बीजों की संख्या तथा प्राथमिक शाखाओं की संख्या से सकारात्मक एवं महत्वपूर्ण ढंग से कायिक और आनुवंशिक स्तर पर सह-सम्बन्धित हैं। पथ गुणांक विश्लेषण में यह पाया गया कि कायिक और आनुवंशिक स्तर पर प्रति पौधा फलियों की संख्या तथा मध्य पत्ती की लम्बाई का प्रति पौधा बीज उत्पादन पर प्रत्यक्ष रूप से अधिकतम सकारात्मक प्रभाव पड़ा। नौरंगी के अट्ठाईस जननद्रव्यों को भौगोलिक एवं आनुवंशिक विविधता के आधार पर छः समूहों में समूहबद्ध किया गया। उच्च अन्तर समूह दूरी से यह निष्कर्ष निकाला गया कि समूह IV एवं V, समूह II एवं IV, समूह I एवं IV, समूह III एवं IV, के बीच अधिकतम अंतर समूह दूरी देखी गयी। समूह IV के जननद्रव्यों को समूह II, I एवं समूह III के जननद्रव्यों के साथ संकरण करने पर उच्च उपज तथा बेहतर गुणवत्ता की नौरंगी किस्में प्राप्त हो सकती है।

(अरुण भट्ट)
सलाहकार

(मेघना सिंह)
लेखिका