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Research Article

Genetic diversity, variability and character association in local common Bean (*Phaseolus vulgaris* L.) germplasm of Kashmir

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Abstract

Rajmash or common bean is regarded as "Grain of hope" as it is an important component of subsistence agriculture and feeds about 300 million people in tropics and 100 million people in Africa alone. The present investigation was conducted during *kharif* 2008. The experimental material comprised 75 diverse germplasm accessions collected from diverse ecological regions of Kashmir and temperate areas of Jammu division. The material was evaluated at three diverse locations representing three diverse agro-ecological regimes in a randomized complete block design with three replications at each location. Classification of genotypes led to formation of 3 clusters in the pooled data of 75 common bean genotypes. The clustering pattern gave a different picture with cluster II containing 51 genotypes while cluster I had 23 genotypes the remaining one cluster had only one genotype. Analysis of the traits contributing maximum to the divergence in the pooled analysis revealed the traits viz., days to maturity (22.52%), 100-seed weight (14.63%), protein content (12.605), seed yield plant^{-1} (11.215) and days to 50 per cent flowering (10.46%) to contribute maximum to the divergence in the present experimental material. Estimates of heritability (bs) were high (>60%) for all the traits except number of branches plant^{-1} and number of seeds pod^{-1}. The expected genetic gain (per cent of mean) was high (>30%) for days to maturity, number of pods plant^{-1}, 100-seed weight and seed yield plant^{-1} while it was moderate (10.0-30.0%) for days to 50 per cent flowering, number of branches plant^{-1}, pod length, number of seeds pod^{-1} and protein content. The genotypic correlation coefficients were, in general higher in magnitude though similar in direction, as compared to corresponding phenotypic correlation coefficients. Seed yield plant^{-1} was observed to have a highly positive and significant correlations, both at phenotypic and genotypic levels with number of branches plant^{-1}, number of pods plant^{-1}, pod length, number of seed pod^{-1} and 100-seed weight. But negative and significant correlation with days to 50 per cent flowering and days to maturity were estimated from the pooled analysis.

Key words: common bean, genetic diversity, variability, heritability, correlation

Introduction

Rajmash or common bean is regarded as "Grain of hope" as it is an important component of subsistence agriculture and feeds about 300 million people in tropics and 100 million people in Africa alone. Besides, it is emerging as an important income generation especially in Central America where beans are No. 1 income generators among field crops. Globally, with 21 million tones produced from about 26 million hectares, it accounts for about half of the total pulse production. In India, common bean is grown over an area of about 6 million hectares with a production of about 2.5 million tones (FAO, 2010). Beans also offer an alternative for diversification of agricultural system but poor yield renders them poor competitors of cereals, oilseeds and other cash crops. Therefore, there is an urgent need to enhance the yielding ability of bean cultivars to make pulse cultivation a profitable venture. In the present investigation genetic diversity, variability and association analysis in local common bean is attempted.

Material and Methods

The present investigation was conducted during *kharif* 2008. The experimental material comprised 75 diverse germplasm accessions collected from diverse ecological regions of Kashmir and temperate areas of Jammu division. The material was evaluated at three diverse locations representing three diverse agro-ecological regimes in a randomized complete block design with three replications at each location. The random locations were i) Pulse Research Sub-Station Naseembag Habak, Srinagar, ii) Regional Research Station and Faculty of Agriculture, Wadura, Sopore, Baramullah, iii) Krishi Vigyan Kendra, Pombay, Kulgam. The experimental plot consisted of three rows each of 3 m length. The material was sown with 30 cm spacing between the rows and plant to plant spacing of 10 cm. The experimental fields were well prepared and standard recommended package of practices were followed to raise a good crop. The geneic divergence, variability parameters and correlation co efficient among yield components were estimated as per the standard methods.

Results and Discussion

Genetic diversity**:** Analysis of genetic diversity is a platform for stratified sampling of breeding population and to identify the genotypes for hybridization. Involving genetically diverse parents is known to provide an opportunity for bringing together gene constellation yielding desirable transgressive segregants in advanced generations. In order to classify large number of potential genotypes into few numbers of homogenous clusters, the D^2 statistic of Mahalanobis (1936) is now well established in plant breeding. The use of Mahalanobis D^2 statistic for estimating genetic divergence have been emphasized by Chohata *et al.*, (1994) because it permits precise comparison among all the possible pair of populations in any group before effecting actual crosses. Multi-variate analysis quantifies the degree of divergence between populations so as to understand the trend of their evolutionary pattern and to assess the relative contribution of different components to the total divergence together with nature of forces operating at intra and inter-cluster levels. In common bean, utility of multivariate analysis in selecting genetically divergent parents, for successful hybridization programme has been described by Sharma *et al*. (2009).

In the present study 75 common bean genotypes were evaluated in three random environments to estimate genetic divergence and identify putative parents as per Mahalanobis D^2 statistics. The data of three individual environments was also used to estimate the genetic divergence on the pooled analytical basis. Analysis of variance for divergence revealed that the values of V-statistic (measuring Wilk's criteria) were high and significant, indicating presence of substantial genetic diversity in the material as expresse in the individual environments and pooled over the environments. Similar results have been reported by Mirjana (2005).

Classification of genotypes led to formation of 3 clusters in the pooled data of 75 common bean genotypes, the clustering pattern gave a different picture with cluster II containing 51 genotypes while cluster I had 23 genotypes and the remaining one cluster had only one genotype (Table-1). The pattern of group constellations in the present study, both in individual environments and pooled analysis, suggested that geographical diversity was not an essential factor to group the genotypes from a particular source or origin into one particular cluster. This means that, geographical diversity, though important, was not the only factor in determining the genetic divergence. Earlier workers have discussed genetic drift, selection pressure and environment as major factors that could cause greater diversity than geographical distance. Genetic diversity is the outcome of several factors, including geographical diversification. Therefore, selection of parents should be based on genetic diversity rather than geographical diversity and statistical distance D^2, presented the index of genetic diversity among these clusters.

Cluster means of the experimental material under investigation revealed that substantial genetic variability existed for all the morpho-agronomic traits in all individual environments and the data pooled over environments. The pooled analysis over environments (Table 3) revealed that the highest cluster means for days to 50 per cent flowering (64.70) was observed in cluster III, similarly for days to maturity highest mean (142.55) in cluster I; for number of branches plant^{-1} (9.71) in cluster III; for number of pods plant^{-1} (11.03) in cluster III; for pod length (13.10 cm) in cluster III; for number of seeds pod^{-1} (6.21) in cluster III; for 100-seed weight (35.53 g) in cluster II; for seed yield plant^{-1} (19.24 g) in cluster III and protein content (22.15%) in cluster I. Cluster means of different clusters identify the characters to be chosen for hybridization.

In the present study the traits contributing maximum to the divergence in the pooled analysis revealed the traits viz., days to maturity (22.52%), 100-seed weight (14.63%), protein content (12.605), seed yield plant^{-1} (11.215) and days to 50 per cent flowering (10.46%) to contribute maximum to the divergence in the present experimental material (Table 7). Characters contributing to divergence are reported to vary from crop to crop. In general, the traits contributing maximum to genetic divergence in common bean has been identified as 100-seed weight, number of pods plant^{-1}, days to flowering, seed length, and grain oil content (Mirjana, 2005 and Coelin *et al.*, 2007). It has been generally agreed that traits contributing maximum towards the D^2 value need to be given great emphasis for deciding on the clusters to be chosen for the purpose of further selection and choice of parents for hybridization.

Improvement over existing germplasm is a continuous process in plant breeding. Any successful hybridization programme for varietal improvement depends mainly on the selection of parents with high genetic divergences so that desirable character combinations could be selected for the target traits to be improved upon. It is a well established fact that, more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining the higher magnitude of heterotic expression in F_1's and subsequently result in the release of broad spectrum of genetic variability in the segregating generations. Selection of parents based on the extent of genetic divergence has been successfully utilized in different crop species. Sharma *et al.* (2009) suggested that while selecting parents for hybridization on the basis of genetic diversity, it is also advisable to take into consideration their *per se* performance for the traits to be improved. Selection of parents for hybridization should be done from different clusters having wider inter-cluster distance, and the parents to be selected from the clusters should also have the high *per se* performance of the traits that are contributing maximum towards the divergence.

The results obtained in present investigation indicate that considerable variability and diversity were available in the experimental material for converging the elite allelic resources though a systemic breeding and selection approach to recover high yielding segregants that possess good quality characteristics as well. Therefore, selection of parents for hybridization should be done form different clusters having wider inter-cluster distance. The parents to be selected form such clusters should also have high *per se* performance for traits that are contributing maximum towards divergence. In general, combining high yielding potential with wide genetic diversity is emphasized for further selection and choice of parents for hybridization. Thus, crosses between genotypes of the cluster I and cluster III are likely to exhibit high heterosis and produce superior recombinants with desired traits.

<u>Genetic variability, heritability and expected genetic gain:</u> The study of the morphological, yield, yield component and quantitative traits revealed that significant genetic variability existed in these genotypes. Analysis of the quantitative characters (Table-4) revealed presence of significant genetic variation for all the characters. Interaction resulting form G x E was also significant for all the traits and thus estimates from the data pooled over the environments are more appropriate and enable more effective selection for desirable genotypes.
Perusal of Table-5 revealed that days to 50 per cent flowering ranged from 39.80 (PBG-29) to 67.53 (PBG-03) with a mean of 55.46, while days to maturity ranged from 71.81 (PBG-29) to 153.67 (PBG-17) with a mean of 115.43; number of branches plant^{-1} ranged from 7.16 (SKUA-R-35) to 12.00 (SKUA-R-16) with a mean of 9.65; number of pods plant^{-1} ranged from 5.14 (SKUA-R-18) to 13.46 (Shalimar Rajmash-1) with a mean of 8.80; pod length ranged from 6.84 cm (PBG-09) to 13.57 cm (PBG-29) with a mean of 9.66 cm; number of seeds pod^{-1} ranged from 3.52 (SKUA-R-24) to 7.35 (PBG-37) with a mean of 4.84; 100-seed weight ranged from 20.22 g (PBG-18) to 54.93 g (Canadian Red), with a mean of 33.34 g. The most important trait viz., grain yield plant^{-1} ranged from 6.11 g (PBG-03) to 33.15 g (SKUA-R-28) with a mean of 14.29 g and protein content ranged from 17.13 per cent (SKUA-R-22) to 25.01 per cent (SKUA-R-35) with a mean of 21.36 per cent.

The estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance for all the traits. The trend was observed both in individual environments as well as on the basis of pooled analysis, indicating thereby, the influence of environment in the expression of these traits. Since these estimates individually or solely do not provide means to assess the nature of genetic variability, phenotypic and genotypic coefficient of variation were also estimated (Table-5). Highest genotypic coefficient of variation was recorded for seed yield plant^{-1} and moderate for 100-seed weight, number of pods plant^{-1} and days to maturity, days to 50 per cent flowering, pod length and number of seeds pod^{-1}. The estimates of phenotypic coefficient of variation followed the same trend suggesting that the scope of improvement for these traits during selection could be based on the phenotypic variability. Similar results were also reported by Rafi and Nath (2004) and Dursun (2007).

The coefficient of variation (PCV and GCV) reveals the extent of variability present for different characters but not the heritable portion of variability. To have the knowledge of heritable portion of variability, it is necessary to estimate the heritability of each character. The ‘Broad Sense’ heritability gives an idea about portion of observed variability attributable to genetic difference. In other words, heritability indicates the accuracy with which a genotype can be identified by its phenotypic performance. Indeed, heritability in broad sense contains both additive and non-additive effects (Hanssen *et al.,* 1956).

Estimates of heritability (bs) were high (>60%) for all the traits except number of branches plant^{-1} and number of seeds pod^{-1} (Table-5). The expected genetic gain (per cent of mean) was high (>30%) for days to maturity, number of pods plant^{-1}, 100-seed weight and seed yield plant^{-1} while as it was moderate (10.0-30.0%) for days to 50 per cent flowering, number of branches plant^{-1}, pod length, number of seeds pod^{-1} and protein content. However, Samal *et al.* (1995) reported low heritability estimate for plant high and a relatively moderate one for 100-seed weight. Rafi and Nath (2004) observed high heritability for days to flowering, plant height, 100-seed weight and days to maturity.

Presence of high GCV and PCV helps in isolation of desirable genotypes however genotypic coefficients of variation alone will not be sufficient for determination of magnitude of heritable variation. Genotypic coefficient of variation together with heritability estimates will give a better picture of expected genetic gain from selection. Higher heritability estimates along with high genetic gain is usually useful than either of the parameters taken alone in predicting the result of selecting best individuals (Johnson *et al.,* 1955).

Panse (1957) reported that high genetic advance and high heritability is the outcome of additive gene action and vice versa indicates presence of more non-additive gene action. In the present set of material the traits like days to maturity, number of pods plant^{-1}, 100-seed weight and seed yield plant^{-1} had high heritability and expected genetic gain. These traits are expected to be governed more by additive gene effects and improvement could be made through selection in the existing material. For other traits like pod length and protein content hybridization followed by selection is expected to yield some good recombinants.

Correlation coefficient analysis: Correlation measured by a correlation coefficient is important in plant breeding because it measures the degree of association (genetic and non-genetic) between two or more traits. The concept of correlation was first given by Galton (1889) and since then it is believed that knowledge of the nature and magnitude of genetic association among components of economic worth can help in improving the efficiency of selection by making possible use of suitable combination of characters. The phenotypic correlations among traits reflect observed relationship between traits arising from the combined effects of genotype and environment, whereas genetic correlations estimate the association between traits, resulting either from linkage or pleiotropic effects between the traits. In crop improvement, breeding value correlations are more useful, especially for indirect selection and this type of selection can be advantageous over direct selection, only when the selected trait has very high heritability, and breeding value correlation between two traits is very high. Compensation between yield components may lead to variation in correlation pattern, and therefore, he stressed the need for investigation of inter-relationship between yield components. Johnson *et al.* (1955) emphasized the importance of genotype-environment interaction and their contribution to “genetic slippage” in the selection of complex characters. Thus, studies under different environments might give a clear and reliable picture of association which can be effectively utilized during selection of breeding programmes. The correlated changes in yield and yield components may at times lead to physiological efficient genotypes for expression of yield. In presence of substantial breeding value correlation between two traits, selection in one trait will cause a change in its mean through additive gene effects of selected individuals and simultaneously cause an indirect change in the mean of the other trait.

Knowledge of correlations among common bean traits is important for several reasons; it is possible to fully perceive the diversity of breeding material, to identify traits needed by a common bean genotype to grow successfully under certain ecological conditions, to identify and avoid characters that have little or no importance and use of some traits in the selection programmes, to define breeding target and cultivars model and to recognize impediments and benefits of a breeding progress well in advance. Hence in the present investigation an attempt was made to study the degree of inter-relationship between different traits in the material under consideration. Perusal of results (Table-6) indicated that genotypic correlation coefficients were, in general higher in magnitude though similar in direction, as compared to corresponding phenotypic correlation coefficients. Seed yield plant^{-1} was observed to have a highly positive and significant correlations, both at phenotypic and genotypic levels, with number of branches plant^{-1}, number of pods plant^{-1}, pod length, number of seed pod^{-1} and 100-seed weight. But negative and significant correlation with days to 50 per cent flowering and days to maturity were estimated from the pooled analysis. Days to 50 per cent flowering revealed positive and significant correlation with days to maturity and number of branches plant^{-1}, but negative and significant correlation with number of pods plant^{-1}, pod length and 100-seed weight. Days to maturity had positive and significant correlation with number of branches plant^{-1}, but negative and significant correlation with number of pods plant^{-1}, pod length and 100-seed weight, whereas number of branches plant^{-1} expressed positive and significant correlation with number of pods plant^{-1}, pod length and number of seed pod^{-1}. Number of pods plant^{-1} expressed positive and significant correlation with pod length and number of seeds pod^{-1}. Pod length expressed significant and positive correlation with number of seeds pod^{-1} where as number of seeds pod^{-1} had negative and significant correlation with 100-seed weight. Protein content expressed negative and significant correlations with number of pods plant^{-1} at genotypic level only.

The correlations at the phenotypic level were similar in direction though lower in magnitude as compared to genotypic correlations. Variation in the magnitude of correlation coefficients was observed in the individual environments at both phenotypic and genotypic levels whereas, the direction in majority of the trait associations was similar both at phenotypic and genotypic levels. In several correlation studies conducted in common beans positive and significant correlation has been reported between seed yield plant^{-1} with number of pods plant^{-1} and number of seeds pod^{-1} (Dursun, 2007) with 100-seed weight (Coimbra *et al.*, 1998). However, Mirjana(2005) reported negative correlation of seed yield with 100-seed weight. Leliji *et al.* (1972) observed negative correlation of crude protein with pod plant^{-1} which is in agreement with the present results.

Apastolova *et al.* (2009) in their studies on common bean genotypes reported significant positive correlation of pod weight with seed yield and length of pods; number of pods with seed weight plant^{-1}; number of pods plant^{-1} with number of pod bearing nodes. Negative correlations were reported between height of the set on lowest pod with number of pods, number of branches and pods plant^{-1}. Johnson *et al.* (1955) proposed that besides genotypic and phenotypic variances, estimation of genotypic and phenotypic correlations are also important for the improvement of a trait.

Refrences

Al-Jibouri, K.A., Mider, R.A. and Robinson, H.F. 1958. Genotype and environmental variances and covariance in upland cotton crosses of inter-specific origin. *Agron. J.*, **50**: 633-637.

Apostolova, E., Dimova, D. and Svetleva, E. 2009. Correlation dependence between twenty one traits of some Bulgarian common bean genotypes. *Acta Horti.*, 830 : 191-197.

Box, G.E.P., Hunter, W.G. and Hunter, J.S. 1978. *Statistics for Experimenters*. New York : John Wiley.

Burton, G.W. and Devane, C.H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.*, **45** : 478-481.

Ceolin, A.C.G., Vidigal, M.C.G., Filho, P.S.V., Kvitschal, M.V., Gonela, A. and Scapim, C.A. 2007. Genetic divergence of the common bean (*Phaseolus vlgaris* L.) group carioca using morpho-agronomic traits by multivariate analysis. *Hereditas,* **144** : 1-9.

Chohata, R.K., Sharma, S.K. and Lal, C. 1994. Genetic divergence in micro sperma lentil. *Legume Res.*, **17**(2) : 132-134.

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

Coimbra, J.L.M., Carvalho, F.I.F., Hemps, S., Silva, S.A. and de-Carvalho, F.I.F. 1999. Adaptability and phenotypic stability of coloured bean (*Phaseolus vulgaris* L.) genotypes in three district environments. *Ciencia Rural,* **29**(3) : 441-448.

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

FAO. 2010. *FAO STAT, 2010*

Galton, F. 1989. Natural Inheritance, London.

Hanssen, C.H., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron. J.,* 48 : 268-272.

Johnson, H.F., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.*, **47** : 314-318.

Leliji, O.I., Dickson, M.H., Crow der, L.V. and Bourke, J.B. 1972. Inheritance of crude protein percentage and its correlation with seed yield in beans, *Phaseolus vulgaris* L. *Crop Sci.,***12** : 168-171.

Mahalanobis, P.C. 1936. On test and measure of group divergence. *J. Asiatic Society*, Bengal 26 : 541-588.

Mirjana, V. 2005. Principal Component Analysis of Dry Bean Collection. Bean *Improv. Corporative* 48 : 16-17.

Panse, V.G. 1957. Genetic of quantitative characters in relation to plant breeding. *Indian J. Genet.*,**17** : 318-328.

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

Rao, C.R. 1952. Advanced Statistical methods in Biometric Research. John Wiley and Sons, Inc., New York.

Rao, C.R. 1960. Multivariate analysis : An indispensable tool in statistical and in applied research. *Sankhya,* **22** : 317-338.

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

Sarma, M.K., Agarwal, R.K. and Richaria, A.K. 1997. Genetic diversity in rice under rainfed upland and irrigated ecosystems. *ORYZA* 34 : 19-24.

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

Singh, R.K. and Choudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Revised Ed. Kalyani Publishers, Ludhiana, New Delhi.

Table 1.Classification of the common bean genotypes into different clusters on the basis of divergence (Pooled over environments)

Cluster	No. of genotypes	Germplasm name
I	23	PBG-03, PBG-13,PBG-12, PBG-14, PBG-20, PBG-01, PBG-07, PBG-09, PBG-22 PBG-21,PBG-02, PBG-19 PBG-16,PBG-08,PBG-11, PBG-04, SKUA-R-01 PBG-18, PBG-15, PBG-05 PBG-06, PBG-17, SKUA-R-19
II	51	PBG-34, SKUA-R-11, PBG-33, SKUA-R-09, SKUA-R-17, PBG-31, SKUA-R-32, SKUA-R-36, PBG-27, Shalimar Rajmash-1, SKUA-R-21, SKUA-R-05, SKUA-R-34, SKUA-R-06, SKUA-R-22, SKUA-R-26, SKUA-R-27, PBG-26, SKUA-R-30, PBG-36, SKUA-R-07, SKUA-R-14, Canadian Red, SKUA-R-02, SKUA-R-03, PBG-37, SKUA-R-24 SKUA-R-23, SKUA-R-29, PBG-24, SKUA-R-10, SKUA-R-20, SKUA-R-25, SKUA-R-18, PBG-10, SKUA-R-28, SKUA-R-12, SKUA-R-31, PBG-25, SKUA-R-13, PBG-35, PBG-28 , SKUA-R-35, SKUA-R-08, SKUA-R-04, PBG-32, PBG-23, SKUA-R-33, SKUA-R-15, SKUA-R-16, PBG-30
III	1	PBG-29

Table 2. Mean intra and inter-cluster distance (D^2) among common bean (*Phaseolus vulgaris* L.) genotypes (Pooled over environments)

Cluster No.	Cluster I	Cluster II	Cluster II
Cluster I	364907.50	3513124.00	11913160.00
Cluster II	-	455080.50	3001391.00
Cluster III	-	-	0.00

Table 3 . Cluster means for different traits in common bean (*Phaseolus vulgaris* L.) genotypes (Pooled over environments)

Cluster No.	No. of genotypes in the cluster	Days to 50% flowering	Days to maturity	No. of branches plant^{-1}	Pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100-seed weight (g)	Seed yield plant^{-1} (g)	Protein content (%)
I	23	64.70	142.53	9.37	6.87	8.13	4.45	27.62	8.52	22.15
II	51	53.55	106.71	9.27	9.19	9.58	4.63	35.53	15.18	22.04
III	01	40.19	73.12	9.91	11.03	13.10	6.21	28.10	19.24	21.28

Table 4. Pooled Analysis of variance for morphological, maturity, quality, yield and yield component traits of the common bean (*Phaseolus vulgaris* L) genotypes

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Number of branches plant^{-1}	Number of pods plant^{-1}	Pod length (cm)	Number of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1}	Protein content (%)
Environments	2	348.31**	868.00**	24.10**	27.919**	22.45**	13.988**	28.43**	334.88**	100.43*
Replications	2	117.19**	285.50**	9.25**	10.64**	6.93**	6.93**	8.75*	101.71**	36.97*
Treatment	74	458.53**	3204.47**	8.74**	31.05**	12.16**	5.48**	567.76**	203.21**	28.60**
Environment x treatment	148	5.33**	17.92**	3.61**	4.75**	2.44	1.30**	3.34**	7.53**	4.36**
Error	450	2.03	3.00	2.89	2.16	1.73	0.81	2.04	1.87	1.30

Table 5.Pooled estimates of variability parametrs for different morphological, maturity, quality, yield and yield component traits in common bean (*Phaseolus vulgaris* L.)

Parameter	Days to flowering	Days to maturity	No. of branches/ plant	Pods/plant	Pod length	Seed yield/plant	100-Seed Weight	Seed yield/plant	Protein content
Mean	55.46	115.43	9.65	8.80	9.66	4.84	33.34	14.29	21.36
Range	39.80-67.53	71.81-152.67	7.16-12.00	5.14-13.76	6.84-13.57	3.52-7.35	20.22-54.93	6.11-33.15	17.13-25.01
PCV	12.97	16.45	10.22	23.00	13.21	18.67	23.89	39.90	9.50
GCV	12.75	16.30	7.82	19.42	10.76	14.09	23.75	38.78	7.68
Heritability (bs)	0.97	0.98	0.55	0.71	0.66	0.56	0.98	0.94	0.70
Genetic advance	14.38	38.21	1.15	2.96	1.73	1.04	16.08	11.04	2.81
Expected genetic gain (GA as % of mean)	25.92	33.10	11.91	33.63	17.90	21.48	48.23	77.25	13.15

Table 6 .Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for morphological, maturity, yield, yield attributing and quality traits in the common bean (*Phaseolus vulgaris* L.) genotypes (Pooled over environments)

Traits	Days to 50% flowering	Days to maturity	No. of branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	Number of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Protein content (%)
Days to 50% flowering	-	0.9375**	0.3150**	-0.4276**	-0.4200**	0.0437	-0.4937**	-0.5290**	-0.0543
Days to maturity	0.9298**	-	0.3028**	-0.4793**	-0.3627**	0.0355	-0.4794**	-0.5241**	-0.0067
No. of branches plant^{-1}	0.2485*	0.2468*	-	0.3389**	0.2267*	0.4239**	-0.2213*	0.2882**	0.0454
No. of pods plant $^{-1}$	-0.4245**	-0.4732**	0.3484**	-	0.5891**	0.4846**	0.0629	0.8444**	-0.2042*
Pod length (cm)	-0.4088**	-0.3522**	0.2327*	0.5654**	-	0.5836**	0.0931	0.6779***	-0.1632
No. of seeds pod^{-1}	0.0347	0.2120	0.3732**	0.4399**	0.5276**	-	-0.4755**	0.4256**	-0.1672
100 seed weight (g)	-0.4899**	-0.4772**	-0.1930	0.0667	0.00916	-0.4340**	-	0.4462**	0.0757
Seed yield plant^{-1} (g)	-0.5248**	-0.5180**	0.2942**	0.8431**	0.6328**	0.4010**	0.4409**	-	-0.1105
Protein content (%)	-0.0445	-0.0083	-0.0298	-0.1840	-0.1438	-0.1364	0.0711	-0.0979	-

* Significant at p=0.05; ** significant at p=0.01

Table 7. Per cent contribution of different morphological traits towards total divergence among common bean (*Phaseolus vulgaris* L.) genotypes

Traits	Number of times appearing first in the rank	Percent contribution towards total divergence among the material studied
Days to 50% flowering	290	10.46
Days to maturity	625	22.52
Number of branches	186	6.71
Number of pods plant $^{-1}$	203	7.34
Pod length (cm)	133	4.79
Number of seeds pod^{-1}	271	9.74
100 seed weight (g)	406	14.63
Seed yield plant^{-1} (g)	311	11.21
Protein content (%)	350	12.60
Total	**2775**	**100.00**