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Morphological characterization of common bean (Phaseolus vulgaris L.) genotypes grown in Kashmir Valley

Amir B. Wani[1], Irtiza[2], S. A. Mir[3]

[1]*Division of Plant Biotechnology SKUAST-K, Shalimar (India)*
[2]*Division of Basic Science & Humanities SKUAST-K, Shalimar (India)*
[3]*Division of Statistics SKUAST-K, Shalimar (India)*

ABSTRACT

Experimental material composed of 10 genotypes of common bean (Phaseolus vulgaris L.) { WB-494, SR-1, WB-939, WB-399, WB-640, WB-375, WB-967, WB-359, WB-335 & WB-933*}selected for extensive studies like morphological characterization, estimation of genetic variability and other genetic parameters, presence of genetic diversity at phenotypic. The experiment was conducted at Research Farm, SKUAST-K, Shalimar, Srinagar during 2014.*

Morphological traits of qualitative nature viz., growth habit, flower colour, days to 50% flowering, days to maturity, no. of pods plant^{-1}, no. of seeds pod^{-1}, seed colour, 100 seed weight and grain yield (q ha^{-1}) were analyzed which indicated presence of sufficient variability with respect to their traits. Analysis of variance revealed presence of significant genetic variation among these genotypes for all the traits studied. Genotypic coefficient of variation (GCV) was high for 100 seed weight, yield ha^{-1}; moderate for no of pods plant^{-1} and for no of seeds pod^{-1} and low for 50% flowering and for days to maturity. For all the traits, estimates of phenotypic coefficient of variation (PCV) were higher in magnitude than the corresponding estimates of genotypic coefficient of variation (GCV), indicating the presence of environmental effect. Heritability estimates (broad sense) were high for 100 seed weight, yield ha^{-1}.

Estimation of genetic divergence using Mahalanobis D^2 among bean genotypes was highly significant, while these genotypes got grouped into 4 clusters with cluster I having maximum of 4 genotypes and cluster III was monogenotypic. Inter-cluster distance was maximum between cluster-I and cluster-IV followed by cluster-II and cluster-IV. The maximum divergence came from yield ha $^{-1}$ (55.56%).

Keywords: ANOVA, common bean, D^2, morphological traits, qualitative nature

I.INTRODUCTION

Common bean (*Phaseolus vulgaris* L.), locally known as "Rajmash" is one of the most widely grown grain legume crop around the world [1]covering an area of about 28.78 million hectares with an annual production of 23.14 million tonnes [2]. In India, it is cultivated both as dry and snap bean in an area of about 9.1 million hectares with an annual production of 3.63 million tonnes and average yield of 0.363 tonnes [2]. Common bean is a major commercial pulse crop in the north-western Himalayan region of India and is known for its quality. The crop is mainly cultivated by the small and marginal hill farmers of Himachal Pradesh, Jammu & Kashmir and Uttrakhand over an area of about 26.75 thousand hectares. North-Western Indian Himalayan state of Jammu and Kashmir (33°17′-37° 20′ N latitude, 73°25′-80°30′ E longitude) exhibits a great variation in the physiographic features and agroclimates at macro and micro-level, involving cold arid, temperate, intermediate and sub-tropical zones, within a small geographical area of 2.22 lakh sq. km. indicating the inherent agricultural potential of the state [3].

II. MATERIALS AND METHODS

Experimental material composed of 10 genotypes of common bean (*Phaseolus vulgaris* L.) selected for extensive studies like morphological characterization, estimation of genetic variability and other genetic parameters, presence of genetic diversity at phenotypic. The experiment was conducted at Research Farm, SKUAST-K, Shalimar, Srinagar during 2014. The Plant material was studied for following Morphological characters as per method suggested by NBPGR, New Delhi.

a) Growth habit

This observation was recorded before maturity under the following codes:

Codes
1 = Determinate
2 = Indeterminate
3 = Semi-determinate

b) Flower color

The color of standard petals was recorded at full flowering stage under following code:

Code
1 = Creamish white
2 = White
3 = Purple
4 = Pinkish white
4 = Light violet

c) Days to 50% flowering

Number of days taken from the date of sowing to the date on which nearly fifty percent plants completed the opening of first flower.

d) Days to maturity

Number of days taken from the seed sowing to complete yellowing of 80 percent plants in each experimental plot.

e) No. of pods plant^{-1}

The total number of pods per plant were counted and recorded, when the flowering was complete.

f) No. of seeds pod^{-1}

The number of seeds were counted from the randomly selected pods in each plant and average was calculated.

g) Seed colour

This observation was recorded after the harvesting of the crop.

Code

1 = Dark red
2 = Creamy or grey white
3 = Black
4 = White
5 = Purple
6 = any other (specify)

h) 100 seed weight

100 seed weight of three randomly drawn samples of sun dried seeds from each experimental plot was weighed in grams and averaged.

i) Grain yield ha^{-1}

Grain yield ha^{-1} was calculated for each genotype from the yield of each genotype.

III.EXPERIMENTAL FINDINGS

Growth habit

Description of the growth habit revealed that six genotypes (WB-494, SR-1, WB-399, WB-640, WB-967 AND WB-933) were determinate and 4(WB-939, WB-375, WB-359, WB-335) were indeterminate type.

Flower colour

It was observed that two genotypes (WB-939, WB-640) had pinkish white flower colour and 8 genotypes (WB-494, SR-1, WB-399, WB-640, WB-375, WB-967, WB-359, WB-335 AND WB-933) had white flower colour.

Seed colour

Two genotypes (WB-933, and WB-967) had dark red seed colour, genotype (SR-1) had maroon seed colour, genotypes (WB-494, WB-399) had grey seed colour, genotypes (WB-640, WB-359, AND WB-355) had white seed colour, genotypes (WB-939 AND WB-375) has black seed colour.

Genotypes	Growth habit	Seed colour	Flower colour
WB-494	Bush type	Grey	White
SR-1	Bush type	Maroon	White
WB-939	Pole type	Black	Pink
WB-399	Bush type	Grey	White
WB-640	Bush type	White	Pink
WB-375	Pole type	Black	White
WB-967	Bush type	Red	White
WB-359	Pole type	White	White
WB-335	Pole type	White	Whitish yellow
WB-933	Bush type	Red	White

Analysis of variance

Perusal of the TABLE 1 revealed that the genotypes tested displayed significant variability for all the traits studied.

Mean, CD @ 5%, phenotypic and genotypic coefficient of variation, heritability (broad sense) and expected genetic gain

The estimates were computed on a single analysis data (TABLE 2). Days to 50% flowering with a mean of 45.45 had CD @ 5% of 0 , days to maturity had CD @ 5% of 0 and a mean of 80.68, no of pods plant^{-1} had CD @ 5% of 0 and a mean of 5.81, no of seeds pod^{-1} had CD@5% of 0 and a mean of 4.10, 100 seed weight had CD @ 5% of 4.34 and a mean of 38.64, yield (q ha^{-1}) had CD @ 5% of 0.18 and a mean of 4.53.

The estimates of phenotypic coefficient of variation were observed to be higher in magnitude than the corresponding estimates of genotypic coefficient of variation. The magnitude of phenotypic and genotypic coefficient of variation (TABLE 3) for 50% flowering and for days to maturity was low (<10.0%) in the materials; it was moderate (10-20%) for no of pods plant^{-1} and for no of seeds pod^{-1}, and high (>20%) for 100 seed weight, yield (q ha^{-1}).

Estimates of heritability (broad sense) was low (<10%) for 50% flowering, no of pods plant^{-1} and no of seeds pod^{-1} in environment taken in (TABLE 4). It was moderate (10-60%) for days to maturity, and it was high

(>60%) for 100 seed weight, yield (q ha^{-1}). Very high value of heritability of 99.62 per cent was exhibited by yield/hac whereas, 50% flowering exhibited -14.80 per cent in the same environment.

Genetic advance was estimated at 5% of selection intensity (TABLE 5) and concerted into genetic gain (% of mean). The estimate revealed that the expected genetic gain was high (30%) for 100 seed weight, yield (q ha^{-1}). Whereas, it was low (<20%) for 50% flowering, No. of pods plant^{-1}, No. of seeds plant $^{-1}$ and for days to maturity in the same environment.

Table 1: Analysis of variance for yield and yield component traits among 10 genotypes of common beans (*Phaseolus vulgaris* L.)

Source of variation	d.f	Mean squares					
		Days to 50% flowering	Days to maturity	No of pods plant^{-1}	No of seeds plant^{-1}	100 seed weight (g)	Yield ha^{-1}
Replication	2	1.69	1.95	1.86	0.02	20.35	0.04*
Treatment	9	1.75	3.81	0.80	0.21	249.26 **	3.51**
Error	18	2.86	2.14	0.74	0.16	6.41	0.01

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

Table 2: Magnitude of variability for yield and yield component traits in 10 common beans (*Phaseolus vulgaris* L.) genotypes

Trait	Mean	C D @ 5%
50% flowering	45.45	-
Days to maturity	80.68	-
No. of pods plant^{-1}	5.81	-
No. of seeds pod^{-1}	4.10	-
100 seed wt.	38.64	4.34
Yield ha^{-1}	4.53	0.18

Table 3: Phenotypic and genotypic coefficient of variation for yield and yield component traits in 10 common bean (*Phaseolus vulgaris* L.) genotypes

Traits	PCV	GCV
50% flowering	3.4781	1.3381
Days to maturity	2.0359	0.9241
No of pods plant^{-1}	15.0517	2.4237
No of seed pod^{-1}	10.4580	3.1418

100 seed wt.	24.1899	23.2850
Yield ha^{-1}	23.9802	23.8653

Table 4: Heritability, genetic advance and expected genetic gain for yield and yield component in 10 common beans (*Phaseolus vulgaris* L.) genotypes

Traits	Heritability (broad sense)	Genetic advance	Expected genetic gain (%)
50% flowering	-0.15	-0.48	-1.06
Days to maturity	0.20	0.69	0.86
No of pods plant^{-1}	0.02	0.04	0.80
No of seeds pod^{-1}	0.090	0.07	1.94
100 seed wt.	0.92	17.84	46.17
Yield ha^{-1}	0.99	2.21	48.92

Estimates of phenotypic and genotypic correlation coefficient

Correlation coefficient were estimated at the phenotypic and genotypic levels among quality, yield and yield component traits in same environment (TABLE 5). Genotypic correlation coefficient, were by and large, higher in magnitude, though similar in direction than their corresponding correlation coefficients at phenotypic level.

50% flowering exhibited positive and significant correlation with no. of pods plant^{-1}, no. of seeds pod^{-1} at phenotypic level only but exhibited negative and significant correlation with days to maturity, 100 seed weight(g), yield ha^{-1} (q ha^{-1}) at both levels. Days to maturity exhibited positive and significant correlation with, 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels and had negative and significant correlation with no. of pods plant^{-1} and no. of seeds pod^{-1} at genotypic level. No. of pods plant^{-1} exhibited positive and significant correlation with 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels and had negative and significant correlation with no. of seeds plant^{-1} at both levels. No. of seeds pod^{-1} had positive and significant correlation with 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels. 100 seed weight exhibited positive and significant correlation with yield ha^{-1} (q ha^{-1}). Yield ha^{-1} (q ha^{-1}) exhibited positive and significant correlation of all traits at both levels.

Table 5: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient for yield and yield traits in 10 common beans (*Phaseolus vulgaris* L.) genotypes

Trait	50% flowering	Days to maturity	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed wt (g)	Yield (q ha^{-1})
50% flowering		-1.04	-0.08	0.96	-0.24	-0.07

Days to maturity	-1.07		-0.51	-2.53	0.39	0.31
No of pods plant^{-1}	0.28	0.26		-3.39	1.48	2.33
No of seeds pod^{-1}	0.09	-0.04	-0.06		1.34	1.20
100 seed wt (g)	-2.67	3.17	2.27	1.76		0.95
Yield ha^{-1} (q ha^{-1})	-0.09	0.26	0.37	0.18	9.54	

*, **significant at 5% and 1% level of significance respectively

Estimation of genetic divergence

Genetic divergence was estimated in 10 common beans genotypes grown in the same environment. Based on the performance of the genotypes in the same environment, 10 genotypes got grouped into 4 clusters (TABLE 6) as per Mahalanobis D^2 analysis employing Tocher's method [4]. Cluster-I and cluster-II expressed maximum (7) genotypes whereas, cluster-IV was having 2 genotypes and cluster-III was mono-genotypic.

The mean intra and inter-cluster distance (D^2) values for the same environment (TABLE 7) revealed that the cluster-IV has the highest intra-cluster distance (D^2) value of (92.52) followed by cluster-II (38.78) then by cluster-I (10.44). The inter-cluster distance (D^2) value was highest (853.03) between cluster-I and cluster-IV followed by cluster-II and cluster-IV (627.50), cluster-III and cluster-IV (613.38), cluster-I and cluster-II (443.57) cluster- II and cluster III (128.58). The minimum inter-cluster distance was observed between cluster-I and cluster-III (103.13).

Cluster means of different traits in the same environment (TABLE 8) revealed that the magnitude of differences among the mean of traits for clusters was significant. The range of variation in cluster means for 50% flowering was 45.49 in cluster-II to 45.93 in cluster III. Mean days to maturity ranged from 80.18 in cluster-I to 81.40 in cluster-IV. Mean no of pods plant $^{-1}$ ranged from 5.40 in cluster-I to 6.27 in cluster-II. Mean no of seeds pod^{-1} ranged from 3.70 in cluster-IV to 4.00 in cluster-III. Mean 100 seed weight (g) ranged from 29.71 in cluster-I to 46.10 in cluster-II. Mean yield ha^{-1} (q ha^{-1}) ranged from 3.42 in cluster-I to 5.68 in cluster-II.

The per cent contribution of a trait towards the total divergence (TABLE 9) revealed that the yield (q ha^{-1}) was the main factor contributing to total divergence accounting (55.56%) in the same environment. The minimum contribution (0%) was from 50% flowering, no of pods plant^{-1} and from no of seeds plant^{-1}. The contribution from rest traits were (2.22%) for days to maturity.

Table 6: Distribution of 10 common beans (*Phaseolus vulgaris* L.) genotypes into clusters based on D^2 statistics (Clustering by Tocher Method)

Cluster	No of genotypes	Variety/accession No. of genotypes
1	4	WB-399, WB-640, WB-359 & WB-375
2	3	WB-494, WB-933 & WB-939
3	1	WB-335

4	2	SR-1 & WB-967

Table 7: Average inter-cluster and intra-cluster D^2 values among 10 common beans (*Phaseolus vulgaris* L.) genotypes

Cluster	I	II	III	IV
I	10.44	443.57	103.13	853.03
II		38.78	128.58	627.50
III			0.00	613.38
IV				92.52

Table 8: Cluster means for yield and yield component traits in 10 common beans (*Phaseolus vulgaris* L.) genotypes

Cluster	50% flowering	Days to maturity	No. of pods $plant^{-1}$	No. of seeds pod^{-1}	100 seed wt (g)	Yield ha^{-1} (q ha^{-1})
I	45.62	80.18	5.40	4.33	29.71	3.42
II	45.49	80.84	6.27	4.09	46.10	5.68
III	45.93	80.80	5.80	4.00	39.70	4.58
IV	44.83	81.40	5.97	3.70	44.78	5.01

Table 9: Contribution of different traits to total divergence in common beans (*Phaseolus vulgaris* L.)

S. No.	Trait	Times ranked I^{st}	Contribution (%)
1	50% flowering		0%
2	Days to maturity	1	2.22%
3	No of pods $plant^{-1}$		0%
4	No of seeds pod^{-1}		0%
5	100 seed wt	3	6.67%
6	Yield ha^{-1}	25	55.56%

Discussion and Conclusion

The results of the following study are discussed under the following heads:

Morphological characterization

Description of the growth habit revealed that six genotypes (WB-494, SR-1, WB-399, WB-640, WB-967 and WB-933) were determinate and 4(WB-939, WB-375, WB-359, WB-335) were indeterminate type. It was observed that two genotypes (WB-939, WB-640) had pinkish white flower colour and 8 genotypes (WB-494, SR-1, WB-399, WB-640, WB-375, WB-967, WB-359, WB-335 AND WB-933) had white flower colour. Two genotypes (WB-933, and WB-967) had dark red seed colour, genotype (SR-1) had maroon seed colour, genotypes (WB-494, WB-399) had grey seed colour, genotypes (WB-640, WB-359, AND WB-355) had white seed colour, genotypes (WB-939 AND WB-375) has black seed colour.

Genetic variability, heritability and expected genetic gain

In the present study 10 common bean genotypes were evaluated for presence of genetic variability, estimation of genetic parameters and genetic diversity. Analysis of quantitative characters (TABLE 1) revealed presence of significant genetic variation for all the characters.

Perusal of TABLE 2 revealed that the Days to 50% flowering with a mean of 45.45 had CD @ 5% of 0 , days to maturity had CD @ 5% of 0 and a mean of 80.68, no of pods plant^{-1} had CD @ 5% of 0 and a mean of 5.81, number of seeds pod^{-1} had C D@5% of 0 and a mean of 4.10, 100 seed weight had CD @ 5% of 4.34 and a mean of 38.64, yield ha^{-1} had CD @ 5% of 0.18 and a mean of 4.53.

Coefficient of variation (both phenotypic and genotypic) to be higher in magnitude than the corresponding estimates of genotypic coefficient of variation. The magnitude of phenotypic and genotypic coefficient of variation (TABLE 3) for 50% flowering and for days to maturity was low (<10.0%) in the materials; it was moderate (10-20%) for no. of pods plant^{-1} and for no. of seeds pod^{-1}, and high (>20%) for 100 seed weight, yield ha^{-1}. The similar results were also reported by [5], [6], [7], [8], [9] and [10].

Estimates of heritability (broad sense) was low (<10%) for 50% flowering, no of pods plant^{-1} and no of seeds pod^{-1} (TABLE 4). It was moderate (10-60%) for days to maturity, and it was high (>60%) for 100 seed weight, yield ha^{-1}. Very high value of heritability (99.62 per cent) was exhibited by yield/hac whereas, 50% flowering exhibited -14.80 per cent in the same environment. Results reported by [11] and [12] are supportive to present study. [13] observed high heritability for days to maturity and 100 seed weight, [14] reported high heritability for days to flowering and days to maturity and seed yield. However, [8] reported relative moderate heritability estimate for 100 seed weight. [9] observed high heritability for days to flowering, 100 seed weight and days to maturity.

The expected genetic gain was high (30%) for 100 seed weight, yield ha^{-1}. Whereas, it was low (<20%) for 50% flowering, no of pods plant^{-1}, no of seeds plant $^{-1}$ and for days to maturity in the same environment.

IV.GENOTYPIC AND PHENOTYPIC CORRELATIONS

The practical utility of selection of a given character as measure of improving another character depends on extent to which they are related and this relation depends on genotypic and phenotypic correlation of all characters. Correlation coefficient is important in plant breeding because it measures the degree of association (genetic and non-genetic) between two or more traits. Progress of selection, therefore, depends on nature and magnitude of inter-relationship existing among characters of economic importance and the ones that contribute to their performance directly or indirectly. Indirect selection methods make it possible to select individuals that are likely to be superior and enable the breeder to eliminate material that may probably exhibit poor performance.

In the present study, the data revealed 50% flowering exhibited positive and significant correlation with no. of pods plant^{-1}, no. of seeds pod^{-1} at phenotypic level only but exhibited negative and significant correlation with days to maturity, 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both genotypic and phenotypic levels. Days to maturity exhibited positive and significant correlation with, 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels and had negative and significant correlation with no. of pods plant^{-1} and no. of seeds pod^{-1} at genotypic level. No. of pods plant^{-1} exhibited positive and significant correlation with 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels and had negative and significant correlation with no. of seeds plant^{-1} at both levels. No. of seeds pod^{-1} had positive and significant correlation with 100 seed weight (g), yield ha^{-1} (q ha^{-1}) at both levels. 100 seed weight exhibited positive and significant correlation with yield ha^{-1} (q ha^{-1}). Yield ha^{-1} (q ha^{-1}) exhibited positive and significant correlation of all traits at both levels. [15]; [16]; [8] and [10]. 100 seed weight exhibited positive and significant correlation with yield ha^{-1} (q ha^{-1}). Yield ha^{-1} (q ha^{-1}) exhibited positive and significant correlation of all traits at both levels

The correlation at genotypic level were by and large similar in direction though higher in magnitude as compared to phenotypic correlation. Variation in magnitude of correlation coefficient was observed in the same environment at both levels, whereas, direction in majority of character associations was similar, both at genotypic and phenotypic level. Higher magnitude of genotypic correlation helps in selection of genetically controlled characters and gives a better response for grain yield improvement that would be expected on the basis of phenotypic associations alone.

V.GENETIC DIVERSITY

Analysis of genetic diversity is a platform for stratified sampling of breeding population and to identify the genotypes for hybridization [17]. 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 [18] is now well established in plant breeding. The use of Mahalanobis D^2 statistic for estimating genetic divergence have been emphasized by many workers [19]; [20]; [21] because it permits precise comparison among all the possible pair of populations in any group before effecting actual crosses. [19] hypothesized that [22] generalized distance as a measure of metric distance between population centroids could be very useful multivariate statistical tool for effective discrimination among parents, as high yield pattern, with greater genetic diversity and expected to develop productive hybrids. 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 multi-variate analysis in selecting genetically divergent parents, for successful hybridization programme has been discussed by [23], [24], [25].

In the present study 10 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 of divergence revealed that the values of 'V' static (measuring Wilk's criteria) were high and significant, indicating presence of substantial genetic diversity in the genotypes as expressed in the same environment.

Classification of genotypes led to the formation of 4 clusters (TABLE 6). Cluster I comprised of maximum genotypes (4) followed by cluster II (3). The remaining two clusters contain 1 and 2 genotypes respectively.

The pattern of group constellations in the present study, 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.

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.

The inter-cluster distance (D^2) (TABLE 7) value was highest (853.03) between cluster-I and cluster-IV followed by cluster-II and cluster-IV (627.50), cluster-III and cluster-IV (613.38), cluster-I and cluster-II (443.57) cluster-II and cluster III (128.58). The high magnitude of D^2 values in the above case showed that genotypes in different clusters are genetically more divergent probably due to geographical and reproductive isolation and may provide basis for consideration in hybridization programme. The minimum inter-cluster distance was observed between cluster-I and cluster-III (103.13). The minimum value indicates narrow genetic diversity among the genotypes. The similarity in the base material from which they have been evolved might be the cause of genetic uniformity. Inter-crossing of genotypes from divergent groups would lead to the greater opportunity for crossing-over, which release hidden variability by breaking linkage. Emphasis should be laid on characters contributing maximum D values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. This has been also reported by [26].

The data (TABLE 8) revealed that the magnitude of differences among the mean of traits for clusters was significant. The range of variation in cluster means for 50% flowering was 45.49 in cluster-II to 45.93 in cluster III. Mean days to maturity ranged from 80.18 in cluster-I to 81.40 in cluster-IV. Mean no. of pods plant $^{-1}$ ranged from 5.40 in cluster-I to 6.27 in cluster-II. Mean no. of seeds pod^{-1} ranged from 3.70 in cluster-IV to 4.00 in cluster-III. Mean 100 seed weight (g) ranged from 29.71 in cluster-I to 46.10 in cluster-II. Mean yield ha^{-1} (q ha^{-1}) ranged from 3.42 in cluster-I to 5.68 in cluster-II. The results clearly indicate that cluster II exhibited highest mean performance for all the traits studied. Cluster means of different clusters identify the characters to be chosen for hybridization. Hence, it is worthy to note that in calculating the cluster means, the superiority of particular genotype with respect to a given character gets diluted by other genotypes that are related and grouped in the same cluster but which are inferior or intermediary for that character in question. Hence, apart from selecting genotypes from clusters which have higher inter-cluster distance for hybridization, we should think of selecting parents based on extent of divergence with respect to a particular character of interest. It means that if a breeder's intention is to improve seed yield, one can select parents which are highly divergent with respect to these characters.

[27] proposed that traits contributing maximum towards D^2 value need to be given great emphasis for deciding the clusters to be chosen for the purpose of further selection and choice of parents for hybridization. The contribution of each character towards genetic diversity was given in (TABLE 9) revealed that the yield ha^{-1} was the main factor contributing to total divergence accounting (55.56%). Similar results were also reported by [28], [24], [29] and [30].

Genotypes under study

Genotypes	Accession no.	Country of origin
WB-494NGB	13468-2	Sweden
WB-939G	193	Turkey
WB-399PHA	12179	Russia
WB-640PAS	276	Kashmir India
WB-375	PHA-12122	Mexico
WB-967G	1318	Mexico
WB-335PHA	13701	Russia
WB-933G	701	
SR-1		Kashmir India
WB-359		Not known

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