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DUS Characterization of Rajmash (*Phaseolus vulgare* L.) Genotypes for Morpho-physiological Traits under Rainfed Conditions

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ABSTRACT

Background: The current investigation was carried out in the year 2021-22 at Dryland Agriculture Research Station (DARS), Budgam. The experiment was laid out in randomized complete block design with three replications in field and completely randomized design (CRD) *in vitro* conditions for evaluating different traits of genotypes. DUS characterization was conducted as per the DUS testing guidelines by Protection of Plant Varieties and Farmers Act, Authority, Descriptors for rajmash (*Phaseolus vulgaris* L.) GOI, New Delhi [reproduced from Plant Variety Journal of India. Vol.1 (1), 2007].

Methods: The observations were recorded on 18 DUS characters including morphological and quality attributes and physiological characters. For all the features studied, the analysis of variance for morpho-physiological and qualitative attributes found significant differences, providing adequate chance to select the genotypes with desired qualities. DUS traits were examined in accordance with the descriptor, “state” and “code” provided for each character.

Result: The observed range of variation were recorded for different traits for different genotypes. Cluster analysis for morphological, maturity, yield and quality characteristics arranged the rajmash genotypes into 11 clusters, as per Mahalanobis D^2 analysis using Tocher’s method with cluster III having the maximum number of genotypes (8), followed by cluster I, II, IV and V with 6 genotypes, 2 genotypes were grouped in cluster VII and XI and the remaining clusters with 1 genotype each. Diversity analysis showed grouping of genotypes in 11 clusters, which will help in selection of genetically divergent parents for exploitation in hybridization programme and would constitute an essential gene pool for future breeding programme.

Key words: DUS testing, Morphological and quality attributes, Physiological, Rajmash.

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.), a member of the Leguminosea family, is the most important legume crop for direct human consumption with a higher yield than gram and pealt boasts high nutrient content, as noted by (Mwanauta *et al*., 2015). This crop holds the second position in terms of production and cultivated area, primarily due to its early maturity, ability to be intercropped with other crops such as maize, soil fertility enhancement, suitability as animal feed, and its potential for commercial applications, as highlighted by (Demelash, 2018). The common bean is a diploid plant with a chromosome count of 2n=2x=22. It is predominantly a self-pollinating annual species. It plays a significant role in global nutrition, providing 15% of the world’s protein requirements and 30% of its caloric intake when its seeds are consumed. Moreover, it constitutes approximately 50% of all grain legumes consumed on a global scale, as outlined in (McConnell’s, 2010). Common bean is major crop in Jammu and Kashmir, particularly in the rain-fed highlands, where it is farmed under a maize-bean intercropping system across an area of around 30 thousand hectares, with a yield of approximately 17 thousand tonnes and a productivity of approximately 0.56 t ha^{-1}. Common bean is grown over an area of around 2 thousand hectares in Kashmir valley, with a production of about 1.6 thousand tonnes and yield of about 0.8 t ha^{-1} (Saba *et al.,* 2016).

The growing season for beans is 80-100 days and the crop requires 350-500 mm of water depending on soil depth, environment and genotype. The bean crop is divided

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into ten stages, five for vegetative growth and five for reproductive development. Germination (V0), emergence (V1), primary leaves (V2), first trifoliate leaf (V3), third trifoliate leaf (V4) are the vegetative stages. Pre-flowering (R5), flowering (R6), pod development (R7), pod filling (R8) and maturity (R9) are the reproductive stages (Miranda *et al*., 2021); (Cavalcante *et al*., 2022).

Numerous biotic and abiotic factors have an impact on bean yields and disease is the greatest barrier to bean production. Drought is one of the abiotic factor that could cause yields to drop by 10% to 100% (Polania *et al.,* 2016). Drought is the second largest contributor to crop yield decline behind diseases, affecting around 60% of the regions that produce beans (Begna, 2020). The French bean are rich source of calcium necessary for maintaining bone structure and overall health, iron essential for blood production, and various types of vitamin B, which have a positive impact on the nervous system, as highlighted by (Karasu and Oz, 2010). It also exhibits carminative properties to alleviate constipation and reparative properties to address diarrhoea, as noted by (Duke, 1981).

Protection of Plant Varieties and Farmers Rights (PPV &FR) act passed by government of India provides the registration of new variety of plant if it confirms to the criteria of Distinctness, Uniformity, and Stability (DUS) (Joshi *et al*., 2011). Regarding this act, DUS creates a description of the variety, using its pertinent characteristics that can be defined as a variety. The variety deemed to be distinct, uniform and stable, if its important characteristics remain unchanged after repeated propagation (Dutfield, 2012). Genetic diversity analysis may serve as a platform for a representative sampling of the breeding population and to identify the genotypes for hybridization Mohammadi and Prasana (2003). The Mahalanobis (1936) D^2 statistic is now well established in plant breeding as a way to group a sizable amount of possible genotypes into a small number of homogenous clusters. Many researchers (Murthy and Arunachalam, 1966; Singh and Bains, 1968) emphasize the use of the Mahalanobis D^2 statistic in several crops.

MATERIALS AND METHODS

The basic experimental material comprises of 40 genotypes *viz.,* SKAU-R-91, ALR-83, ALR-77, ALR-78, ALR-79, SR-1, ALR-27, SR-2, ALR-19, ALR-32, ALR-14, ALR-48, ALR-64, ALR-91, ALR-49, ALR-26, ALR-11, KDR-18, KDR-11, KDR-99, KDR-97, KDR-5, KDR-85, ALR-63, ALR-13, ALR-20, ALR-12, ALR-80, ALR-90, ALR-28, ALR-18, ALR-16, KDR-1, KDR-25, KDR-77, KDR-96, KDR-98, KDR-75, KDR-41, KDR-60. The experiment was conducted at Dryland Agriculture Research Station (DARS), Budgam for the field experiment under natural rainfed conditions and the laboratory experiment was laid at SKUAST-K (FoH), Shalimar, Srinagar during 2021-22. The altitude of the location is 1587 m above MSL with coordinates of 34.08°N of latitude and 74.83°E of longitude. Recommended agronomical practices were followed to ensure optimum plant stand. The characterization was carried out using 18 morpho-physiological descriptors (Table 1). Four types of assesments were followed which are., Visual assessment by observations of individual plants or parts of plants (VS), Visual assessment by a single observation of a group of plants or parts of plants (VG), Measurements of a number of individual plants or parts of plants (MS), and Measurements by a single observations of a group of plants or parts of plants (MG).

Data obtained throughout the investigation was examined using appropriate analytical techniques. Critical differences were used to compare the significant results. Randomized complete block design (RCBD) and complete randomize design (CRD) were employed in the current study for the field and laboratory experiments respectively. Frequency distribution will be used to analyze the pattern of variance for visually assessed traits. To evaluating the degree of genetic divergence among the test genotypes including quantitative features, Mahalanobis (1936) D^2 was used. Genotypes were grouped into various clusters using Torcher's technique (1952). Genetic distance between clusters is equal to the square root of average D^2. The scale proposed by the Roa (1952) was adopted for rating of the distance based on D^2 values (inter-cluster distance).

RESULTS AND DISCUSSION

DUS (Distinctiveness, Uniformity and Stability) characterization

The frequency of genotypes for several attributes is provided in the following Table 2 where, 40 genotypes of rajmash (*Phaseolus vulgaris* L.) were subjected to DUS (Distinctiveness, Uniformity and Stability) characterization in accordance with the recommendations provided by the DUS descriptor of PPV and FR Authority 2007, GOI, New Delhi. Forty (40) DUS traits were examined in accordance with the descriptor, "state" and "code" provided for each character. For various DUS characters, the frequency distribution of these genotypes is provided in (Table 2 and Plates 1-14).

The frequency of genotypes for several attributes reveals a substantial degree of variation. Analysis of data in Table 2 demonstrated that the "medium" flowering period (50-75 days) contributed to a frequency of (60%) for the genotypes with the highest flowering time, followed by "early" flowering period (<50 days) contributing to frequency of 40% and not any single genotype showed "late" or "very late" flowering.

For plant characters like growth habit, maximum genotypes were of "spreading" and "erect type" with a frequency of (47.50% each) and (5%) were "semi-erect" and the character *i.e.,* plant twining habit, maximum genotypes showed "Viny" type of twining habit with a frequency of (60%) and the rest genotypes showed "non-Viny" type of twining habit with a frequency of (40%). AlBallat and Al-Araby (2019) indicated a wide genetic variability for indeterminate growth habit traits among 27 accessions. Jan *et al*. (2021) also

Table 1: Table of characterization of Rajmash.

Characteristics	States	Note	Stage of observations	Types of assessments
Time of flowering	Early (<50 days)	3	50% plants with at least	VG
	Medium(50-75 days)	5	one open flower	
	Late (76-100 days)	7		
	Very late (> 100 days)	9		
Leaflet: Size (at the	Small	3	Peak flowering	MS
terminal leaflet ofMedium	5			
first flowering node)	Large	7		
Plant: Growth type	Erect	3	Peak flowering	VG
	Semi-erect	5		
	Spreading	7		
Plant: Twining habit	Viny	1	Peak flowering	VG
	Non-viny	9		
Plant: habit	Determinate	1	Peak flowering	VG
	Indeterminate	3		
Leaf: Intensity of green colour	Light	3	Peak flowering	VG
	Dark	7		
Leaf: Shape of central leaflet	Cordate	1	Peak flowering	VG
	Ovate	2		
	Rhombohedric	3		
	Hastate	4		
Flower: Colour of standard petal	White	1	Peak flowering	VG
	Yellow	2		
	Pink	3		
	Violet	4		
Flower: Outer surface	Striped	1	Peak flowering	VG
ofstandard petal	Nin-striped	3		
Pod: Curvature	Absent	1	Fully grown green pod	VG
	Medium	5		
	Strong	7		
Pod: Shape of cross	Cordate	1	Fully grown green pod	VG
Section (through seed)	Circular	2		
	Eight shaped	3		
	Oval	4		
Pod: Shape	Concave	1	Fully grown green pod	VG
(in relation tosuture)	S-shaped	2		
	Convex	3		
Pod: Shape of distal	Acute	3	Fully grown green pod	VG
part(excluding beak)	Acute to truncate	5		
	Truncate	7		
Pod: Colour	Pale green	1	Fully grown green pod	VG
	Green	2		
	Purple	3		
Pod: Stringiness	Absent	1	Fully grown green pod	VS
	Present	9		
Seed: Shape	Circular	1	Mature seed	VG
	Circular to elliptical	2		
	Elliptical	3		
	Kidney shaped	4		

Continous................

Table 1: Continue....

Table 1: Continue....

Seed: Size (weight of1000 seeds	Small (<250 g)	3	Mature seed	MG
	Medium (250-350 g)	5		
	Large (351-450 g)	7		
	Very large (>450 g)	9		
Seed:Testa colour	White	1	Mature seed	VG
	Brown	2		
	Red	3		
	Dark red	4		
	Black	5		

Table 2: Frequency distribution of DUS traits in rajmash (Phaseolus vulgaris L.) genotypes based on DUS descriptor of PPV and FR, GOI, New Delhi (2007).

Characteristics	States	Code	Absolute number	Frequency
Time of flowering	Early (<50 days)	3	16	40%
	Medium(50-75 days)	5	24	60%
	Late (76-100 days)	7	0	0%
	Very late (> 100 days)	9	0	0%
Leaflet: Size (at the terminal leaflet of first flowering node)	Small	3	25	62.50%
	Medium	5	9	22.50%
	Large	7	6	15%
Plant: Growth type	Erect	3	19	47.50%
	Semi-erect	5	2	5%
	Spreading	7	19	47.50%
Plant: Twining habit	Viny	1	24	60%
	Non-viny	9	16	40%
Plant: habit	Determinate	1	14	35%
	Indeterminate	3	26	65%
Leaf: Intensity of green colour	Light	3	26	65%
	Dark	7	14	35%
Leaf: Shape of central leaflet	Cordate	1	11	27.50%
	Ovate	2	15	37.50%
	Rhombohedric	3	6	15%
	Hastate	4	8	20%
Flower: Colour of standard petal	White	1	15	37.50%
	Yellow	2	10	25%
	Pink	3	14	35%
	Violet	4	1	2.50%
Flower: Outer surface of standard petal	Striped	1	21	52.50%
	Non-striped	3	19	47.50%
Pod: Curvature	Absent	1	10	25%
	Medium	5	23	57.50%
	Strong	7	7	17.50%
Pod: Shape of cross section(through seed)	Cordate	1	12	30%
	Circular	2	11	27.50%
	Eight shaped	3	6	15%
	Oval	4	11	27.50%
Pod: Shape (in relation tosuture)	Concave	1	28	70%
	S-shaped	2	0	0%
	Convex	3	12	30%
Pod: Shape of distal part(excluding beak)	Acute	3	10	25%
	Acute to truncate	5	16	40%
	Truncate	7	14	35%

Table 2: Continue....

Table 2: Continue....

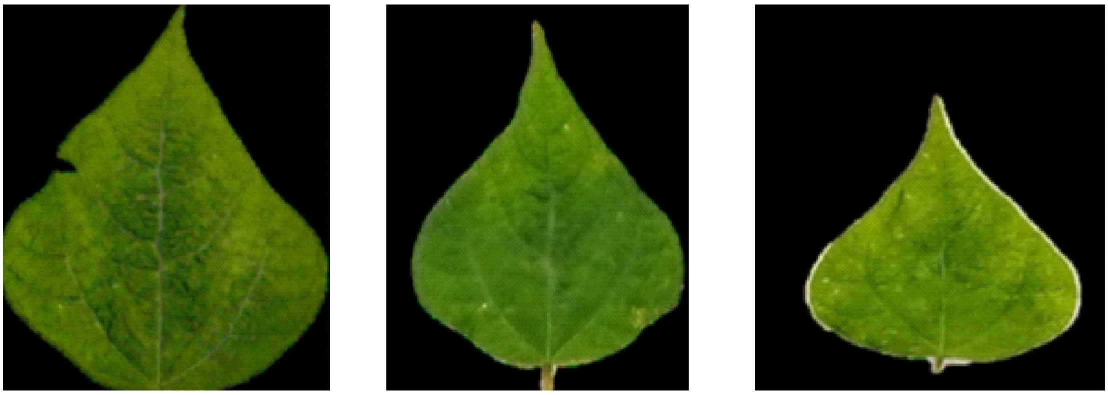
Pod: Colour	Pale green	1	17	42.50%
	Green	2	21	52.50%
	Purple	3	1	2.50%
Pod: Stringiness	Absent	1	14	35%
	Present	9	26	65%
Seed: Shape	Circular	1	3	7.50%
	Circular to elliptical	2	18	45%
	Elliptical	3	18	45%
	Kidney shaped	4	1	2.50%
Seed: Size	Small (<250g)	3	0	0%
(weight of 1000 seeds)	Medium (250-350g)	5	5	12.50%
	Large (351-450g)	7	23	57.50%
	Very large (>450g)	9	12	30%
Seed: Testa colour	White	1	6	15%
	Brown	2	6	15%
	Red	3	12	30%
	Dark red	4	16	40%


Vinyl

Non-vinyl

Leaf character

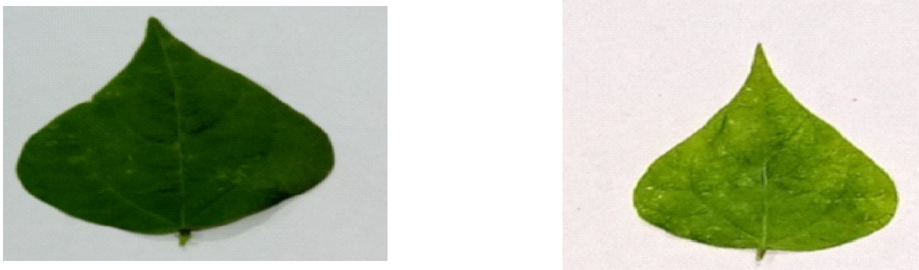
Plate 1: Recording the twining habit.


Large

Medium

Small

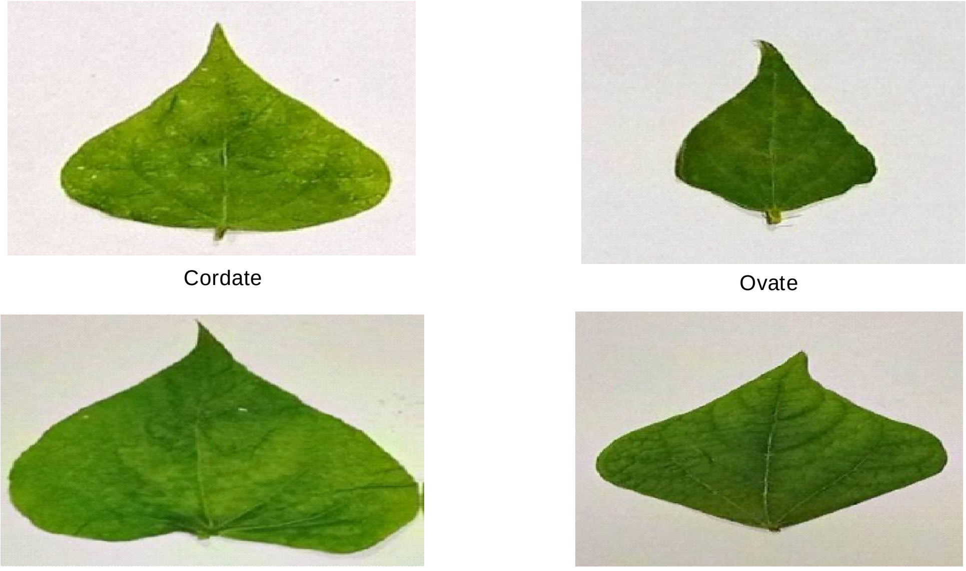
Plate 2: Recording of leaf size.



Dark green

Light green

Plate 3: Recording of intensity of green colour in leaves.



Cordate

Ovate

Rhombo hedric

Hastate

Plate 4: Recording of Shape of central leaflet.

Yellow

Voilent

Pink

White

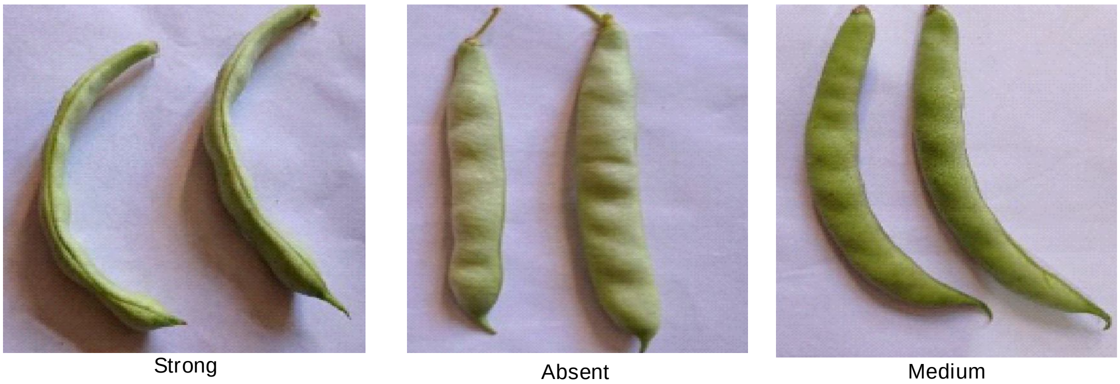
Flower character

Plate 5: Recording the colour of flowers.

Non stripted

Stripted

Plate 6: Recording of surface of standard petal.



Strong

Absent

Medium

Plate 7: Shape of curvature of pod in rajmash.

Acute

Truncate

Acute to truncate

Plate 8: Shape of distil part of pod excluding beak **.**

Purple

Green

Yellow

Plate 9: Colour of pod.

Concave

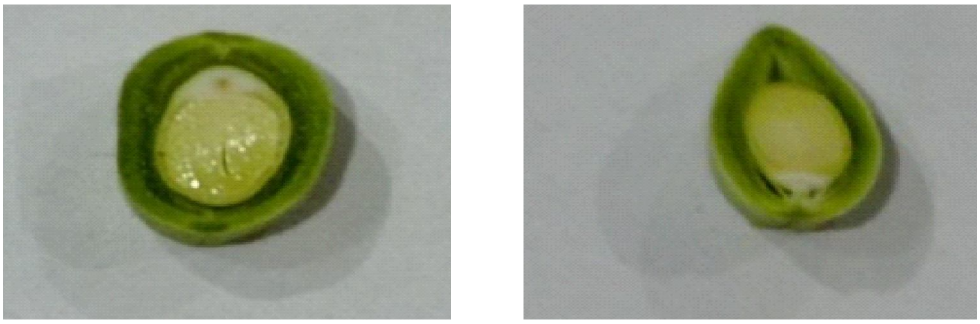
Convex

Plate 10: Shape of pod in relation to its suture.

Absent

Present

Plate 11: Shape of pod stringiness in rajmash.



Chordate

Circular

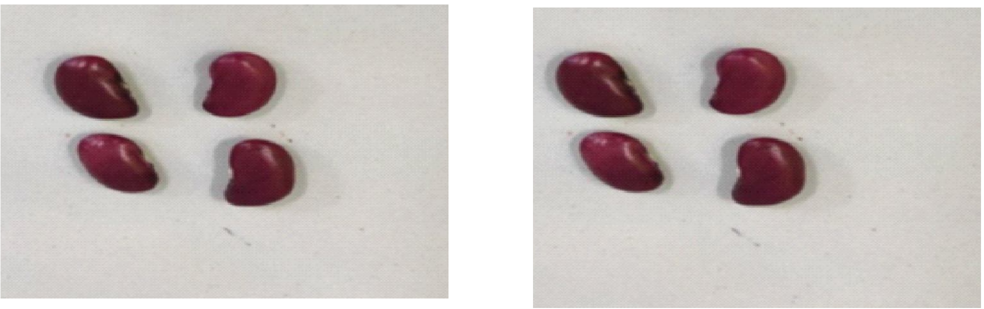
8-shaped

Oval

Plate 12: Shape of pod cross section through seed.

Circular

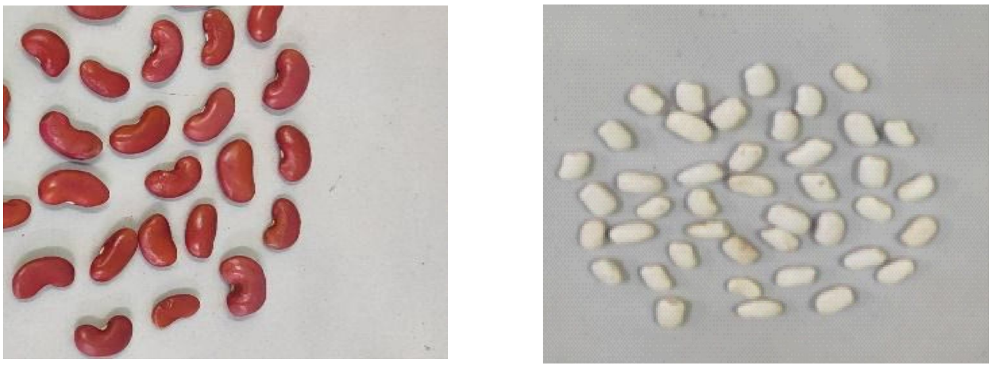
Circular



Elliptical

Elliptical

Plate 13: Shape of seed.



Brown

White

Plate 14: Colour of seed.

revealed spreading growth type, vinyl twining habit frequently noticed among genotypes for growth habit and growth type during screening of 109 French bean.

In leaf characters, like size of terminal leaflet of first flowering node, intensity of green colour in leaf and the leaf shape. In case of leaflet size, maximum frequency of (62.50%) was observed for “small” state of expression and (22.50%) was observed for “medium” and rest (15%) was observed for “large” state of expression, whereas intensity of “light green” colour of leaf was shown by maximum genotypes with a frequency of (65%) and intensity of “dark green” colour of leaf was shown by rest of the genotypes with a frequency of (35%) and shape of central leaflet was cordate, ovate, rhombohedric and hastate. Maximum frequency was observed for “ovate” (37.50%) followed by “cordate” (27.50%), “hastate” (20%) and “rhombohedric” (15%). With regard to flower colour, “white” colored flowers were recorded for (37.50%) genotypes, which was followed by “pink” colored flowers (35%), “yellow” colored flowers (25%) and “violet” colored flowers (2.50%). The frequency for “striped” outer surface of standard petal was recorded in (52.50%) genotypes followed by “non-striped” (47.50%). Leaflet shape differs among the cultivars, but leaflets generally have broad bases and pointed tips Singh *et al.* (1991). Duran *et al*. (2005) adopted morphological descriptor leaf shape (cordate, ovate, rhombohedric, or hastate) to characterize French bean landraces and cultivars from the Caribbean.

In pod characters like, curvature of pod, shape of pod viz., cross section of pod through seed, in relation tom suture and shape of distil part of pod excluding beak, pod colour and pod stringiness. “Medium” curvature was recorded in maximum genotypes with the frequency of (57.50%), curvature of pod was “absent” in 25% of genotypes and “strong” curvature was recorded in (17.50%) of genotypes. Shape of cross section of pod through seed was cordate, circular, eight shaped and oval. Maximum genotypes showed “cordate” shape with the frequency of (30%), followed by “circular” (27.50%), “oval” (27.50%) and “eight shaped” (15%). 70% of genotypes showed “concave” shape in relation to its suture followed by “convex” with a frequency of (30%) and “S-shaped” suture was absent. The shape of distil part of pod excluding beak was acute, acute to truncate and truncate. Maximum genotypes had “acute to truncate” shape with a frequency of (40%) followed by “truncate” (35%) and “acute” (25%). The frequency of “green” colour pod was recorded in (52.50%), was followed by “pale green”colour pod (42.50%) and the pod stringiness was present in (65%) of genotypes and was “absent” in (35%). Massimo *et al*. (2013) found statistically significant differences in pod morphological traits and slightly curved pod are predominant. Doriana *et al*. (2013) observed a great variability for pod colour, pod cross-section, pod curvature, pod beak position, pod beak orientation in French bean. Singh *et al*. (2014) characterized 18 French bean genotypes and inferred that pod curvature, pod shape of cross section (through seed), pod shape (in relation to suture), pod shape of distal part (excluding beak), pod colour, pod stringiness, pod pigmentation on pod shell are important morphological markers.

The seed shape showed variation for all states however state “circular to elliptical and elliptical” was having highest frequency of (45%) for both and was followed by “circular” and “kidney shaped” with the frequency of (7.50%) and (2.50%) respectively. Seed size 1000-seed weight also revealed variability for all the states, “large” state was having highest frequency of (57.50%) followed by “very large” and “medium” with the frequency of (30%) and (12.50%) respectively. The frequency of “dark red” seed was maximum (40%) followed by “red”, “white” and “brown” with the frequency of (30%) (15%) and (15%) respectively. Papa and Gepts, (2003) and Langarica *et al*. (2014) inferred that purple and pink flowers confer black seed coats.

A new genotype must meet three basic criteria before it can be licensed as a commercial variety: it must be distinct (D), Uniform (U) and Stable (S) Tomassini *et al*. (2003). DUS testing serves as the foundation for both plant variety protection and the discovery of new varieties from the reference set (Know *et al*., 2005). Based on character classification, the *Phaseolus vulgaris* L. genotypes used for

DUS assessment were divided into the number of classes. All the 40 genotypes in our analysis had distinctive morphological features. This is explained by the fact that practically all of the genotypes in the current study could be distinguished using a combination of distinct particular traits, demonstrating the value of DUS guidelines.

For days to flowering, maximum genotypes (24) took 50 to 75 days to flowering followed by early *i.e.*, less than 50 days (16). Maximum number of genotypes were of spreading (19) and erect type (19) followed by semi-erect (2), Viny (24) and indeterminate (26) type of plants were predominant over non-Viny (16) and determinate (14) type. Maximum genotypes had small sized leaves (25) followed by medium (9) and large (6). Maximum foliage colour was light green (26) followed by dark green (14) and ovate (15) leaves were maximum than other shapes of leaf. Flower colour was mostly white (15) followed by pink (14) and there were more striped flowers (21) as compare to non-striped (19). Pod shape through seed was cordate (12) followed by circular (11) and oval (11). For pod shape in relation to suture maximum number of genotypes was concave (28) followed by convex (12). Pod distil shape was acute to truncate (16) followed by truncate (14) and acute (10). The pod colour was green in maximum genotypes followed by pale green and purple with a frequency of 52.40%, 42.50% and 2.50% respectively.

Most of the genotypes had stringiness in pod with a frequency of 65% and in 35% pod stringiness is absent. The shape of seeds showed good variability for all the states having maximum frequency (45%) for “circular to elliptical” and “elliptical”. 1000 seed weight was large for maximum number of genotypes (23) having of total frequency (57.50%). Maximum genotypes showed dark red seeds (40%) followed by red colored seeds (30%). Similarly huge variability was observed in accessions by (Singh *et al*., 2014); (Saba *et al*., 2016) and (Kanwar and Mehta, 2018).

Estimation of genetic divergence

Based on the performance of the genotypes, 40 genotypes were grouped into 11 clusters as per Mahalanobis D^2 analysis using Tocher’s method (Rao, 1952) in Table 3. Maximum number of genotypes were found in cluster III (8 genotypes), followed by cluster I, II, IV, and V. Cluster VIII and cluster XI were found to have 2 genotypes each, and the remaining clusters were solitary containing only one genotype. These findings clearly demonstrate the potential of identifying various genotypes that can serve as a source of heritable traits for the creation of new varieties. These genotypes can serve as a source of divergent resources and can be utilized to identify potential parents for development of high yielding varieties through selection. In the present divergence analysis, major clusters commonly contained the genotypes of heterogeneous origin. Parents belonging to the most divergent clusters are generally advantageous for selection or production of new varieties, resulting in a vast diversity in genetic architecture.

The highest genotypic divergence was identified by mean intra and inter distances, which quantify the degree of divergence as per Table 4. It was found that the distances within the cluster (intra cluster) were higher, with cluster IV having the maximum distance (572.32), indicating that the genotypes were sufficiently diverse. Cluster VII and Cluster VIII had the highest inter cluster distance (16655.88), followed by cluster XI and cluster VII (14373.27), cluster I and cluster VIII (11442.41) and cluster VI and cluster VIII (11116.69). Cluster VI and cluster IX had the least inter cluster distance (372.91), followed by cluster I and cluster VI (724.90). These findings clearly demonstrate the potential of identifying various genotypes that can serve as a source of heritable traits for the creation of new varieties. These genotypes can serve as a source of divergent resources and can be utilized to identify potential parents for development of high yielding varieties through selection. The findings in this study are similar to those reported by Mishra *et al*. (2010); Gangadhara *et al*. (2014).

Contribution of genotypes towards total divergence

The per cent contribution of various characters (Table 5) showed that the plant height (44.74%) had the highest contribution towards divergence, followed by the pod weight

Table 3: Distribution of rajmash genotypes (*Phaseolus vulgaris* L.) into clusters based on D^2 statistics for maturity, morphological, yield and quality traits.

Clusters	No. of genotypes	Name of genotypes
Cluster 1	6	ALR-48, ALR-91, ALR-49, ALR-78, KDR-41, ALR-63
Cluster 2	6	ALR-13, ALR-16, 17, KDR-98, ALR-19, ALR-80
Cluster 3	8	ALR-90, KDR-1, ALR-28, ALR-26, ALR-32, KDR-97, ALR-64, ALR-12
Cluster 4	6	KDR-11, ALG-96, ALR-83,ALR-20, 18, ALR-14
Cluster 5	6	ALR-18, KDR-75, ALR-79, KDR-5, KDR-99, ALR-27
Cluster 6	1	KDR-77
Cluster 7	2	KDR-85, KDR-60
Cluster 8	1	SR-2
Cluster 9	1	KDR-25
Cluster 10	1	ALR-77
Cluster 11	2	SKAU-R-91, SR-1

Table 4: Average inter-cluster (above diagonal) and intra-cluster (diagonal) D^2 values among different *Phaseolus vulgaris* L. genotypes.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11
Cluster 1	345.61	7584.84	3355.15	2967.98	1037.31	724.90	1104.13	11442.41	1333.11	5466.31	8943.03
Cluster 2		480.51	1347.56	2754.17	4564.05	7735.91	11740.74	1107.36	6401.77	2963.12	1884.31
Cluster 3			426.94	1109.07	1639.78	3513.57	6273.25	3052.80	2801.97	2116.34	2573.16
Cluster 4				572.32	2038.99	2175.03	6386.73	4479.93	1329.68	1176.19	2437.28
Cluster 5					570.83	1684.72	2295.01	7928.49	1929.26	4568.49	6587.60
Cluster 6						0.00	2302.07	11116.69	371.91	3843.38	7519.83
Cluster 7							332.86	16655.88	3656.54	10139.13	14373.27
Cluster 8								0.00	8919.76	3389.70	1316.44
Cluster 9									0.00	2437.81	5435.33
Cluster 10										0.00	1075.67
Cluster 11											519.05

Table 5: Per cent contribution of different characters towards divergence.

Traits	Number of times ranked 1st	Percent contribution towards total divergence%
DTE	-	-
50%F	8	1.03%
DTM	-	-
PH	505	44.74%
NPP	-	-
PWP	196	25.13%
PL	9	1.15%
NSP	-	-
100 SW	4	0.51%
SYP	84	13.25%
SYH	52	8.75%
SL	30	3.85%
SB	28	3.59%
ST	-	-
SI	-	-

DTE= Days to emergence, 50%F= Days to 50% flowering, DTM= Days to maturity, PH= Plant height, NPP= Number of pods per plant, PWP= Pod weight per plant, PL= Pod length, NSP= Number of seeds per pod, 100SW= Hundred seed weight, SYP= Seed yield per plant, SYH= Seed yield per hectare, SL= Seed length, SB= Seed breadth, ST= Seed thickness, SI= Shape index.

per plant (25.13%), seed yield per plant (13.25%), seed yield per hectare (8.75%), seed length (3.85%), seed breadth (3.59%), pod length (1.15%), days to 50% flowering (1.03%) and 100-seed weight (0.51%). Additionally, plant height was ranked 505 times, followed by pod weight per plant at 196 times and seed yield per plant 84 times.

The selection and choice of parents is mostly determined by the contribution of traits to divergence. The number of times each character appears in the first rank has been used to evaluate the contribution of each character to genetic divergence. The result of this study revealed that plant height (44.74%) made the largest contribution to the overall genetic diversity among the genotypes followed by pod weight per plant (25.15%), seed yield per plant (13.25%), seed yield per hectare (8.75%) and seed length (3.85%). Therefore, it was determined that plat height, pod weight, seed yield, seed length etc. were significant factors causing genetic divergence. Gangadhara *et al*. (2014) and Panchbhaiya *et al.* (2017) did similar divergence research.

CONCLUSION

All the DUS characters will serve as a reference for future identification and cataloguing of valuable traits of current genetic resources for characterizing germplasm. To improve crops, germplasm characterization and evaluation is crucial. DUS characterization is a useful method for identifying and preventing duplication in crop plants. The manuscripts described considerable variation for qualitative traits. All of the analyzed characters vast range of variability was reflected by the frequency distribution. Diversity analysis showed grouping of genotypes in 11 clusters, which will help in selection of genetically divergent parents for exploitation in hybridization programme and would constitute an essential gene pool for future breeding programme.

Conflict of Interest

No conflict of interest is there with this article.

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