

Original Research Article

<https://doi.org/10.20546/ijcmas.2019.801.028>

Assessment of Genetic Diversity in Indian Common Bean Germplasm for Yield Traits

S. Sharma*, H.K. Chaudhary, A. Pathania and S. Thakur

Department of Crop Improvement, CSKHPKV, Palampur, Himachal Pradesh-176062, India

*Corresponding author:

ABSTRACT

Keywords

Divergence,
Genetic variability,
Common bean

Article Info

Accepted:
04 December 2018
Available Online:
10 January 2019

D² statistics is a powerful tool for estimating genetic diversity among different genotypes for hybridization programme. On the basis of D² values, the 169 genotypes were grouped into VIII clusters. Cluster II was the largest consisting of sixty two genotypes viz., KRC-2, K-326, HPK-322(2), HPR-396, VLF-106, K-255, KR-110, KR-249, K-249, VL-63, Palchan Local, Mani Rajma, Palchan kath, AK-40, HPR-80, HPR-24, HPR-38, AK-65, HPR-214, KR-296, HPR-8, KR-56-1, KR-118-1, KRC-16, KR-238, KR-155-3, KR-293, KR-52-2, KR-48-1, HUG-33, K-38, HPR-293, EC-84462, KR-256, AK-4, K-319, KRC-12, KR-35, KRC-9, KR-175-1, KR-205, KR-96, KRC-22, Beeses 3 white, KR-171, K-296, Premiere, KR-111, KR-53-2, KR-66-2, KR-24, KR-131, KR-240, KR-82, Ribba Local, R-10-457, KR-196, SR-1-6, SR-6-11, Jawala, Baspa. The next largest is clusters IV, followed cluster VII, V, VI, III, I each containing 42, 29, 16, 12, 1 respectively. The assessment of genetic diversity helps in reducing the number of breeding lines from the large germplasm.

Introduction

Common bean (*Phaseolus vulgaris* L.; 2n=2x= 22) is a predominantly self-pollinated crop plant mainly originated in Latin America, probably Central Mexico and Guatemala. From Latin America, Spanish and Portuguese spreaded it into Europe, Africa and other parts of the World (Gepts and Bliss, 1988; Gepts *et al.*, 1988; Zeven, 1997; Zeven *et al.*, 1999). Nowadays, it is widely cultivated in the tropics, subtropics and temperate regions. Roughly 30% of common bean production in the world comes from Latin American countries. Due to its nutritive components, it is

one of the 10 most important crops of the world. In India, common bean is known as 'Rajmash' and 'Frash bean' (green bean) and grows during summer and the winter in hilly areas of Himachal Pradesh, Jammu and Kashmir and North-Eastern states. In autumn, it is grown in parts of Uttar Pradesh, Maharashtra, Karnataka, and Andhra Pradesh. In Northern Indian plains, it is also cultivated on a limited scale as autumn or spring crop, because of its susceptibility to extreme temperatures. In India, the area under common bean cultivation is 9700 million ha as compared to 27,086 million ha all over the world, while its production is 4340 million

tonnes as compared to 18,943 million tonnes in the world (FAO).

In India, common bean is known by the names of 'Rajmash' and 'Frash bean (green bean)' and grows during the summer and Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. So, the knowledge of genetic diversity and relatedness in the germplasm is a prerequisite for crop improvement programmes. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes. So precise information on the nature and degree of genetic diversity present in collections from its principal areas of cultivation would help to select parents for evolving superior varieties. For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme. D^2 statistics is a powerful tool for estimating genetic diversity among different genotypes for hybridization programme. The assessment of genetic diversity helps in reducing the number of breeding lines from the large germplasm and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants.

Materials and Methods

The present investigation was carried out at the Experimental Farm CSK HPKV, Mountain Agricultural Research and Extension Centre (MAREC), Sangla, Distt. Kinnaur. The experimental material for the present study comprised of 165 local landraces of rajmash and 4 checks G19833 (A1), G4494 (A2) from Andean gene pool and DOR 364 (M1), ICAPIJAO (M2) from Mesoamerican gene

pool of Rajmash (*Phaseolus vulgaris* L.). These landraces along with checks were evaluated for different morphological and agronomic traits in Simple Lattice Design of 13 x 13 with two replications during *kharif* 2015. Two rows of each entry were grown in 1m length with row-to-row and plant-to-plant distance of 50 cm and 5 cm, respectively. Recommended package of practices were followed for raising the crop. Details of landraces used for the present study as given in table 1.

Observations recorded

Observations were recorded for both qualitative traits as well as quantitative traits (viz., Days to flowering, Days to maturity, Plant height (cm), Branches per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Biological yield per plant (g), Seed yield per plant (g), Harvest index (%) and 100-seed weight (g) on five randomly selected plants per replication for all the genotypes except for days to flowering and days to maturity which was recorded on plot basis.

Statistical methods

Statistical analysis of the data was done as per Mahalanobis (1936) and using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1953). Cluster means of common bean genotypes falling under different clusters in individuals as well as combined over environments were also calculated.

On the basis of D^2 values, the 169 genotypes were grouped into VIII clusters (Table 2). Cluster II was the largest consisting of sixty two genotypes viz., KRC-2, K-326, HPK-322(2), HPR-396, VLF-106, K-255, KR-110, KR-249, K-249, VL-63, Palchan Local,, Mani

Rajma, Palchan kath, AK-40, HPR-80, HPR-24, HPR-38, AK-65, HPR-214, KR-296, HPR-8, KR-56-1, KR-118-1, KRC-16, KR-238, KR-155-3, KR-293, KR-52-2, KR-48-1, HUG-33, K-38, HPR-293, EC-84462, KR-256, AK-4, K-319, KRC-12, KR-35, KRC-9, KR-175-1, KR-205, KR-96, KRC-22, Beeses 3 white, KR-171, K-296, Premiere, KR-111, KR-53-2,

KR-66-2, KR-24, KR-131, KR-240, KR-82, Ribba Local, R-10-457, KR-196, SR-1-6, SR-6-11, Jawala, Baspa. The next largest is clusters IV, followed cluster VII, V, VI, III, I each containing 42, 29, 16, 12, 1 respectively. Sharma *et al.* (2009) also used D2 statistics to study genetic diversity and grouped common bean germplasm into six clusters.

Table.1 Details of material used in the present study

S.No.	Local Landraces	Accession No.
1	KR-202-1	AC-1
2	KR-77	AC-2
3	KR-93	AC-3
4	KRC-21	AC-4
5	IC 313623	AC-5
6	AK 61	AC-6
7	K-326	AC-7
8	HPK-322(2)	AC-8
9	K-258	AC-9
10	K-243	AC-10
11	HPR-396	AC-11
12	HPR-415	AC-12
13	VLf-106	AC-13
14	K-255	AC-14
15	HPR-432	AC-15
16	KR-110	AC-16
17	KR-249	AC-17
18	KR-94	AC-18
19	Sarahan Local	AC-19
20	KR-126	AC-20
21	AK-48	AC-21
22	EC-316088	AC-22
23	K-249	AC-23
24	VL-63	AC-24
25	Palchan Local	AC-25
26	Palchan Kath	AC-26
27	Mani Rajma	AC-27
28	AK-23	AC-28
29	Palchan Kath	AC-29
30	AK-40	AC-30
31	AK-64	AC-31
32	HPR-80	AC-32
33	HPR-24	AC-33
34	HPR-38	AC-34
35	AK-65	AC-35
36	AK-73	AC-36
37	HPR-214	AC-37
38	Rakhcham Local	AC-38
39	K-163	AC-39
40	HPR-16	AC-40
41	KRC-11	AC-41
42	KR-253-A	AC-42
43	KR-273	AC-43
44	KR-175	AC-44
45	KR-296	AC-45
46	R-10-453	AC-46
47	KR-176	AC-47

48	AK-6	AC-48
49	Dalhera Local	AC-49
50	AK-37	AC-50
51	AK-16	AC-51
52	HPR-8	AC-52
53	KR-40	AC-53
54	KR-56-1	AC-54
55	KR-280	AC-55
56	KR-118-1	AC-56
57	KRC-16	AC-57
58	KR-51	AC-58
59	KR-238	AC-59
60	KR-155-3	AC-60
61	KR-293	AC-61
62	KR-52-2	AC-62
63	KR-48-1	AC-63
64	HUG-33	AC-64
65	K-38	AC-65
66	KRC-18	AC-66
67	HPR-293	AC-67
68	HPR-44	AC-68
69	EC-84462	AC-69
70	K-158	AC-70
71	KR-142	AC-71
72	AK-77	AC-72
73	K-284	AC-73
74	KR-256	AC-74
75	AK-4	AC-75
76	AK-82	AC-76
77	AK-57	AC-77
78	Saimulchan Local	AC-78
79	KR-32	AC-79
80	KR-9	AC-80
81	KR-142-1	AC-81
82	KR-227	AC-82
83	KR-169	AC-83
84	KR-133	AC-84
85	KRC-4	AC-85
86	AK-68-A	AC-86
87	K-29	AC-87
88	K-319	AC-88
89	K-85	AC-89
90	AK-36	AC-90
91	KR-6	AC-91
92	AK-3	AC-92
93	HPR-159	AC-93
94	K-214	AC-94
95	K-289	AC-95
96	AK-53	AC-96
97	AK-50	AC-97
98	KR-70-3	AC-98
99	K-16	AC-99
100	K-264	AC-100
101	K-191	AC-101
102	KRC-12	AC-102
103	KRC-241	AC-103
104	KR-242-1	AC-104
105	KR-243	AC-105
106	KR-307	AC-106
107	KR-134	AC-107
108	KR-35	AC-108
109	KR-216-1	AC-109
110	KRC-9	AC-110

111	AK-66	AC-111
112	AK-44	AC-112
113	AK-39	AC-113
114	HPR-139	AC-114
115	KR-175-1	AC-115
116	KR-205	AC-116
117	KR-96	AC-117
118	HPR-21	AC-118
119	K-254	AC-119
120	K-168	AC-120
121	HPR-360	AC-121
122	Kalera Local	AC-122
123	AK-1	AC-123
124	HPR-84	AC-124
125	HPR-300	AC-125
126	KRC-22	AC-126
127	KR-70-3	AC-127
128	KR-72	AC-128
129	KR-117	AC-129
130	KR-192	AC-130
131	KR-276	AC-131
132	Beeses 3 White	AC-132
133	HPR-339	AC-133
134	HPR-224	AC-134
135	KR-88	AC-135
136	KR-247	AC-136
137	KR-135	AC-137
138	KR-89	AC-138
139	KR-161	AC-139
140	KR-171	AC-140
141	K-296	AC-141
142	Premiere	AC-142
143	HPR-54	AC-143
144	AK-89	AC-144
145	AK-87	AC-145
146	KR-111	AC-146
147	KR-53-2	AC-147
148	KR-66-2	AC-148
149	KR-29-2	AC-149
150	KR-292	AC-150
151	KR-24	AC-151
152	KR-62-2	AC-152
153	AK-62	AC-153
154	AK-42	AC-154
155	KR-131	AC-155
156	KR-240	AC-156
157	KR-82	AC-157
158	Ribba Local	AC-158
159	R-10-57	AC-159
160	KR-196	AC-160
161	SR-1-6	AC-161
162	SR-6-11	AC-162
163	Kailash	AC-163
164	Jawala	AC-164
165	Baspa	AC-165
166	G19833	A1
167	G4494	A2
168	DOR364	M1
169	ICA PIJAO	M2

Table.2 Distribution of rajmash genotypes into different clusters

	Number of genotypes	Genotypes
I	1	KR-202-1
II	62	KRC-21, K-326, HPK-322(2), HPR-396, VLF-106, K-255, KR-110, KR-249, K-249, VL-63, Palchan Local, Palchan Kath, Mani Rajma, AK-40, HPR-80, HPR-24, HPR-38, AK-65, HPR-214, KR-296, HPR-8, KR-56-1, KR-118-1, KRC-16, KR-238, KR-155-3, KR-293, KR-52-2, KR-48-1, HUG-33, K-38, HPR-293, EC-84462, KR-256, AK-4, K-319, KRC-12, KR-35, KRC-9, KR-175-1, KR-205, KR-96, KRC-22, Beese 3 white, KR-171, K-296, Premiere, KR-111, KR-53-2, KR-66-2, KR-24, KR-131, KR-240, KR-82, Ribba Local, R-10-457, KR-196, SR-1-6, SR-6-11, Jawala, Baspa
III	6	KR-253-A, KR-273, KR-176, AK-6, Dalhera, Local, AK-37
IV	42	KR-93, AK-61, K-258, K-243, KR-94, Sarahan Local, KR-126, AK-23, KR-175, R-10-453, KR-40, KR-51, K-158, AK-77, KR-227, KR-133, AK-53, AK-50, K-16, K-264, KRC-242-1, KR-134, KR-216-I, K-254, Kalera Local, HPR-84, HPR-300, KR-70-3, KR-72, KR-117, KR-192, KR-276, HPR-339, KR-247, KR-135, KR-161, KR-29-2, KR-292, AK-62, AK-42, DOR 364, ICAPIJAO
V	16	IC-313623, HPR-415, AK-64, AK-73, K-163, HPR-16, AK-16, KR-280, K-284, HPR-159, K-214, K-191, K-168, HPR-224, KR-88, Kailash
VI	12	AK-48, EC-316088, KR-142, AK-82, AK-57, KR-32, KRC-241, HPR-360, AK-1, HPR-54, AK-89, AK-87
VII	29	KR-77, HPR-432, Rakcham Local, KRC-11, KRC-18, HPR-44, Saimulchan Local, KR-9, KR-142-1, KR-169, KRC-4, AK-68-A, K-29, K-85, AK-36, KR-6, AK-3, K-289, KR-70-3, KR-243, AK-66, AK-44, AK-39, HPR-139, HPR-21, KR-89, KR-62-2, G19833 ,G4494.
VIII	1	KR-307

Table.3 Average intra and inter-cluster distances among eight clusters

Clusters	I	II	III	IV	V	VI	VII	VIII
I	0.00	161.36	92.31	149.99	135.53	134.63	149.52	153.89
II		16.66	82.14	30.90	37.45	58.36	28.96	69.04
III			19.34	64.59	49.16	47.58	67.86	85.88
IV				15.19	21.43	29.90	25.45	71.60
V					17.57	27.11	21.52	58.50
VI						19.65	41.02	72.99
VII							15.68	48.58
VIII								0.00

*Diagonal values are intra cluster distances

Table.4 Cluster means of eight clusters for different traits of rajmash genotypes

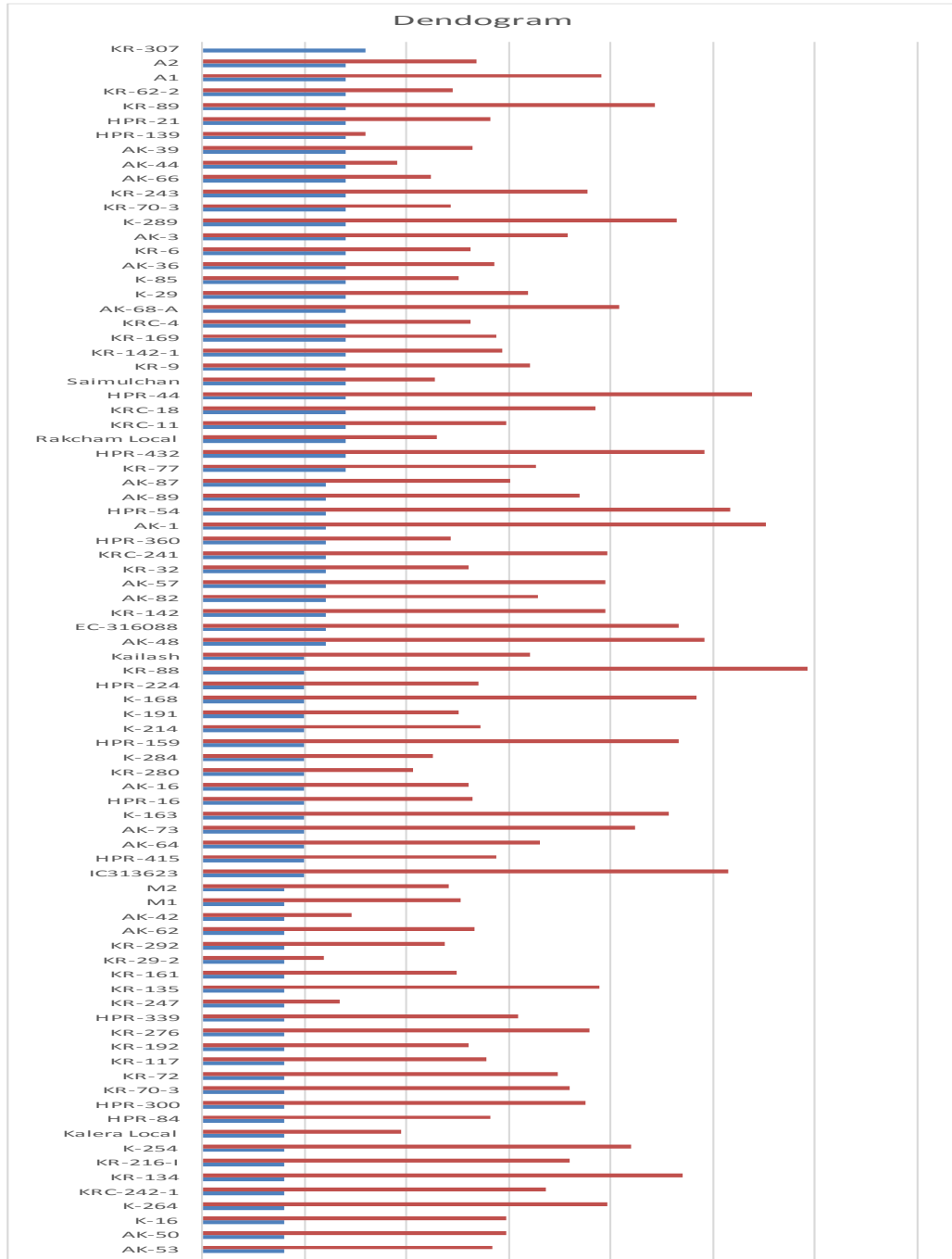
Traits	I	II	III	IV	V	VI	VII	VIII	Mean	Maximum	Minimum
Plant height	85.0	45.96	90.42	73.31	74.44	98.58	66.57	72.50	75.85	98.58	45.96
Branches/plant	3.00	3.39	3.92	3.38	3.50	3.96	3.41	3.50	3.51	3.92	3.00
No. of pods/plant	15.00	10.97	24.04	11.62	15.22	15.41	11.40	10.00	14.21	24.04	10.00
Pod length	9.40	10.18	9.53	9.68	10.41	10.55	10.90	13.80	10.56	13.80	9.40
No. of seed/pod	6.50	4.79	5.75	4.92	5.22	4.63	4.36	4.00	5.02	6.50	4.00
Biological yield	35.10	20.52	16.46	26.55	39.79	36.83	29.66	39.00	30.49	39.79	16.46
Harvest index	11.80	41.78	45.71	38.90	44.57	40.46	40.31	52.58	39.51	52.58	11.80
100 seed wt	33.70	33.32	24.56	24.87	35.67	27.03	48.68	90.54	39.80	90.55	24.56
Days to flowering	21.40	73.89	81.58	77.63	78.34	76.25	75.40	61.50	68.25	81.58	21.40
Days to maturity	74.00	124.68	131.00	133.44	129.53	135.63	133.98	124.00	123.28	135.63	74.00
Seed yield	140.00	8.28	7.37	10.27	17.67	14.96	11.92	20.50	28.87	140.00	7.37

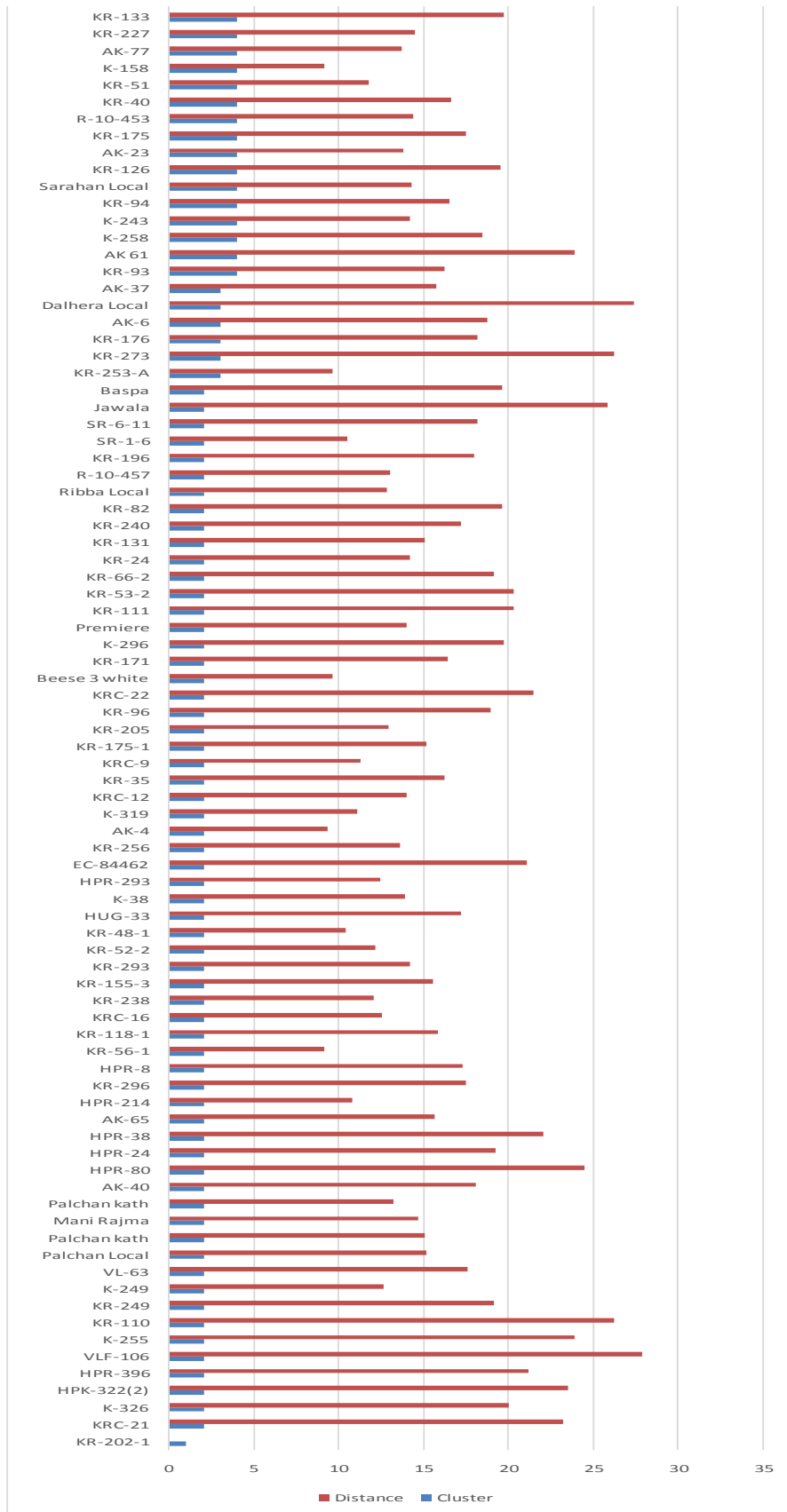
Table.5 Relative contribution (%) of individual trait to the genetic divergence among rajmash genotypes

S. No	Traits	No. of times ranked first	Contribution (%)
1	Plant height (cm)	684	38.14
2	Branches per plant	0	0*
3	No. of pods per plant	19	1.05
4	Pod Length (cm)	1	0.05
5	No. of seeds per pod	0	0*
6	Biological yield per plant (g)	687	38.31**
7	Seed yield per plant (g)	104	5.80
8	Harvest Index (%)	12	0.66
9	100 seed weight	221	12.32
10	Days to flowering	14	0.78
11	Days to maturity	51	2.84

*Minimum; **Maximum

Fig.1 Dendrogram of rajmash genotypes generated using Mahalanobis D²-cluster analysis





Average intra and inter cluster distances

Average intra and inter cluster distances are presented in Table 3. The genotypes which were grouped in same cluster were less divergent than the ones, which were placed in different clusters. In the present study, highest inter-cluster distance was observed between cluster I and cluster VIII (153.89), followed by cluster I and cluster IV (149.99) indicating that the genotypes from divergent clusters can be intercrossed to obtain high heterotic response and also to recover desirable transgressive segregants. Highest intra-cluster distance was only observed for cluster VI (19.65) revealed that genotypes within the same cluster were quite diverse; hence selection of parents within cluster would be effective (Fig. 1).

Cluster means and contribution of individual character toward divergence

Character mean of rajmash genotypes falling under different clusters and percent contribution to genetic divergence is presented in Table 4 and 5, respectively. Cluster I showed maximum values for number of seeds per pod and seed yield and minimum for branches per plant. Cluster II showed no maximum and minimum values for any of the trait. Cluster III showed maximum values for branches per plant, number of pods per plant and days to flowering and minimum values for none of the trait. Cluster IV showed no maximum and minimum values for any of the trait. Cluster V showed maximum value for biological yield per plant and minimum values for none of the trait. Cluster VI showed maximum values for plant height and days to maturity. Cluster VII showed no maximum and minimum values for any of the trait. Cluster VIII showed maximum values for pod length, harvest index, 100 seed weight.

The maximum contribution towards genetic divergence was exhibited by biological yield per plant (38.32%), followed by plant height (38.15%), 100 seed weight (12.33%), seed yield per plant (5.80%), days to maturity (2.84%), number of pods per plant (1.06%), days to flowering (0.78%), harvest index (0.67) and pod length (0.06%). In earlier studies, Mirjana (2005) reported contribution of 100 seed weight, number of pods per plant, days to flowering, seed length towards genetic divergence in common bean. Rodino *et al.* (2006) observed that the number of pods per plant had the greatest effect on the genetic divergence, followed by the number of branches per plant and single plant yield whereas, in present study biological yield per plant contributed maximum towards genetic divergence followed by plant height and 100 seed weight.

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How to cite this article:

Sharma, S., H.K. Chaudhary, A. Pathania and Thakur, S. 2019. Assessment of Genetic Diversity in Indian Common Bean Germplasm for Yield Traits. *Int.J.Curr.Microbiol.App.Sci*. 8(01): 250-260. doi: <https://doi.org/10.20546/ijemas.2019.801.028>