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## Study of genetic divergence for yield and yield contributing traits in soybean (*Glycine max* (L.) Merrill) genotypes

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### Abstract

The present investigation was carried out to order to assess the genetic diversity in fifty-four soybean genotypes using Mahalanobis  $D^2$  statistics. The present investigation comprised 54 genotypes, including three checks (AMS 2014-1, JS 20-116 and NRC 128) in a randomized complete block design with three replications during *Kharif* 2021. The experiment was conducted at the Research Cum Instructional Farm under the Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, C.G., The Cluster-II followed by Cluster-IV, Cluster-I, Cluster-III, Cluster-V and Cluster-VI, showed the maximum intra cluster distance hence belonging to this cluster could be utilized as parent in future breeding programme to get better recombinants. Maximum inter-cluster distance was recorded between Cluster-V with Cluster-VI, followed by between Cluster-IV with Cluster-V, Cluster-II with Cluster-V, Cluster-II with Cluster-VI, Cluster-I with Cluster-IV. Hence, it would be advisable to choose parents from these clusters having different gene pools for important genes to be combined in improved genotypes through hybridization programme.

**Keywords:** Genetic diversity, cluster analysis, cluster means,  $D^2$  statistic, inter and intra-cluster distance, soybean

### Introduction

Soybean (*Glycine max* (L.) Merrill) is a leguminous, autogamous, annual plant belongs to the order Fables, family Fabaceae, subfamily Faboideae with diploid chromosome number  $2n = 40$ . It contains approximately 40% protein (34%–48%), 23% carbohydrates, 20% oil (17%–24%), 8% moisture, 5% mineral and 4% fibre (Gopalan *et al.*, 1974). All of the eight essential amino acids, about 85% of PUFA with linoleic acid (53%), oleic acid (23%) and linolenic acid (7%) which are not synthesized by the human body are available in soybean. (Antalina, 2000; Balasubramanian & Palaniappan, 2003; Fehr. *et al.*, 1992) <sup>[1, 2, 3]</sup>. Genetic divergence is proven to be of tremendous interest to plant breeders and plays an important part in designing a successful breeding programme.  $D^2$  statistics were proposed by Mahalanobis (1936) <sup>[6]</sup> as a measure of group distance on multiple characters.  $D^2$  distinguishes between intra and inter-cluster levels to quantify the degree of divergence and estimate the relative contribution of each component character to total divergence. It allows detailed comparisons between all populations in a given group prior to actual crossovers (Kachhadia *et al.*, 2014) <sup>[5]</sup>. The Mahalanobis  $D^2$  approach has been shown to be a highly valuable tool in the investigation of genotype diversity (Rao, 1952) <sup>[7]</sup>.

### Materials and Methods

The current experiment was performed under AICRP on Soybean, Research Cum Instructional Farm under the Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, C.G. during the *Kharif* 2021. The experiment included 54 diverse soybean genotypes, including three checks (AMS 2014-1, JS 20-116 and NRC 128), planted in randomized complete block design. Genotypes were raised in three replications that were spaced 45 cm (R x R) and 10 cm (P x P) apart in three rows that were 3 m long (1.35 x 3 m<sup>2</sup>). Total 14 characters were used to record all observations. The experimental site had heavy soil with a pH range of 7.5. The fertilizer dose was applied at a rate of 20N: 40P: 20K kg/ha. All of the recommended agronomic practices were implemented. Details of the genotypes that were used in the investigation are given in Table 1.

**Table 1:** Details about the materials used in the experiment

S. No.	Entry	Pedigree	Source
1.	SKAU-WSB-101	-	SKUAST, Srinagar, J.K.
2.	KBS 21-1	-	UAS, Dharwad, K.A.
3.	MAUS 818	-	VNMKV, Parbhani, M.H.
4.	MAUS 791	-	VNMKV, Parbhani, M.H.
5.	AMS 115	AMS-MB5-18 x TAMS106	RRC, Amravati, M.H.
6.	AMS 19-01	Mutant of JS 93-05	RRC, Amravati, M.H.
7.	RVS 13-20	JS 20-29 x JS 93-05	RVSKV, Sehore, M.P.
8.	RVS 13-15	JS 20-88 x JSM 196	RVSKV, Sehore, M.P.
9.	DLSb 3	Dsb-23 x SL 958	UAS, Dharwad, K.A.
10.	DLSb 4	Dsb-21 x SL 958	UAS, Dharwad, K.A.
11.	DSb 39	JS 335 x EC 242104	UAS, Dharwad, K.A.
12.	NRC 128 (C)	JS 97-52 x (EC 389148 x PS 1042)	ICAR-IISR Indore, M.P.
13.	AS 40	G.Soy 1 x AMRS472	JAU-CoA Amreli, G.J.
14.	AS 24	JS 335 x GJ 3	JAU-CoA Amreli, G.J.
15.	JS 23-08	JS 20-29 x JS 93-05	JNKVV, Jabalpur, M.P.
16.	JS 23-05	SL 738 x JS 95-60	JNKVV, Jabalpur, M.P.
17.	DS 1312	SL 688 x DS 3047	IARI, Delhi
18.	DS 3163	DS-2205 x DS 12-13	IARI, Delhi
19.	DS 3168	DS-2210 x DS-2411	IARI, Delhi
20.	DS 3124	DS-2615 x DS-2709	IARI, Delhi
21.	SL 1282	(SL 525 x JS 335) x SL 525	PAU, Ludhiana, P.B.
22.	SL 1230	SL 905 x {(G. soja x Ankur) x SL (E) 28}	PAU, Ludhiana, P.B.
23.	HIMSO-1694	SL-679 x Harasoya	CSKKV, Palampur, H.P.
24.	HIMSO-1693	Pb-1 x Himsoya	CSKKV, Palampur, H.P.
25.	VLS 103	VLS 63 x VLS 2007-24	VPKAS, Almora, U.K.
26.	VLS 102	VLS 74 x EC 361360	VPKAS, Almora, U.K.
27.	JS 20-116 (C)	JS 97-52 x JSM 120 A	JNKVV, Jabalpur, M.P.
28.	PS 1605	-	GBPUAT, Pantnagar, U.K.
29.	PS 1689	JS 93-52 x PK 472 (F9-1)	GBPUAT, Pantnagar, U.K.
30.	PS 1682	PS 1583 x Bragg (F6-1)	GBPUAT, Pantnagar, U.K.
31.	RSC 11-48	MAUS 504 x MACS 1336	IGKV, Raipur, C.G.
32.	RSC 11-42	JS 97-52 x JS 93-05	IGKV, Raipur, C.G.
33.	BAUS(M)-3	Mutant of BSS-2	BAU, Ranchi, J.H.
34.	BAUS-116	JS 20-65 x JS 20-35	BAU, Ranchi, J.H.
35.	CAUMS 2	From NRC 2012 M-120-B-2	CAU, Imphal, M.N.
36.	NRC 195	-	ICAR-IISR Indore, M.P.
37.	NRC 203	EC 538828 x NRC 7	ICAR-IISR Indore, M.P.
38.	NRC 193	JS 97-52 x JS 88-66	ICAR-IISR Indore, M.P.
39.	NRC 192	JS 97-52 x JS 335	ICAR-IISR Indore, M.P.
40.	NRC 191	NRC 7 x EC -538828	ICAR-IISR Indore, M.P.
41.	NRC 190	JS97-52 X JS 335	ICAR-IISR Indore, M.P.
42.	AMS 2014-1(C)	AMS99-33 x H6P6	RRC, Amravati, M.H.
43.	NRC 189	Davis x Kaevi 651-6	ICAR-IISR Indore, M.P.
44.	RVSM 16-20	-	RVSKV, Morena, M.P.
45.	KDS 1175	KDS-344 X NRC-102	MPKV, Digraj, M.H.
46.	KDS 1187	KDS-344 X NRC-101	MPKV, Digraj, M.H.
47.	KDS 1149	KDS-228 X Type-49	MPKV, Digraj, M.H.
48.	MACS 1672	Himso-1563 x MACS-450	ARI (MACS), Pune, M.H.
49.	MACS 1735	Himso-1563 x SL-710	ARI (MACS), Pune, M.H.
50.	ASb 15	-	PJTSAU, Adilabad, T.S.
51.	TS 21-2	TS 80(Mutant Derivative of JS 80-21)x AMS 33B	BARC, Mumbai, M.H.
52.	TS 21-1	SL 742 X TS 37 (Mutant of DSb-12)	BARC, Mumbai, M.H.
53.	LOKSOY-1	Type 49 x EC 538836	Lokbharti, Sanosara, G.J.
54.	KSS 204	-	Basant Agro Ltd. M.H.

## Results and Discussion

### Group constellation

A D<sup>2</sup> analysis based on Tocher's method (P.C. Mahalanobis, 1936) [6] for 14 characteristics was performed on 54 soybean genotypes. The fifty-four genotypes were grouped into six

clusters with variable number of entries revealing the presence of variable amount of diversity in the material (Table 2). Cluster-II (30 genotypes) had the most, followed by Cluster-I (11 genotypes), Cluster-IV (8 genotypes), Cluster-III (3 genotypes), Cluster-V and VI (each had one-one genotype).

**Table 2:** Grouping of soybean genotypes into different clusters

Cluster No.	Number of genotypes included	Names of genotypes	Seed yield per plant (g) (Cluster mean)
I	11	MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115, MACS 1672	12.63
II	30	LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42, DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693, HIMSO-1694, AS 40, NRC 128 (C)	10.89
III	3	AS 24, JS 20-116 (C), ACS 1735	12.41
IV	8	PS 1689, SL 1282, PS 1682, MAUS 818, SL 1230, NRC 203, DS 3124, BAUS-116	11.29
V	1	SKAU-WSB-101	7.34
VI	1	AMS 19-01	34.73

**Inter and intra cluster distance**

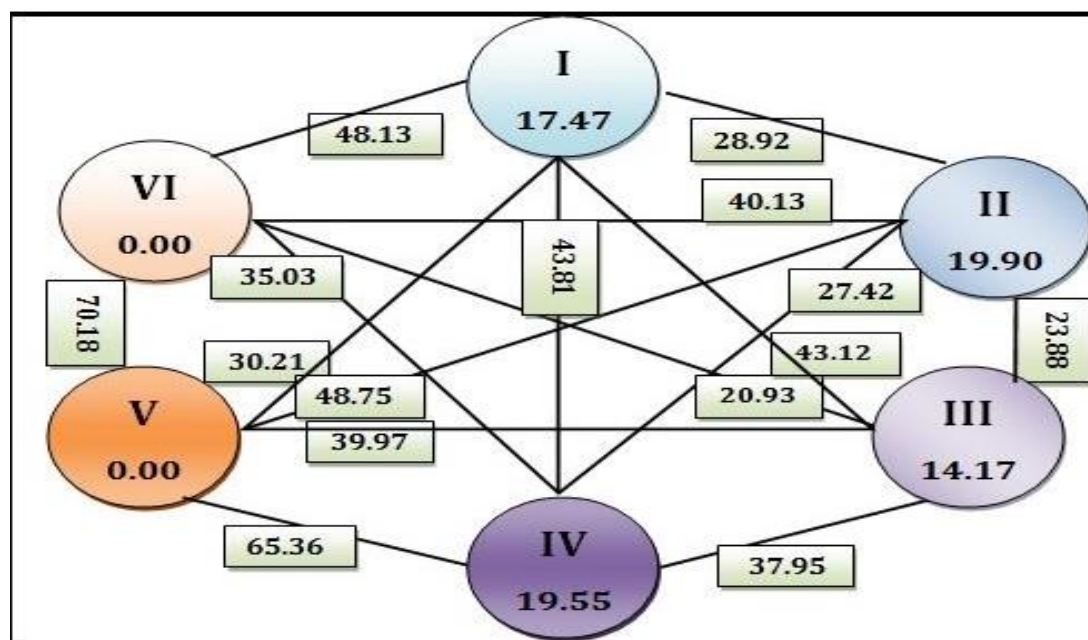
Maximum intra-cluster distances were recorded in Cluster-II (19.90), followed by Cluster-IV (19.55), Cluster-I (17.47), Cluster-III (14.17), Cluster-V (0.00) and Cluster-VI (0.00). Maximum inter-cluster distance was observed between Cluster-V with Cluster-VI (70.18), followed by between Cluster-IV with Cluster-V (65.36), Cluster-II with Cluster-V (48.75), Cluster-II with Cluster-VI (48.13), Cluster-I with

Cluster-IV (43.81), Cluster-III with Cluster-VI (43.12), Cluster-II with Cluster-VI (40.13), Cluster-III with Cluster-V (39.97), Cluster-III with Cluster-IV (37.95), Cluster-IV with Cluster-VI (35.03), Cluster-I with Cluster-V (30.21), Cluster-I with Cluster-II (28.92), Cluster-II with Cluster-IV (27.42) and Cluster-II with Cluster-III (23.88), furthermore minimum inter-cluster distance was observed between Cluster-I with Cluster-III (20.93).

**Table 3:** Average inter and intra cluster distance of soybean genotypes.

S.No.	I	II	III	IV	V	VI
I	<b>17.47</b>	28.92	20.93	43.81	30.21	48.13
II		<b>19.90</b>	23.88	27.42	48.75	40.13
III			<b>14.17</b>	37.95	39.97	43.12
IV				<b>19.55</b>	65.36	35.03
V					<b>0.00</b>	70.18
VI						<b>0.00</b>

\*Intra-cluster values are diagonals  **$\sqrt{D^2}$**  values



**Fig 1:** Diagrammatic representation of inter and intra cluster distances.

**Table 4:** Cluster mean performance of various soybean genotypes.

S. No	Characters	I	II	III	IV	V	VI	Avg.
1.	Days to 50% flowering	37	43	42	42	31	36	38
2.	Days to maturity	95	104	99	113	84	112	101
3.	Plant height (cm)	53.59	71.42	63.72	63.82	41.53	48.74	57.14
4.	Number of primary branches per plant	3.71	3.50	3.62	3.64	2.53	4.84	3.64
5.	Number of pods per plant	51.76	54.16	69.60	54.45	33.53	103.63	61.19
6.	Pod bearing length (cm)	43.90	59.60	56.20	53.87	31.00	43.40	48.00
7.	Number of seeds per pod	2.55	2.49	2.55	2.47	2.45	2.47	2.50
8.	Number of seeds per plant	114.65	106.87	134.16	101.03	36.93	288.80	130.41
9.	100 seed weight (g)	10.05	10.00	8.60	10.26	19.34	9.54	11.30
10.	Biological yield per plant (g)	24.14	25.33	23.45	27.26	17.41	61.43	29.84
11.	Harvest index (%)	53.19	42.40	52.37	41.58	42.11	56.57	48.04
12.	Oil content (%)	20.29	20.12	20.33	20.33	23.54	20.78	20.90
13.	Protein content (%)	37.85	37.81	40.77	37.75	38.75	40.74	38.94
14.	Seed yield per plant (g)	12.63	10.89	12.41	11.29	7.34	34.73	14.88

### Percent contribution to variation

The days to maturity had highest contribution, followed by harvest index, number of seeds per plant, days to 50% flowering, biological yield per plant, protein content, number of pods per plant, pod bearing length, number of primary branches per plant and seed yield per plant and plant height moreover number of seeds per pod and oil content both character had lowest contribution on divergence.

### Components of inter-cluster D<sup>2</sup> values

#### Days to 50% flowering

For days to 50% flowering trait Cluster-II had the highest mean value (43 days), followed by Cluster-IV (42 days), Cluster-III (42 days), Cluster-I (37 days) and Cluster-VI (36 days) and whereas the lowest mean value (31 days) was found in Cluster-V. Top best performing genotypes for this trait are, LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42, DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693, HIMSO-1694, AS 40 and NRC 128 (C).

#### Days to maturity

The Cluster-IV had the maximum mean value for days to maturity (113 days), followed by Cluster-VI (112 days), Cluster-II (104 days), Cluster-III (99 days) and Cluster-I (95 days) and while the lowest mean value for days to maturity was recorded in Cluster-V (84 days). Top best performing genotypes for this trait are, PS 1689, SL 1282, PS 1682, MAUS 818, SL 1230, NRC 203, DS 3124, BAUS-116, AMS 19-01, LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42, DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693, HIMSO-1694, AS 40 and NRC 128 (C).

#### Plant height (cm)

Cluster-II had the highest cluster mean for the plant height (cm) (71.42 cm), followed by Cluster-IV (63.82 cm), Cluster-III (63.72 cm), Cluster-I (53.59 cm) and Cluster-VI (48.74 cm). The lowest cluster mean for the plant height (cm) was in Cluster-V (41.53). Top best performing genotypes for this trait are, LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42,

DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693, HIMSO-1694, AS 40 and NRC 128 (C).

#### Number of primary branches per plant

Cluster-VI had the highest average for the number of primary branches per plant trait (4.84), followed by Cluster-I (3.71), Cluster-IV (3.64), Cluster-III (3.62) and Cluster-II (3.50), while Cluster-V had the lowest (2.53) cluster mean. Top best performing genotypes for this trait are, AMS 19-01, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115 and MACS 1672.

#### Number of pods per plant

Cluster-VI had the greater cluster mean for number of pods per plant character (103.63), followed by Cluster-III (69.60), Cluster-IV (54.45), Cluster-II (54.16) and Cluster-I (51.76), whereas Cluster-V had the lowest (33.53) cluster mean. Top best performing genotypes for this trait are, AMS 19-01, AS 24, JS 20-116 (C), MACS 1735, PS 1689, SL 1282, PS 1682, MAUS 818, SL 1230, NRC 203, DS 3124 and BAUS-116/

#### Pod bearing length (cm)

For pod bearing length (cm), the cluster mean was the highest in Cluster-II (59.60 cm), followed by Cluster-III (56.20 cm), Cluster-IV (53.87 cm), Cluster-I (43.90 cm) and Cluster-VI (43.90 cm). Furthermore, the lowest cluster mean for the pod bearing length (cm) was in Cluster-V (31.00). Top best performing genotypes for this trait are, LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42, DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693 and HIMSO-1694.

#### Number of seeds per pod

Cluster-I and Cluster-III had the highest average for the number of seeds per pod trait (2.55), followed by Cluster-II (2.49), Cluster-IV and Cluster-VI (2.47), while Cluster-V had the lowest (2.45) cluster mean for number of seeds per pod. Top best performing genotypes for this trait are, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115, MACS 1672, AS 24, JS 20-116 and MACS 1735.

**Number of seeds per plant**

Cluster-VI had the maximum mean value for the number of seeds per plant (288.80), followed by Cluster-III (134.16), Cluster-I (114.65), Cluster-II (106.87) and Cluster-IV (101.03), while the lowest mean value for the number of seeds per plant was recorded in Cluster-V (36.93). Top best performing genotypes for this trait are, AMS 19-01, AS 24, JS 20-116 (C), MACS 1735, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115 and MACS 1672.

**100 seed weight (g)**

The maximum cluster mean for 100 seed weight (g) was found in Cluster-V (19.34 g.) followed by Cluster-IV (10.26 g), Cluster-I (10.05 g), Cluster-II (10.00 g) and Cluster-VI (9.54 g). The lowest cluster mean for 100 seed weight (g) was found in Cluster-VI (9.54 g). Top best performing genotypes for this trait are, SKAU-WSB-101, AMS 19-01, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115 and MACS 1672.

**Biological yield per plant (g)**

Cluster-VI had the highest average for biological yield per plant (g) trait (61.43 g), followed by Cluster-IV (27.26 g), Cluster-II (25.33 g), Cluster-III (24.14 g) and Cluster-IV (23.45 g), while Cluster-V had the lowest (17.41 g) cluster mean. Top best performing genotypes for this trait are, AMS 19-01, PS 1689, SL 1282, PS 1682, MAUS 818, SL 1230, NRC 203, DS 3124, BAUS-116, LOKSOY-1, KSS 204, DLSb 4, NRC 195, TS 21-2, VLS 102, DSb 39, DS 3163, KDS 1187, TS 21-1, KDS 1175, AMS 2014- 1(C), NRC 190, PS 1605, VLS 103, RSC 11-42, DS 3168, NRC 193, CAUMS 2, NRC 192, DLSb 3, ASb 15, NRC 189, BAUS(M)-3, KDS 1149, RSC 11-48, HIMSO-1693, HIMSO-1694, AS 40 and NRC 128 (C).

**Harvest index (%)**

Maximum cluster mean for harvest index (%) was found in Cluster-VI (56.57%), followed by Cluster-I (53.19%), Cluster-III (52.37%), Cluster-II (42.40%) and Cluster-V (42.11%). The lowest cluster mean for the harvest index (%) was found in Cluster-IV (41.58%). Top best performing genotypes for this trait are, AMS 19-01, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115, MACS 1672, AS 24, JS 20-116 (C) and MACS 1735.

**Oil content (%)**

Cluster-VI had the highest average for oil content (%) (20.78%), followed by Cluster-V (20.54%), Cluster-IV and Cluster-III (20.33%), Cluster-I (20.29%), while Cluster-II had the lowest (20.12%) cluster mean for oil content (%). Top best performing genotypes for this trait are, SKAU-WSB-101, AMS 19-01, AS 24, JS 20-116 (C), MACS 1735, PS 1689, SL 1282, PS 1682, MAUS 818, SL 1230, NRC 203, DS 3124 and BAUS-116.

**Protein content (%)**

The maximum cluster mean for protein content (%) was found in cluster-III (40.77%), followed by Cluster-VI (40.74%), Cluster-V (38.75%), Cluster-I (37.85%), Cluster-II (37.81%) and the lowest cluster mean for protein content (%) in Cluster-IV (37.75%). Top best performing genotypes for this trait are, AS 24, JS 20-116 (C), MACS 1735, AMS 19-01,

SKAU-WSB-101, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115 and MACS 1672.

**Seed yield per plant (g)**

Cluster-VI had the highest cluster mean for seed yield per plant (g) trait (34.73 g), followed by Cluster-I (12.63 g), Cluster-III (12.41 g), Cluster-IV (11.29 g), Cluster-II (10.89 g) and Cluster-V had the lowest (7.34 g). Top best performing genotypes for this trait are, AMS 19-01, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115, MACS 1672, AS 24, JS 20-116 (C) and MACS 1735.

**Conclusion**

Six clusters were constructed based on D<sup>2</sup> values where Cluster-II (30) was followed by Cluster-I (11), Cluster-IV (8), Cluster-III (3), Cluster-V (1) and VI (1) genotypes. Largest intra-cluster distances had found in, Cluster-II followed by Cluster-IV, Cluster-I, Cluster-III, Cluster-V and Cluster-VI, moreover greatest inter-cluster distance was observed between Cluster-V with Cluster-VI, followed by between Cluster-IV with Cluster-V, Cluster-II with Cluster-V, Cluster-II with Cluster-VI, Cluster-I with Cluster-IV. As a result, it would be wise to select parents from these clusters as they are predicted to produce superior segregates or attractive combinations for the development of valuable genetic stock, gene pools, or varieties with enhanced genotypes through a hybridization programme. AMS 19-01, MAUS 791, RVS 13-15, RVS 13-20, NRC 191, RVSM 16-20, DS 1312, JS 23-08, KBS 21-1, JS 23-05, AMS 115, MACS 1672, AS 24, JS 20-116 (C), MACS 1735, are the top best performance genotypes based on seed yield per plant (g).

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