



# Performance of Horse Gram [*Macrotyloma uniflorum* (L.) Verdc] Germplasm for Seed Yield and Its Component Characters

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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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## ABSTRACT

The present investigation was carried out with 78 diverse horse gram [*Macrotyloma uniflorum* (L.) Verdc] genotypes along with 4 checks during the late *Kharif* season. Data was recorded on days to 50 percent flowering, days to maturity, plant height, number of branches per plant, pod length, number of seeds per pod, number of pods per plant, pod weight (g), seed yield per plant (g), and 100-seed weight (g). Analysis of variance revealed significant differences among all the genotypes for all the characters studied. A wide range of variations had been observed for all the characters except for the number of seeds per pod. The highest coefficient of variation was observed in the number of pods per plant followed by 100 seed weight and seed yield per plant. The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficient of

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variation (GCV) for all the traits but the differences were narrow. The highest magnitude of PCV and GCV were recorded for seed yield per plant (g) followed by pod weight (g) indicating a wide range of variation which provides a chance for yield improvement. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, number of pods per plant, pod weight, seed yield per plant, and 100 seed weight indicating additive gene action and the abundant scope for improvement in these traits through simple selection. This study provides information about the performance of the genotypes and identifies some prominent genotypes. Thirty-three genotypes recorded significantly higher seed yield per plant as compared to the best-performing check. These genotypes were IC 426292, IC 470167, IC 426471, IC 470229, IC 470206, IC 470262, IC 426464, IC 107247, IC 108076, IC 426550, IC 426540, IC 108078, IC 426537, IC 470166, IC 467865, CRHG-1, IC 426539, IC 426478, IC 426524, IC 426549, IC 426522, IC 470170, IC 261278, IC 470188, IC 426535, IC 107222, IC 226533, IC 426574, IC 426523, IC 526965, IC 426571, IC 426517 and IC 426538. These genotypes may be further used for parental selection in breeding programs for the improvement of yield and its attributes in horse gram.

**Keywords:** Horse gram; seed yield; heritability; GCV; PCV; augmented block design.

## 1. INTRODUCTION

Horse gram [*Macrotyloma uniflorum* (L.) Verdc] is an important drought-hardy, climate-resilient dual-purpose rainfed crop adaptable to poor soils with minimal or no input and aftercare. Taxonomically the crop belongs to the family Fabaceae with diploid chromosome number (2n=20). It has its origin in India [1]. In India, Horse gram is grown annually on nearly 4.0 L. ha of area and more than 93% of the area is mainly confined to six states such as Karnataka, Maharashtra, Odisha, Andhra Pradesh, Madhya Pradesh, and Tamil Nadu [2] Being a leguminous crop, it is used as a green manure and cover crop and as a contingent crop in case of delayed monsoon. Horse gram is the cheapest source of nutritious forage for cattle and horses, especially in drylands where fodder shortage is a serious problem during the lean months. Horse gram is also well known for its excellent medicinal and therapeutic properties and is used to cure kidney stones, asthma, bronchitis, urinary discharges, heart diseases, leukoderma, etc. The horse gram on average contains 25% protein, 1% fat, and 57% carbohydrates [3]. Horse gram grains contain up to 27% protein [4] high in lysine content compared to other pulses such as chickpea and red gram [5]. Horse gram is also a very good source of iron and molybdenum micronutrients and the overall chemical composition of grains is as good as other cultivated legumes [6]. The high variability present in germplasm accessions for various traits is of high significance for the advancement of the crop. The present investigation was targeted to study the genetic variability among the horse gram accessions and drawing of

inferences for utilization in the horse gram improvement.

## 2. MATERIALS AND METHODS

The present investigation on evaluation of horse gram [*Macrotyloma uniflorum* (L.) Verdc] germplasm for seed yield was conducted at Hayathnagar research farm, ICAR-CRIDA, Hyderabad, during late *Kharif* 2022. The experimental material for the present study consisted of 78 germplasm lines of horse gram collected from the National Bureau of Plant Genetic Resources (ICAR-NBPGR), Regional Station, Hyderabad along with four released varieties of horse gram from ICAR-CRIDA as checks viz. CRIDA-18R, CRHG-4, CRHG-19 and CRHG-22. The field experiment was laid out in Augmented Block design [7], which consisted of 3 blocks of 26 genotypes each with 4 checks replicated randomly in each block. Row to row distance was 45 cm and plant to plant was maintained at 10 cm. All standard packages of practices were followed to raise a good crop.

A total of 10 characters were recorded which includes days to 50% flowering, days to maturity, plant height, number of branches per plant, pod length (cm), number of seeds per pod, number of pods per plant, pod weight (g), seed yield per plant (g) and 100 seed weight (g). Days to 50% flowering and days to maturity were recorded on the whole plot basis, whereas, the characters like plant height, number of branches per plant, pod length (cm), number of seeds per pod, number of pods per plant, pod weight (g), seed yield per plant (g) and 100 seed

weight were recorded on five randomly selected plants in each entry. The average values for these characters were calculated and used for the statistical analysis. The mean data of genotypes along with checks were analyzed in augmented block design using INDOSTAT software.

### 3. RESULTS AND DISCUSSION

#### 3.1 Anova

The results of analysis of variance for days to 50% flowering, days to maturity, plant height, number of branches per plant, pod length (cm), number of seeds per pod, number of pods per plant, pod weight (g), seed yield (g) and 100 seed weight (g) were presented in Table 1. The statistical analysis revealed significant variability among the genotypes for all the traits studied except for the number of seeds per pod indicating the presence of high variability among the horse gram genotypes (Table 1). The mean sum of squares due to blocks (eliminating check + variety) was non-significant for all the traits. The mean sum of squares due to entries (eliminating blocks) was significant for all the characters except 100 seed weight. The mean sum of squares due to varieties was significant for all the characters. The mean sum of squares due to checks vs. varieties was significant for all the characters except for days to 50% flowering and 100 seed weight.

#### 3.2 Mean Performance

The germplasm material evaluated in the experiment was genetically diverse and exhibited a wide range of variation for all the quantitative characters studied. (Table 2). Among the genotypes including days to 50% flowering ranged from 45 (IC 470196) to 60 (IC 426513, IC 426556, IC 328887, IC 426496) days with a mean of 50.25. The genotype IC 470196 was at par as compared to the earlier check. Days to maturity ranged from 85 (IC 470167) to 97 (IC 426472, IC 426537, IC 470262) among the genotypes with a mean of 91.15. The genotype IC 470167 was at par as compared to the earlier check.

Plant height ranged from 15 to 65 cm with a mean of 34.39 cm in the studied genotypes

including check. The genotype IC 426472 (65 cm) recorded the highest plant height while the genotype IC 261296 (15 cm) was the lowest. However, 18 genotypes were found to be significantly taller with respect to plant height from the best-performing check. Among the experiment material, the number of branches per plant ranged from 1 to 9.33 with a mean of 4.20. The genotype IC 261296 (1) recorded the lowest number of branches per plant while IC 426544 (9.33) genotype recorded the highest number of branches per plant. Nine genotypes were found to have a significantly higher number of branches per plant as compared to the best-performing check. Among the germplasm including the check pod length ranged from 3.4 to 6 with a mean of 4.43 cm. The genotypes IC 470196 (3.4) and IC 107247 (6) recorded the lowest and highest pod length respectively. Only one genotype was found to have a significantly higher pod length as compared to the best-performing check.

Among all the genotypes number of seeds per pod ranged from 4 (IC 426513) to 6.67 (IC 278866) with a mean of 5.46. The genotype IC 278866 was at par with respect to the number of seeds per pod as compared to the best-performing check. Significant variation was observed among the genotypes including checks for the number of pods per plant and it ranged from 9.5 (IC 261296) to 80 (IC 470229) with a mean of 38.17. Three genotypes were found to have a significantly higher number of pods per plant as compared to the best-performing check.

Among all the genotypes, pod weight ranged from 2.84 (IC 426513) to 20.42 (IC 426538) with a mean of 10.37 g. 45 genotypes had significantly higher pod weight as compared to the best-performing check. The genotypes differed significantly for seed yield per plant and it ranged from 1.54 (IC 426493) to 13.24 g (IC 426538) with a mean of 6.81 g. Thirty-three genotypes were found to have significantly higher seed yield as compared to best-performing check. Significant variation was observed among genotypes for 100 seed weight and the value ranged from 2.32 (IC 426555) to 5.01 (IC 313367) with a mean of 3.20 g. 5 genotypes were found to have significantly higher value as compared to check.

**Table 1. Analysis of variance for yield and its component traits in Horse gram genotypes**

Source of variation	d.f	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
Block (ignoring Treatments)	2	11.20	1.34	207.39 **	9.54 **	0.40 *	0.02	160.67 **	262.59 **	188.92 **	0.34 *
Treatment (eliminating Blocks)	81	12.02 *	10.32 **	117.63 **	2.30 **	0.18 *	0.26	243.83 **	19.51 **	8.65 **	0.23
Checks + varieties vs. varieties	78	12.36 *	10.32 **	127.37	2.33 **	0.18 *	0.27	252.61 **	17.23 **	7.85 **	0.23
Block (Eliminating Check + var.)	2	2.58	2.58	0.09	0.03	0.04	0.03	12.01	0.04	0.01	0.03
Entries (ignoring Blocks)	81	12.23 *	10.29 **	122.75 **	2.54 **	0.19 *	0.26	247.50 **	25.99 **	13.31 **	0.24
Checks	3	3.42	10.08 *	22.13	1.22 **	0.10	0.03	83.17 *	0.77	0.93	0.06
Varieties	77	12.73 *	9.68 **	127.50 **	2.61 **	0.19 *	0.27	242.86 **	24.59 **	13.30 **	0.25 *
Checks vs. Varieties	1	0.31	57.56 **	59.09 *	0.55 *	0.27 *	0.02	1098.12 **	209.77 **	51.50 **	0.31
Error	6	2.92	1.25	5.66	0.09	0.04	0.13	13.15	0.23	0.28	0.07

\*Significant at 5% of level of probability; \*\* Significant at 1% level of probability; Note: **d.f** = degrees of freedom, **D50** = Days to 50% flowering, **DM** = Days to maturity, **PH** = Plant height (cm), **BR** = Number of branches per plant, **PL** = Pod length (cm), **SPP** = Number of seeds per pod, **NOP** = Number of pods per plant, **PW** = Pod weight (g), **SY** = Seed yield per plant (g), **100SW** = Seed weight (g)

**Table 2. Mean performance of horse gram genotypes for various characters**

S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
C-1	CRIDA -18R	52.00	87.33	29.56	4.44	4.22	5.44	43.44	6.52	4.33	3.02
C-2	CRIDA- 4	50.00	87.33	30.11	3.67	4.33	5.33	46.67	5.37	4.10	2.85
C-3	CRIDA -19	49.67	90.33	33.72	4.33	4.06	5.33	46.11	6.32	5.15	3.08
C-4	CRIDA- 22	50.00	90.67	35.11	5.22	4.50	5.56	55.56	6.16	5.18	3.19
1.	IC 426513	60.00	91.00	19.00	2.00	3.50	4.00	36.00	2.84	2.71	2.98
2.	IC 426556	60.00	93.00	21.67	2.00	4.67	5.33	37.00	7.76	4.45	3.89
3.	IC 328887	60.00	96.00	27.67	2.00	4.83	6.00	26.67	5.12	4.12	3.83
4.	IC 426456	54.00	90.00	35.00	3.00	4.33	6.00	35.67	4.55	2.17	3.23
5.	IC 470194	48.00	92.00	47.33	6.00	4.33	5.00	40.67	7.98	4.18	2.87
6.	IC 426541	55.00	94.00	38.33	2.00	4.33	5.00	48.33	7.84	4.37	2.78
7.	IC 426496	60.00	97.00	31.33	3.33	4.33	5.00	30.00	6.67	3.93	3.10
8.	IC 426492	59.00	95.00	27.50	4.00	4.25	5.00	53.50	10.81	6.90	3.22

S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
9.	IC 261296	49.00	91.00	15.00	1.00	4.25	5.00	9.50	4.31	2.54	2.96
10.	IC 470172	49.00	88.00	48.00	5.00	4.67	6.33	54.67	9.34	6.84	3.31
11.	IC 426557	50.00	93.00	30.67	3.00	4.33	5.33	24.67	5.41	2.80	3.39
12.	IC 470177	48.00	94.00	39.67	4.00	4.83	5.67	25.00	4.93	4.52	3.13
13.	IC 426471	49.00	87.00	48.67	3.33	4.67	6.00	45.67	12.26	7.61	2.93
14.	IC 278826	49.00	89.00	25.33	2.00	4.67	6.67	18.33	4.45	3.56	4.67
15.	IC 107247	50.00	90.00	50.00	4.00	6.00	6.00	76.00	15.13	10.00	3.30
16.	IC 426537	51.00	95.00	58.67	5.67	5.00	6.00	50.67	18.95	10.22	3.27
17.	IC 467863	47.00	93.00	22.67	1.67	4.33	5.00	20.00	7.41	3.86	2.98
18.	IC 313367	46.00	86.00	28.00	3.67	4.33	5.00	17.67	7.57	4.43	5.01
19.	IC 426486	48.00	92.00	45.33	5.33	4.83	6.00	27.33	7.24	2.64	2.91
20.	IC 470206	47.00	91.00	48.33	6.33	4.50	5.67	45.00	13.48	8.49	3.69
21.	IC 470167	49.00	85.00	49.33	5.67	5.00	6.00	59.33	12.94	7.04	3.60
22.	IC 108079	46.00	93.00	45.00	4.00	3.50	5.00	40.00	8.79	5.14	3.01
23.	IC 426493	50.00	89.00	25.33	2.67	5.00	6.00	13.33	4.06	1.54	3.01
24.	IC 470196	45.00	87.00	26.00	2.00	3.40	5.00	22.00	3.15	2.87	3.78
25.	IC 426524	48.00	87.00	34.00	4.00	4.33	5.67	31.67	15.88	11.38	3.09
26.	IC 426464	47.00	89.00	23.67	3.00	4.17	5.00	17.67	11.07	9.53	2.49

S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
27	IC 18344	50.00	90.00	27.33	4.33	4.50	5.00	14.00	3.09	2.12	2.76
28	IC 426553	52.00	96.00	36.33	5.33	4.50	6.00	35.67	10.54	6.41	2.57
29	IC 426571	51.00	87.00	37.33	3.67	4.67	6.00	59.33	16.34	12.80	2.93
30	IC 108078	50.00	89.00	21.00	2.00	3.75	5.00	19.00	12.41	10.20	3.40
31	IC 467865	49.00	90.00	17.00	1.67	4.50	5.00	22.33	13.37	10.67	3.72
32	IC 426538	48.00	92.00	29.67	3.33	4.00	5.33	51.67	20.42	13.24	2.80
33	IC 426523	46.00	88.00	29.67	7.33	4.00	5.33	40.00	18.28	12.42	2.82
34	IC 426549	47.00	94.00	19.67	4.00	4.00	5.33	25.00	15.08	11.49	2.56
35	IC 426575	49.00	91.00	35.00	6.00	4.50	5.50	25.50	4.97	3.47	3.01
36	IC 426574	50.00	90.00	43.00	7.00	4.50	6.00	50.00	19.56	12.33	3.08
37	IC 526965	51.00	97.00	41.00	6.33	4.17	5.33	41.67	18.60	12.49	2.69
38	IC 426517	48.00	94.00	29.50	4.67	4.00	5.00	54.67	19.89	12.97	2.55
39	IC 426550	49.00	91.00	17.33	2.67	4.00	5.67	24.67	13.21	10.08	3.37
40	IC 426539	51.00	89.00	27.00	5.00	3.50	5.00	49.00	11.80	11.01	3.35

S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
41	IC 426533	52.00	90.00	29.33	4.67	4.50	5.67	39.00	17.63	12.30	2.80
42	IC 426522	50.00	88.00	28.33	3.67	4.33	5.33	46.33	16.02	11.57	2.47
43	IC 261278	49.00	95.00	35.33	3.00	4.00	5.33	43.67	19.46	12.18	3.24
44	CRHG-1	47.00	93.00	40.00	5.00	4.00	5.00	56.00	15.68	10.94	3.75
45	IC 107222	48.00	92.00	21.33	4.00	4.33	6.00	33.33	19.02	12.29	4.49
46	IC 14351	51.00	90.00	23.00	2.00	4.75	6.00	24.00	8.45	3.48	3.86
47	IC 470170	50.00	89.00	42.33	4.33	4.17	5.00	53.67	19.85	11.90	2.92
48	IC 108076	52.00	86.00	17.83	2.00	4.50	5.00	17.00	12.28	10.02	4.34
49	IC 426535	49.00	88.00	36.33	4.33	4.17	5.67	40.33	18.00	12.26	3.29
50	IC 470188	50.00	93.00	30.33	5.00	4.83	6.33	53.33	14.79	12.24	3.30
51	IC 106914	51.00	96.00	42.00	4.00	4.67	5.67	32.67	7.63	6.58	4.17
52	IC 470262	49.00	90.00	55.67	7.33	4.83	5.67	54.00	10.77	9.04	3.47
53	IC 426544	59.00	89.00	26.33	9.33	4.33	4.67	20.00	7.17	6.03	2.66
54	IC 470166	59.00	90.00	26.17	4.33	4.17	5.00	16.67	11.07	10.56	2.81
55	IC 426551	46.00	92.00	40.00	4.67	4.67	6.00	46.67	11.06	5.89	3.43
56	IC 426526	50.00	86.00	26.33	7.33	4.00	4.33	22.67	5.38	2.53	3.23
S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
57	IC 426543	51.00	95.00	34.00	3.67	4.33	5.00	30.00	6.88	4.68	2.75
58	IC 426478	50.00	93.00	28.33	7.33	4.33	5.33	29.00	14.56	11.18	3.39
59	IC 426472	48.00	88.00	65.00	5.00	4.83	6.00	38.67	10.33	5.45	2.93
60	IC 426540	49.00	87.00	43.33	4.00	4.33	6.00	50.00	14.25	10.10	2.93
61	IC 313366	54.00	95.00	18.00	2.00	4.00	4.00	20.00	6.18	4.20	3.40
62	IC 470197	47.00	97.00	38.00	4.00	4.33	5.33	34.33	7.19	2.99	3.52
63	IC 426555	55.00	91.00	24.33	2.67	3.83	5.67	37.67	6.44	3.22	2.32
64	IC 426518	50.00	94.00	16.00	3.33	4.33	5.33	22.67	7.35	4.95	2.97
65	IC 426470	52.00	90.00	40.67	4.67	4.83	5.33	71.00	12.50	4.42	3.23
66	IC 426572	48.00	96.00	42.00	4.67	4.83	5.67	36.00	6.38	4.30	2.86
67	IC 426577	47.00	95.00	54.00	4.67	4.83	5.33	34.00	7.80	3.14	2.90
68	IC 470289	51.00	92.00	40.33	4.33	4.83	6.33	46.00	9.84	5.32	3.31
69	IC 526966	49.00	90.00	25.50	5.50	5.50	6.00	37.50	5.85	3.30	2.90
70	IC 470208	46.00	86.00	35.33	6.00	4.50	5.00	64.33	11.18	6.76	3.02
71	IC 526968	48.00	93.00	37.33	4.33	4.50	5.67	37.67	5.14	2.60	3.12
72	IC 470244	49.00	88.00	55.33	4.33	4.33	5.67	45.67	9.98	4.76	3.17

S. No	Genotype	D50	DM	PH	BR	PL	SPP	NOP	PW	SY	100SW
73	IC 426536	51.00	89.00	25.33	3.00	4.50	5.33	18.67	3.83	2.61	3.52
74	IC 470313	50.00	92.00	48.00	4.67	4.50	5.33	67.00	12.77	5.18	3.28
75	IC 470229	52.00	94.00	47.00	5.00	5.00	5.50	80.00	15.42	7.69	3.38
76	IC 470267	49.00	96.00	40.33	4.00	4.50	5.33	32.67	5.78	3.14	3.12
77	IC 470288	48.00	91.00	48.00	6.33	4.50	6.33	55.67	8.28	4.52	3.28
78	IC 343872	48.00	95.00	42.50	4.00	5.50	5.50	31.50	5.91	5.56	2.72
	Minimum	45.00	85.00	15.00	1.00	3.40	4.00	9.50	2.84	1.54	2.32
	Maximum	60.00	97.00	65.00	9.33	6.00	6.67	80.00	20.42	13.24	5.01
	Mean	50.25	91.15	34.39	4.20	4.43	5.46	38.17	10.37	6.81	3.20
	C.V(%)	3.40	1.23	6.96	7.09	4.40	6.52	9.29	4.77	8.02	8.04
	C.D at 5%	5.39	3.53	7.51	0.94	0.61	1.12	11.45	1.50	1.68	0.81

**Table 3. List of superior genotypes for different characters**

S.no	Character	Rank	Genotypes	Values
1	Days to 50% flowering	1	IC 470196	45.00
		2	IC 313367	46.00
		3	IC 108079	46.00
		4	IC 426523	46.00
		5	IC 426551	46.00
2	Days to maturity	1	IC 470167	85.00
		2	IC 313367	86.00
		3	IC 108076	86.00
		4	IC 426526	86.00
		5	IC 470208	86.00
3	Plant height (cm)	1	IC 426472	65.00
		2	IC 426537	58.67
		3	IC 470262	55.67
		4	IC 470244	55.33
		5	IC 426577	54.00
4	Number of branches per plant	1	IC 426544	9.33
		2	IC 426523	7.33
		3	IC 470262	7.33
		4	IC 426526	7.33

S.no	Character	Rank	Genotypes	Values
5	Pod length (cm)	5	IC 426478	7.33
		1	IC 107247	6.00
		2	IC 526966	5.50
		3	IC 343872	5.50
		4	IC 426493	5.00
6	Number of seeds per pod	5	IC 470229	5.00
		1	IC 278826	6.67
		2	IC 470172	6.33
		3	IC 470188	6.33
		4	IC 470289	6.33
7	Number of pods per plant	5	IC 470288	6.33
		1	IC 470229	80.00
		2	IC 107247	76.00
		3	IC 426470	71.00
		4	IC 470313	67.00
8	Pod weight (g)	5	IC 470208	64.33
		1	IC 426538	20.42
		2	IC 426517	19.89
		3	IC 470170	19.85
		4	IC 426574	19.56
9	Seed yield per plant (g)	5	IC 261278	19.46
		1	IC 426538	13.24
		2	IC 426517	12.97
		3	IC 426571	12.80
		4	IC 526965	12.49
10	100 seed weight (g)	5	IC 426523	12.42
		1	IC 313367	5.01
		2	IC 278826	4.67
		3	IC 107222	4.49
		4	IC 108076	4.34
		5	IC 106914	4.17



**Table 4. Estimates of variability, heritability and genetic advance as percent of mean for yield and component parameters in Horse gram**

S. No	Characters	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV(%)	GCV(%)	Heritability inbroad sense ( $h^2$ ) (%)	Genetic Advance as %mean
			Min.	Max						
1.	Days to 50% flowering	50.25	45.00	60.00	12.73	9.82	7.10	6.23	77.09	11.29
2	Days to maturity	91.15	85.00	97.00	9.68	8.43	3.41	3.19	87.09	6.13
3	Plant height (cm)	34.39	15.00	65.00	127.50	121.84	32.83	32.09	95.56	64.73
4	Number of Branches	4.20	1.00	9.33	2.61	2.52	38.52	37.85	96.58	76.74
5	Pod length (cm)	4.43	3.40	6.00	0.19	0.16	9.94	8.92	80.52	16.52
6	Seed per pod	5.46	4.00	6.67	0.27	0.14	9.53	6.96	53.25	10.47
7	Number of pods	38.17	9.50	80.00	242.86	229.71	40.83	39.71	94.59	79.67
8	Pod weight (g)	10.37	2.84	20.42	24.59	24.36	47.84	47.62	99.08	97.79
9	Seed yield (g)	6.81	1.54	13.24	13.30	13.02	53.57	53.00	97.88	108.18
10	100 seed weight (g)	3.20	2.32	5.01	0.25	0.18	15.47	13.24	73.25	23.37

### 3.3 Variability, Heritability and Genetic Advance

The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the traits. The narrow difference between PCV and GCV indicated the less influence of the environment on these characters. The results are similar with Singhal et al., [8] in horse gram and Owusu et al., [9] in cowpea. The character's plant height, number of branches, number of pods, pod weight, and seed yield per plant exhibited high estimates of GCV and PCV which indicated that a large amount of variability is present among the genotypes studied. Similar results were obtained by Sharma et al., [10] for plant height, number of branches, and seed yield per plant in cowpea, Singh et al., [11], Gomashe et al., [12] and Nimbale et al., [13] for seed yield per plant in horse gram, Mate et al., [14] for seed yield per plant and number of pods per plant in horse gram, Rakesh et al., [15] and Hemalatha et al., [16] for number of pods per plant in horse gram and black gram crops respectively. High heritability coupled with high genetic advance was observed for plant height, number of branches per plant, number of pods per plant, pod weight, seed yield per plant, and 100 seed weight which indicated that the characters are controlled by additive gene action and thus simple and direct selection is effective for the improvement of these traits. Similar results are found with Gowsalya et al., [17] for plant height in black gram, Kumar et al., [18] for number of branches, number of pods per plant, Seed yield per plant and plant height in black gram, Mate et al., [19] for number of pods per plant and Nimbale et al., [20] for seed yield per plant in horse gram, Verma et al., [21] for plant height, number of branches per plant, number of pods per plant, pod weight and 100 seed weight in cowpea. Moderate estimates of heritability and genetic advance was observed for number of seeds per pod. High estimates of heritability and moderate levels of genetic advance was observed for days to 50% flowering and pod length. High heritability and low genetic advance values were observed for days to maturity. The variability estimates along with heritability and genetic advance as per cent of mean are presented in the Table 4.

### 4. CONCLUSION

In any crop improvement program, knowledge of certain genetic parameters like heritability

estimates and genetic advance is essential for proper understanding and their manipulation. The quantitative characters under study had high heritability, which suggests that selecting for these traits may result in genetic improvement. High estimates of genetic advance expressed as a per cent of mean suggested the possibility of regulation of additive genes through effective selection techniques. A breeding program's effectiveness in improving quantitative traits is heavily dependent on the size of the diversity of the accessible germplasm [22]. Goodman [23] highlighted the value of breeding stock and germplasm accessions by suggesting that even if the lines seem uninteresting phenotypically, but may have unrealized potential alleles or potential allelic combinations. Promising accessions for different traits are reported in Table 3, which may be used in breeding programs for parental selection to increase production and to enhance yield attributing traits in horse gram.

### COMPETING INTERESTS

Authors have declared that no competing interests exist.

### REFERENCES

1. Bogdan AV. The more important species: Tropical pastures and fodder plants (Grasses and Legumes). Longmen, London. 1977;236-241.
2. Annual report, All India Network Research Project on Arid Legumes, 2021-2022.
3. Gopalan C, Ramasastri BV, Balasubramaniam SC. Nutritive values of Indian foods. 2012;48.
4. Kumar D. Production technology for horse gram in India. ICAR-Central Arid Zone Research Institute, Jodhpur, Rajasthan. 2007;1-20.
5. Yadav S. Protein and oil rich wild horse gram. Genetic Resources and Crop Evolution. 2004; 51:629-633.
6. Viswanatha KP, Yogesh LN, Amitha K. Morphological diversity study in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc] based on Principal Component Analysis (PCA) Electronic Journal of Plant Breeding. 2016;7(3):767- 770.
7. Federer WT. Augmented design with one-way elimination of heterogeneity. Biometrics. 1961;17(3):447-473.
8. Singhal HC, Tomar SS, Baraiya BR, Sikarwar RS, Tomar IS. Study of genetic divergence in horse gram (*Macrotyloma*

- uniflorum* L.). Legume Research-An International Journal. 2010;33(2):119-123.
9. Owusu EY, Karikari B, Kusi F, Haruna M, Amoah RA, Attamah P, Adazebra G, Sie EK, Issahaku M. Genetic variability, heritability and correlation analysis among maturity and yield traits in Cowpea (*Vigna unguiculata* (L) Walp) in Northern Ghana. Heliyon. 2021;7(9).
  10. Sharma M, Sharma PP, Sharma H, Meghwal DR. Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm lines. Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1384-1387.
  11. Singh R, Salam JL, Mandavi NC, Saxena RR, Sao A. Genetic diversity estimation in horse gram [*Macrotyloma uniflorum* (L.) Verdcout] genotypes collected from Bastar plateau. International Journal of current Microbiology and Applied sciences. 2019;8(12):613-620.
  12. Gomashe SS, Dikshit N, Chand D, Shingane SN. Assessment of genetic diversity using morpho-agronomical traits in horse gram. International journal of current microbiology and Applied sciences. 2018;7:2095-2103.
  13. Nimbale AM, Vijaykumar AG, Naik VR. Genetic variability and association studies for yield and yield attributing traits in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. The Pharma Innovation. 2021; 10(12):2545-2548
  14. Mate PA, Bhavsar VV, Matere BS, Girase VS. screening of genetic variability for yield and its components in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. local germplasm. Journal of Agriculture Research and Technology. 2021; 47(1):078-082
  15. Rakesh A, Hemalatha V, Eswari KB, Swarnalatha, V. Genetic variability correlation and path analysis for yield and its components in horse gram (*Macrotyloma uniflorum* [Lam.] Verdc). Green farming. 2016;7(4):1-4.
  16. Hemalatha K, Lal SS, Lal GM. Study on genetic variability and correlation in black gram (*Vigna mungo* L. Hepper). Journal of Pharmacognosy and Phytochemistry. 2017;6(4):674-676.
  17. Gowsalya P, Kumaresan D, Packiaraj D, Kannan Bapu JR. Genetic variability and character association for biometrical traits in black gram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding. 2016;7(2):317-324.
  18. Kumar P, Singh SK, Shukla RS, Elahi T, Prajapati SS, Rahangdale S, Upadhyay S. Estimation of genetic parameters for yield and yield contributing characters in black gram [*Vigna mungo* (L.) Hepper] genotypes. The pharma innovation. 2022; 11(9):2622-2624.
  19. Mate PA, Bhavsar VV, Matere BS, Girase VS. Screening of genetic variability for yield and its components in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. local germplasm. Journal of Agriculture Research and Technology. 2021;47(1): 078-082.
  20. Nimbale AM, Vijaykumar AG, Naik VR. Genetic variability and association studies for yield and yield attributing traits in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. The Pharma Innovation. 2021; 10(12):2545-2548.
  21. Verma AK, Mehta AK, Gontia AS, Sharma D, Singh RP, Singh P. Genetic variability, heritability and genetic advance studies for yield components in F2 generation of cowpea (*Vigna unguiculata* L. Walp). International Journal of Chemical studies. 2019;7(6):3084-3088.
  22. Hanna W, Ozias-Akins P, Roche D. Apomixis and heterosis. Genetics and Exploitation of Heterosis in Crops. 1999;335-342.
  23. Goodman MM. Broadening the genetic diversity in maize breeding by use of exotic germplasm. Genetics and exploitation of heterosis in crops. 1999;139-148.

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