



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(12): 2545-2548
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www.thepharmajournal.com
Received: 10-10-2021
Accepted: 23-11-2021

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Genetic variability and association studies for yield and yield attributing traits in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.]

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Abstract

Present investigation was carried out with 29 horsegram genotypes at Seed Unit, UAS, Dharwad, to assess genetic variability, correlation and path analysis of for seven quantitative characters. The Analysis of variance exhibited highly significant differences among the genotypes for most of the traits. Higher PCV coupled with high GCV was observed for seed yield per hectare (25.04% and 23.10%), revealing a wide range of variation for yield improvement. High heritability coupled with high genetic advance as percent of mean was observed for seed yield per hectare (85.10% and 43.91) indicating additive gene action and the ample scope for improvement in these characters through simple selection. Significant and positive correlation coefficients were recorded between number of branches per plant, plant height and number of seeds per pod; Significant and positive correlation was exhibited between pod length and number of seeds per pod whereas, significant and negative association between number of pod per plant and pod length. Seed yield per witnessed positive correlation was with all the traits except number of seeds per pod. Except number of seeds per pod (-0.7007) all other traits had recorded direct positive effect on seed yield. Residual effect (0.5785) revealed influence of other factors on yield were not considered in the model and requires further study.

Keywords: Horsegram, genetic variability, quantitative traits, correlation and path analyses

Introduction

Horsegram (*Macrotyloma uniflorum* (Lam) Verdc.) is a hardy, drought tolerant legume crop adapted to wide range of Indian agricultural regimes. It has origin in India (Bogdan, 1977) [3]. Karnataka is one of the major states with large area under horsegram cultivation. Horsegram having very high nutritional value forms an important protein source to the farmers in rural/tribal areas (Dikshit *et al.*, 2014) [6]. Horse gram seeds contains nearly 27% protein (Kumar, 2007) [8] and relatively high in lysine content compared to other pulses like chick pea and red gram (Yadav, 2004) [16]. Taxonomically the crop belongs to the family Fabaceae with diploid chromosome number (2n=20, 22, 24). Horse gram has extraordinary therapeutic properties and enriched with medicinal benefits thus occupy an important role in Indian traditional ayurvedic treatments. It also plays very important role for sustainable farming system due its atmospheric nitrogen fixation ability. Generally, the crop is cultivated in marginal lands or resource poor soils as a rainfed crop which led to low productivity and hence requires focused scientific efforts in development of climatic resilient (Vijayakumar *et al.*, 2016) [15] varieties with yield potential. Breeding for high yielding varieties in horsegram would help to attain the nutritional security in developing countries. Information on genetic improvement of this crop is very limited and very few efforts have been made for the improvement. Looking into the importance of this crop an investigation was carried out to assess the genetic variability parameter, nature and degree of association among the characters and their direct and indirect effects on yield. Generally, due to low heritability direct selection for yield is not so effective. Thus, selection based on its contributing characters could be more efficient and reliable (Kumar *et al.*, (2013a) [9]; Kumar *et al.*, (2013b) [10].

In any crop improvement programme, knowledge on certain genetic parameters like heritability estimates and genetic advance is essential for proper understanding and their manipulation. Estimates of correlation coefficients, gives information on direction of character association. The estimation of direct and indirect relationship between traits is important for yield improvement in plant breeding (Dewey and Lu, 1959) [5]. Path coefficient analysis is helpful under such situation.

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The present investigation was carried out for estimating the nature and magnitude of variability; inheritance pattern of favorable traits, association between traits and importance of direct and indirect effect of traits on yield in horsegram.

Materials and Methods

A total of 29 diverse genotypes collected from diverse sources (Table 1). Were evaluated in a randomized complete block design (RCBD) with three replications at Seed Unit, University of Agricultural Sciences, Dharwad during the year 2019-20. The meteorological data of experimentation plot is presented in the Table 2. The experiment was carried out with the plot size of 4 x 2.25 m² of each genotype having 6 rows. Row to row and plant to plant distance were maintained at 45 and 10cm respectively. All the recommended agronomic practices to raise a healthy crop were followed. The observations were recorded on five randomly selected plants per replication for each genotype. The observations for eight quantitative traits viz., days to fifty percent flowering, plant height (cm), primary branches per plant, pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per hectare (kg). The genotypic and phenotypic variances and genetic advance were calculated as suggested by Johnson *et al.*, (1955) [7]. Genotypic and phenotypic coefficients of variations (Burton, 1952) [4], heritability in broad sense (Lush, 1940) [12] and path coefficients for yield and its components traits (Dewey and Lu., 1959) [5] were computed.

Results and Discussion

The results of variances for yield and its related traits are presented in the Table 3. The analysis of variance (ANOVA) exhibited significant variation ($P < 0.05$) for the quantitative traits under study (Table 1) indicating presence of variability and offers some scope for bringing improvement in horsegram.

The mean performance of all 29 horsegram genotypes for yield and yield attributing characters along with checks is presented in Table 2. In the present study, among the 29 genotypes evaluated, Paiyur-1 recorded highest seed yield per ha (1261.50 kg) compared to the check PHG-9 (1047.64 kg).

Many of the genotypes have recorded significant superiority for 100 seed weight and pod length. The genotype VHG-44 (5.83 cm) recorded longest pod length compared to check PHG-9 (5.10 cm). Similarly, GHG-4 exhibited highest test weight of 4.5 g against best check GPM-06 (4.27 g). Shortest and longest plant height was noticed in genotypes CHG-1 (49.17 cm) and KBHG-1 (74.33.5 cm) respectively. The genotype GHG-4 is superior for number of seeds per pod, pod length, and 100 seed weight. The results of the present study is in accordance with Lata, (2013) [11], Alle *et al.*, (2016) [1], Priyanka *et al.*, (2019) [14] and Nileema *et al.*, (2020) [13].

Genotypic and Phenotypic coefficient of variability

The estimates of genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance (GA) were presented in Table 3. The phenotypic coefficients of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the traits. So it is evident that the expression of the characters was mainly governed by the genotypes itself along with meager effect of

environment. This finding is in accordance with Lata, (2013) [11] and Nileema *et al.*, (2020) [13].

High phenotypic and genotypic coefficient of variability was exhibited by the trait seed yield per hectare (25.04% and 23.10%). Moderate coefficient of variability both at phenotypic and genotypic level was observed for number of seeds per pod (18.29% and 12.82%), 100 seed weight (11.14% and 10.12%). While the traits, days to 50% flowering and number of seeds per pod were observed to have low values of phenotypic and genotypic coefficient of variability *i.e.*, (6.25% and 5.69%) and (6.86% and 4.20%), respectively. This estimate of the present study were authorised with the findings of Alle *et al.*, (2016) [1] and Priyanka *et al.*, (2019) [14]. Heritability and Genetic advance over mean acts as a predictive measure for designing the selection procedure in a breeding programme. Heritability in broad sense helps in identifying the appropriate character for selection and enable the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits (Robinson 1966). In the present investigation there was wide range in the heritability observed *i.e.*, 32.80%-85.10% suggesting for adoption of simple selection technique on basis of phenotypic expression of character since there is less influence of environment. The high heritability was recorded for the characters *i.e.*, days to 50% flowering (82.70%), test weight (81.00%) and grain yield per hectare (85.10%). Genetic gain is the genetic advance expressed as percent of population mean (GAM). In the present study, genetic gain was high for only for grain yield per hectare (43.91%). While it was moderate for days to 50% flowering (10.65%), plant height (11.25%), number of branches per plant (10.25%), number of pods per plant (18.52%), 100 seed weight (16.91%) and it was observed low for pod length (5.13% and number of seeds per pod (5.29%). Heritability estimates coupled with genetic advance provide a reliable measure for predicting the genetic gain under selection. High heritability coupled with high estimates of genetic gain were observed for trait grain yield per. The trait viz., days to flowering exhibited moderate GAM with high heritability which signifies the importance of non-additive effects and the high heritability results due to favorable influence of environment Priyanka *et al.*, (2019) [14] and Nileema *et al.*, (2020) [13].

Correlation and path analysis

In the present study, the correlation coefficients at genotypic level (Table 4). Were generally of higher magnitude than the corresponding phenotypic level. Significant and positive correlation coefficients were recorded between number of branches per plant, plant height and number of seeds per pod; Significant and positive correlation was exhibited between pod length and number of seeds per pod whereas, significant and negative association between number of pod per plant and pod length. Seed yield per witnessed positive correlation was with all the traits except number of seeds per pod. These results concur with those reported by Priyanka *et al.*, (2019) [14] and Nileema *et al.*, (2020) [13]. Except number of seeds per pod (-0.7007) all other traits had recorded direct positive effect on seed yield (Table5). Residual effect (0.5785) indicated that other factors influencing the yield were not considered in the model and requires further study.

Table 1: Analysis of variances for different traits in horsegram

Source of variation	Df	DF	PH	NBP	NPP	PL	NSP	100 SW	SY/ha
Replication	2	7.537	17.769	5.138	80.261	0.251	0.118	0.058	10587.13
Genotype	28	51.020**	99.032**	1.089*	66.220*	0.166	0.210**	0.434*	146057.23**
Error	56	3.317	29.471	0.376	16.976	0.067	0.075	0.031	8038.31
CD at 5%		2.979	8.8795	1.003	6.739	0.424	0.449	0.290	146.644
CV %		2.599	9.2862	10.079	13.042	6.215	5.426	13.753	9.658

DF=days to fifty percent flowering, PH=plant height (cm), NBP= No. of branches per plant, NPP= No. of pods per plant, NSP=No. of seeds per pod, 100SW= 100 seed weight (g), PL=pod length (cm), SYP=seed yield per ha (kg).

Table 2: Mean values for yield and its component traits in horsegram

Sl. No.	Genotypes	DF	PH	NBP	NPP	NSP	PL	100 SW	SY/ha
1.	CRHG-4	61.83	52.87	6.20	42.76	4.10	5.27	3.60	661.50
2.	CRHG-19	62.33	52.33	4.87	31.20	4.10	5.10	3.73	457.30
3.	White Seeded HG	61.83	52.20	5.10	29.00	4.27	4.90	3.30	634.40
4.	PHG-4	71.66	55.66	6.00	35.90	3.90	4.80	3.50	1259.37
5.	VHG-44	71.00	68.90	6.80	39.70	4.20	5.83	4.40	960.40
6.	GHG-4	73.00	53.87	6.10	26.00	4.63	5.50	4.50	713.53
7.	CHG-1	74.33	49.17	6.50	28.30	4.33	5.40	4.23	882.30
8.	Paiyur-1	66.67	57.40	6.50	32.90	4.33	4.80	4.33	1261.50
9.	Paiyur-2	68.33	52.60	5.80	27.50	3.80	4.90	4.23	1083.33
10.	AK-21	73.00	64.43	5.50	28.60	4.40	4.80	3.97	1029.20
11.	AK-44	67.00	56.00	5.90	27.60	4.30	5.10	4.30	740.60
12.	AK-42	72.66	55.33	6.30	25.30	4.43	5.20	4.00	1051.03
13.	AK-22	74.66	73.53	7.00	23.30	4.57	5.50	2.93	1218.77
14.	DWD Local-3	72.66	62.17	5.30	28.47	4.47	5.10	4.10	602.07
15.	VLG-19	70.00	53.13	5.47	26.57	4.33	4.90	4.10	899.87
16.	VLG-14	71.50	56.97	6.40	29.90	3.90	4.70	4.27	846.87
17.	CRHG-6	67.00	61.30	6.30	29.50	4.23	5.00	4.07	1069.80
18.	DWD Local-1	73.00	63.00	7.50	36.40	3.97	5.10	3.80	924.00
19.	VLG-15	68.66	62.27	5.80	28.70	4.00	5.10	4.40	1014.60
20.	CRHG-10	71.00	54.73	6.10	31.60	4.03	5.10	4.37	948.97
21.	AK-41	73.67	54.57	5.80	35.20	3.93	4.90	4.20	786.47
22.	VLG-10	70.33	60.27	5.60	28.80	4.30	5.30	4.37	925.03
23.	KBHG-1	74.33	55.27	6.10	33.70	4.30	5.00	4.23	1237.0
24.	BGB1183	73.00	66.50	6.30	31.90	4.00	5.00	4.23	1162.50
25.	DWD Local-2	72.33	58.60	7.00	34.40	4.40	5.00	4.03	1182.30
26.	BLH-1	70.66	61.66	6.57	39.20	3.90	4.66	3.93	942.70
27.	GPM-6	73.00	61.80	6.60	33.70	3.70	4.70	4.27	826.03
28.	CRIDA-18 R	60.00	54.00	5.40	32.20	4.17	5.00	3.60	550.00
29.	PHG-9	72.33	64.90	5.77	37.80	4.07	5.10	3.47	1047.93
CD at 5%		2.979	8.879	1.004	6.790	0.424	0.449	0.291	146.645

DF=days to fifty percent flowering, PH=plant height (cm), NBP= No. of branches per plant, NPP= No. of pods per plant, NSP=No. of seeds per pod, 100SW= 100 seed weight (g), PL=pod length (cm), SYP=seed yield per ha (kg).

Table 3: Estimates of variability parameters for different quantitative traits in horsegram

Characters	Mean	Range		PCV	GCV	h ² bs (%)	GA	GAM
		MIN	MAX					
Days to 50% flowering	70.06	60.00	74.67	6.25	5.69	82.70	7.47	10.65
Plant height(cm)	58.46	49.16	73.53	12.41	8.23	44.0	6.582	11.25
Number of branches/plant	6.088	4.86	7.53	12.87	8.01	38.7	0.624	10.25
Number of pods/plant	31.58	23.33	42.76	18.29	12.82	49.2	5.852	18.52
Pod Length (cm)	5.06	4.66	5.83	7.584	4.34	32.8	0.214	5.13
Number of seeds/pod	4.17	3.70	4.63	6.862	4.20	37.5	0.268	5.29
100 Seed Weight(g)	4.016	2.90	4.50	11.14	10.12	81.0	0.679	16.91
Seed Yield/ha(kg)	928.24	457.30	1261.50	25.04	23.10	85.1	407.670	43.91

GCV: Genotypic coefficients of variation, PCV: Phenotypic coefficients of variation, h²bs: heritability (broad sense), GA: Genetic advance, GAM: Genetic advance as percent of mean

Table 4: Genotypic and phenotypic correlation coefficients among various characters in horsegram

Character		PH	NBP	NPP	100 SW	PL	NSP	SY/ha
PH	P	1.00	0.3018 **	0.2272 *	-0.1612	0.1428	0.3366 **	0.3504
	G	1.00	0.5497	0.0725	-0.1816	0.0962	0.0752	0.4482
NBP	P		1.00	0.2824 **	0.0635	-0.0007	0.2028	0.4205
	G			1.00	0.0635	0.0007	0.2028	0.4205

	G		1.00	0.2446	0.0722	-0.1590	0.1820	0.6158
NPP	P			1.00	0.1283	-0.2912 **	0.0543	0.0820
	G			1.00	-0.0666	-0.7598	-0.2661	-0.1536
100 SW	P				1.00	0.0340	0.0176	0.0053
	G				1.00	-0.1597	0.0126	0.0725
PL	P					1.00	0.4794 ***	0.0318
	G					1.00	0.5832	0.0426
NSP	P						1.00	-0.0192
	G						1.00	-0.1536
SY/ha	P							1.00
	G							1.00

*Significant at 5%, **significant at 1%; PH=plant height (cm), NBP= No. of branches per plant, NPP= No. of pods per plant, NSP=No. of seeds per pod, 100SW= 100 seed weight (g), PL=pod length (cm), SYP=seed yield per ha (kg). G – Genotypic correlation coefficients, P – Phenotypic correlation coefficients.

Table 5: Estimates of direct and indirect effects of various traits on seed yields per ha in horsegram

Traits	PH	NBP	NPP	100 SW	PL	NSP	SY/ha	R
PH	0.2970	0.1633	-0.0215	-0.0539	-0.0286	0.0223	0.4482	0.1331
NBP	0.3453	0.6282	0.1536	0.0454	-0.0999	0.1143	0.6158	0.3868
NPP	-0.0193	0.0651	0.2661	-0.0177	-0.2021	-0.0708	-0.0543	-0.0543
100 SW	-0.0433	0.0172	-0.0159	0.2386	-0.0381	0.0030	-0.0543	0.0173
PL	-0.0433	-0.1304	-0.6230	-0.1309	0.8200	0.4782	0.0426	0.0350
NSP	-0.0527	-0.1275	0.1864	-0.0088	-0.4086	-0.7007	-0.1536	-0.1536

*Significant at 5%, **significant at 1%; Residual effect= 0.5785 r= Genotypic correlation, Diagonal and bold indicates the direct effect. PH=plant height (cm), NBP= No. of branches per plant, NPP= No. of pods per plant, NSP=No. of seeds per pod, 100SW= 100 seed weight (g), PL=pod length (cm), SYP=seed yield per ha (kg).

Conclusion

In the present study, the values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the influence of environmental factors. The genetic analysis showed that high heritability coupled with high genetic advance as per cent of mean was recorded for plant height, test weight and grain yield per hectare which implies that these characters were under the control of additive type of gene action and possess high selective value and thus, suggesting employment of simple selection techniques for improvement of these traits would be more rewarding too.

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