

Original Research Article

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Investigation on Genetic Variability Parameters and Association of Traits in Horsegram (*Macrotyloma uniflorum* (Lam) Verdc.)

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ABSTRACT

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The extent of genetic variability and association between twelve quantitative traits in 252 horsegram genotypes was assessed. The study revealed the existence of wide range of variability in the genotypes. The difference between GCV and PCV was narrow which indicated less influence of environment on trait expression. High variability coupled with greater heritability and genetic advance was recorded in six traits viz., plant height, number of clusters per plant, number of primary branches, number of pods per plant, number of pods per cluster and single plant yield indicating better scope for improvement of these traits through adoption of simple selection techniques. Correlation and path analysis revealed that six traits viz., number of cluster per plant, plant height, pod length, number of pods per plant, number of pods per cluster and number of seeds per pod had positive and direct effects with yield. Additionally these traits were also found to be influencing with yield indirectly through other yield attributing traits. Therefore, prioritized selection of these traits would be more promising for horsegram yield improvement.

Introduction

Horsegram (*Macrotyloma uniflorum* (Lam) Verdc.) is a hardy, drought tolerant legume crop adapted to wide range of Indian agricultural regimes. Horsegram is a promising nutritious crop; seeds contain relatively high lysine content compared to chickpea and red gram (Yadav, 2004). It is enriched with medicinal benefits which occupy an important role in Indian traditional medicine. Owing to these virtues, it is commonly known as poor man's pulse crop. Horsegram is also grown as a green manure

crop because of its high potential towards atmospheric nitrogen immobilization. Generally, the crop is cultivated in marginal lands which led to low productivity and hence warrants focused scientific efforts like development of climatic resilient (Vijayakumar *et al.*, 2016) varieties with yield potential. Breeding for high yielding varieties in horsegram would pave way to cater the nutritional security in developing countries.

Germplasm is serving as a genetic wealth of a nation as it possesses the pool of favorable genes. Tamil Nadu Agricultural University,

India is maintaining a germplasm of 790 accessions. The knowledge on genetic variability of a germplasm collection/pre breeding stock is an essential prerequisite for initiating any crop improvement programme through plant breeding (Babu *et al.*, 2012). Estimates of genetic parameter would offer better understanding on nature and magnitude of variability present in a population and thereby helpful in deciding appropriate selection techniques. Yield is a complex trait governed by polygenes; exhibiting low heritability too and hence direct selection for yield is offering limited scope. Hence selection based on components associated with yield would be more efficient and reliable (Kumar *et al.*, 2013). Estimates of correlation coefficients, gives information on direction of trait association. The estimation of indirect relationship between traits is essential for targeted success in plant breeding (Dewey and Lu, 1959). A clear understanding on association of traits and its direct and indirect effects on yield would improve selection efficiency. Joshi *et al.*, (2018) in a chickpea RIL population, Rakesh Gandhi *et al.*, (2018) in a blackgram segregating population and Narmada Varma *et al.*, (2018) in a greengram germplasm had estimated the GCV, PCV, genetic advance and heritability of yield attributing traits and suggested the appropriate breeding methodology. Alle *et al.*, (2015) estimated the extent of variability parameters and association between traits in horsegram. The present experiment was focused on 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 a part of TNAU germplasm accession.

Materials and Methods

The experimental material comprises of 252 horsegram germplasm accessions of Tamil

Nadu Agricultural University (TNAU) which includes 250 accessions and two varieties *viz.*, PAIYUR 2 (released by TNAU) and CRIDA1-18 R (released by Central Research Institute for Dryland Agriculture) (Table 1). The genotypes were sown in 4m lengthened row with a spacing of 30 cm x 10 cm during *rabi* season of 2017 at experimental farms of Department of Pulses, TNAU, Coimbatore. The accessions were raised in Randomized Block Design and replicated twice. Data was recorded on five randomly selected plants for 12 quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, pod length (cm), pod width (cm), number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). Except days to flowering and maturity, other yield contributing traits were recorded at harvest. Computation of genotypic variance, phenotypic variance and genetic advance was done as per formula of Johnson *et al.*, (1955a). Genotypic and phenotypic coefficient of variation (Burton, 1952), heritability in broad sense (Lush, 1940), correlation coefficient (Singh and Chaudhary, 1995) and path analysis (Dewey and Lu, 1959) were estimated as per the procedure of the authors given in the parentheses. The statistical analyses were done using Indostat-version 7.1 software.

Results and Discussion

Horsegram, the underutilized but therapeutic and nutritionally potential fabaceae crop requires less or no water and sustains the livelihood of marginal and poor Indian farmers during *rabi* season. It requires attentive scientific intervention to enhance the yield potential and thereby to gratify the nutritional requirements of downtrodden farmers. Development of multiple stress tolerant; better yielding and quality

possessing varieties is the major part of such intrusion. The probability of success in any breeding programme depends on the existence of wide range of variability for the trait concerned. Collection and conservation of germplasm offers a possible mean for restoration of genetic variability and also act as a reservoir for future breeding strategies. On the mission of germplasm conservation, TNAU is maintaining a total of 790 horsegram accessions. Of this totality, 252 accessions were utilized to study the magnitude of variability and correlation analyses. The analysis of variance (ANOVA) exhibited significant differences among genotypes for all 12 quantitative traits studied; indicated the existence of greater variability and offers some scope for bringing improvement in horsegram.

The estimates of genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance (GA) were presented in table 2. The values of PCV and GCV values were categorized as low (below 10%), moderate (11%-20%) and high (above 20%) according to the scale given by Sivasubramanian and Menon, 1973. The traits studied in this experiment showed all the above three classes of GCV and PCV. Traits *viz.*, single plant yield (48.881% and 49.371%) followed by number of pods per plant (45.370% and 45.657%) recorded the highest GCV and PCV. Similar results were also noticed by Alle *et al.*, (2015) and Vijayakumar *et al.*, (2016) in horsegram. The lowest percent of GCV and PCV were recorded in days to maturity (2.913% and 2.996%) followed by days to 50% flowering (5.299% and 5.374%). Moderate GCV and PCV values were scored by pod length, pod width, number of seeds per pod and hundred seed weight. The PCV was found to be slightly higher than GCV in all traits studied indicating the importance of greater genetic variability with less influence of environment.

Hence selection based on phenotype will be more reliable in horsegram improvement. Akin suggestion was also opined by Latha *et al.*, 2013.

Heritability (h^2) acts as a predictive measure for designing the selection procedure in a breeding programme. It provides information on heritable portion of observed effects. Classification of heritability into low (below 30%), medium (30% - 60%) and high (above 60%) was suggested by Johnson *et al.*, (1955a). All the characters involved in this study exhibited high heritability which ranged from 0.793 to 0.987 suggesting for adoption of simple selection technique on basis of phenotypic expression of trait since there is less influence of environment. Heritability estimates along with genetic advance provide a reliable measure for predicting the genetic gain under selection. High genetic advance as percent of mean (GAM) coupled with high heritability was observed for all the experimented traits except days to 50% flowering and days to maturity indicating the preponderance of additive gene action in expression of these traits. Hence, suggesting employment of simple selection techniques for improvement of these traits and would be more rewarding too. The trait *viz.*, days to maturity exhibited low GAM with high heritability which signifies the importance of non-additive effects and the high heritability results due to favourable influence of environment. On a nutshell, high variability coupled with high heritability and genetic advance was observed for six traits *viz.*, plant height, number of clusters per plant, number of primary branches, number of pods per plant, number of pods per cluster and single plant yield. Thus there is a great scope for improvement of these traits through selection.

The genotypic (r_g) and phenotypic correlation coefficients (r_p) among 12 quantitative traits were presented in table 3.

Table.1 List of horsegram germplasm accessions

No. of genotypes	Nature of genotypes	Genotypes
250	Accessions	PLS 6007, PLS 6196, PLS 6199, PLS 6229, PLS 6008, PLS 6232, PLS 6040, PLS 6206, PLS 6039, PLS 6038, PLS 6025, PLS 6019, PLS 6036, PLS 6041, PLS 6037, PLS 6179, PLS 6013, HG 19, HG 119, HG 14, PLS 6001, PLS 6213, PLS 6063, PLS 6023, 8606/2-1, PLS 6060, PLS 6073, PLS 6048, PLS 6172, PLS 6074, PLS 6068, PLS 6197, PLS 6208, PLS 6164, PLS 6184, PLS 6006, PAIYUR 2, PLS 6131, PLS 6052, PLS 6089, PLS 6193, PLS 6190, PLS 6177, HG 68, PLS 6216, PLS 6234, PLS 6140, PLS 6231, PLS 6194, PLS 6099, PLS 6186, PLS 6154, PLS 6169, PLS 6181, PLS 6161, PLS 6083, PLS 6107, PLS 6115, PLS 6104, PLS 6175, PLS 6119, PLS 6168, PLS 6141, PLS 6110, PLS 6114, PLS 6081, PLS 6185, PLS 6049, PLS 6165, PLS 6151, PLS 6109, PLS 6230, PLS 6192, PLS 6120, PLS 6102, PLS 6092, PLS 6062, PLS 6112, PLS 6103, PLS 6135, PLS 6085, PLS 6118, PLS 6050, PLS 6242, HG 35, HG 50, PLS 6279, PLS 6262, HG 5A, PLS 6096, PLS 6266, PLS 6018, HG 86, PLS 6237, PLS 6268, PLS 6236, HG 57, HG 58, PLS 6278, PLS 6272, HG 41, PLS 6281, PLS 6280, PLS 6132, 8602/1-2, HG 28, 8514/4-1, PLS 6275, HG 94, PLS 6245, 8605/2-1, 8601/2-5, HG 59, PLS 6117, HG 36, PLS 6240, HG 473, PLS 6263, HG 12, HG 23, HG 21, HG 63, PLS 6055, 8602/2-2, HG 31, HG 121-4, PLS 6282, HG 4, HG 122, 8515/4-1, HG 37, 8515/2-1, 8606/2-3, 8606/2-2, HG 79, HG 18, HG 115, 8606/1-3, PLS 6246, HG 30, HG 125, PLS 6260, HG 121, 8515/1-2, PLS 6252, HG 204, HG 72, HG 9A, PLS 6070, 8605/2-2, PLS 6244, HG 5, PLS 6251, HG 96, HG 93, HG 47, HG 92, PLS 6247, 8605/2-4, PLS 6078, PLS 6125, PLS 6061, PLS 6142, PLS 6077, PLS 6071, PLS 6113, PLS 6106, PLS 6150, PLS 6116, PLS 6047, PLS 6046, PLS 6183, PLS 6090, PLS 6121, PLS 6097, PLS 6088, PLS 6072, PLS 6082, PLS 6201, PLS 6080, PLS 6095, PLS 6051, PLS 6035, PLS 6064, PLS 6270, PLS 6094, PLS 6014, PLS 6009, PLS 6002, HG 67, HG 78, HG 61, PLS 6034, HG 80, HG 43, HG 95, HG 38, PLS 6016, PLS 6003, PLS 6021, 8601/2-1, PLS 6200, PLS 6212, HG 8, 8516/1-1, HG 9, 8606/2-4, PLS 6261, PLS 6043, HG 101, HG 54, PLS 6111, HG 27, PLS 6069, PLS 6005, PLS 6015, PLS 6256, PLS 6258, HG 116, PLS 6217, PLS 6218, PLS 6253, HG 376, PLS 6255, PLS 6227, HG 34, PLS 6066, PLS 6030, PLS 6224, PLS 6219, HG 114, HG 112, PLS 6202, PLS 6205, PLS 6228, HG 120, PLS 6211, PLS 6059, PLS 6233, PLS 6226, HG 90, PLS 6250, 8512/2/1, PLS 6221, 8513/4-3, HG 85, PLS 6105, PLS 6004, PLS 6269, PLS 6033 & HG 2.
2	Varieties in cultivation	PAIYUR 2 CRIDA 1-18 R

Table.2 Estimates of variability and heritability parameters

Traits	GCV	PCV	h ²	GA	GAM
Days to 50 % flowering	5.299	5.374	0.972	6.122	10.762
Days to maturity	2.913	2.996	0.945	6.241	5.833
Plant height	22.156	23.412	0.896	26.215	43.194
Pod length	12.395	12.967	0.914	1.233	24.407
Pod width	16.335	16.887	0.936	0.184	32.551
Number of clusters per plant	31.526	32.016	0.970	29.035	63.947
Number of primary branches	27.140	30.469	0.793	2.967	49.798
Number of pods per plant	45.370	45.657	0.987	106.543	92.877
Number of pods per cluster	29.779	30.144	0.976	1.516	60.602
Number of seeds per pod	13.356	13.840	0.931	1.450	26.551
Hundred seed weight	10.819	11.005	0.967	0.909	21.912
Single plant yield	48.881	49.371	0.980	22.907	28.081

GCV: Genotypic coefficients of variation, **PCV:** Phenotypic coefficients of variation, **ECV:** Environmental coefficients of variation, **h²:** heritability (broad sense), **GA:** Genetic advance, **GAM:** Genetic advance as percent of mean

Table.3 Estimates of genotypic and phenotypic correlation coefficients in horsegram accessions

		DFE	DTM	PH	PL	PW	NCP	NPB	NPP	NPC	NSP	HSW	SPY
DFE	G	1.0000	0.9873**	-0.1289*	-0.0215	-0.2168**	0.0320	0.0378	-0.0872	-0.1960**	-0.1243*	0.0525	-0.0760
	P	1.0000	0.9519**	-0.1220	-0.0180	-0.2073**	0.0295	0.0319	-0.0873	-0.1921**	-0.1186	0.0498	-0.0758
DTM	G		1.0000	-0.1377*	-0.0801	-0.1903**	-0.0183	0.0610	-0.1358*	-0.2119**	-0.1473*	0.0998	-0.1125
	P		1.0000	-0.1253*	-0.0722	-0.1781**	-0.0219	0.0380	-0.1321*	-0.2037**	-0.1403*	0.0959	-0.1108
PH	G			1.0000	0.1153	-0.1594*	0.2886**	0.2492**	0.3740**	0.2939**	0.0552	-0.2042**	0.3266**
	P			1.0000	0.1091	-0.1407*	0.2688**	0.2006**	0.3549**	0.2809**	0.0501	-0.1736**	0.3154**
PL	G				1.0000	-0.4105**	0.2742**	-0.2690**	0.5096**	0.4573**	0.6334**	-0.3606**	0.5659**
	P				1.0000	-0.3606**	0.2570**	-0.2201**	0.4760**	0.4222**	0.5902**	-0.3304**	0.5332**
PW	G					1.0000	-0.1216	0.2622**	-0.1813**	-0.0885	-0.0190	0.3103**	-0.1457*
	P					1.0000	-0.1160	0.2359**	-0.1732**	-0.0865	-0.0107	0.2963**	-0.1356*
NCP	G						1.0000	0.2173**	0.7966**	0.1533*	0.0222	-0.3953**	0.6876**
	P						1.0000	0.1965**	0.7881**	0.1369*	0.0155	-0.3786**	0.6793**
NPB	G							1.0000	0.1412*	0.0163	-0.0782	-0.0681	0.0949
	P							1.0000	0.1253*	0.0183	-0.0691	-0.0554	0.0860
NPP	G								1.0000	0.6927**	0.3082**	-0.4709**	0.9412**
	P								1.0000	0.6861**	0.2910**	-0.4580**	0.9365**
NPC	G									1.0000	0.4746**	-0.3339**	0.7170**
	P									1.0000	0.4544**	-0.3236**	0.7060**
NSP	G										1.0000	-0.1963**	0.4877**
	P										1.0000	-0.1909**	0.4755**
HSW	G											1.0000	-0.3110**
	P											1.0000	-0.2935**

* Significant at 5 per cent level

G – Genotypic correlation coefficients

** Significant at 1 per cent level

P – Phenotypic correlation coefficients

DFE - Days to 50 % flowering, **DTM** - Days to maturity, **PH** - Plant height, **PL** - Pod length, **PW** - Pod width, **NCP** - Number of clusters per plant, **NPB** - Number of primary branches, **NPP** - Number of pods per plant, **NPC** - Number of pods per cluster, **NSP** - Number of seeds per pod, **HSW** - Hundred seed weight, **SPY** - Single plant yield

Table.4 Estimates of direct and indirect effects of different quantitative traits (partitioned by path analysis)

	DFE	DTM	PH	PL	PW	NCP	NPB	NPP	NPC	NSP	HSW	SPY
DFE	-0.3026	-0.2987	0.0390	0.0065	0.0656	-0.0097	-0.0114	0.0264	0.0593	0.0376	-0.0159	-0.0760
DTM	0.3272	0.3314	-0.0456	-0.0265	-0.0631	-0.0061	0.0202	-0.0450	-0.0702	-0.0488	0.0331	-0.1125
PH	0.0010	0.0010	-0.0075	-0.0009	0.0012	-0.0022	-0.0019	-0.0028	-0.0022	-0.0004	0.0015	0.3266**
PL	0.0003	0.0011	-0.0015	-0.0134	0.0055	-0.0037	0.0036	-0.0068	-0.0061	-0.0085	0.0048	0.5659**
PW	0.0051	0.0044	0.0037	0.0096	-0.0233	0.0028	-0.0061	0.0042	0.0021	0.0004	-0.0072	-0.1457*
NCP	-0.0008	0.0004	-0.0071	-0.0067	0.0030	-0.0244	-0.0053	-0.0195	-0.0037	-0.0005	0.0097	0.6876**
NPB	-0.0006	-0.0009	-0.0038	0.0041	-0.0040	-0.0033	-0.0154	-0.0022	-0.0002	0.0012	0.0010	0.0949
NPP	-0.0877	-0.1366	0.3762	0.5126	-0.1824	0.8011	0.1420	1.0057	0.6967	0.3099	-0.4736	0.9412**
NPC	0.0023	0.0024	-0.0034	-0.0053	0.0010	-0.0018	-0.0002	-0.0080	-0.0115	-0.0055	0.0039	0.7170**
NSP	-0.0295	-0.0349	0.0131	0.1502	-0.0045	0.0053	-0.0185	0.0731	0.1126	0.2372	-0.0465	0.4877**
HSW	0.0094	0.0178	-0.0364	-0.0643	0.0553	-0.0705	-0.0122	-0.0840	-0.0595	-0.0350	0.1783	-0.3110**

Residual effect = 0.2017; **Diagonal and bold indicates the direct effects**

* Significant at 5 per cent level

** Significant at 1 per cent level

DFE - Days to 50 % flowering, **DTM** - Days to maturity, **PH** - Plant height, **PL** - Pod length, **PW** - Pod width, **NCP** - Number of clusters per plant, **NPB** - Number of primary branches, **NPP** - Number of pods per plant, **NPC** - Number of pods per cluster, **NSP** - Number of seeds per pod, **HSW** - Hundred seed weight, **SPY** - Single plant yield.

In general, genotypic correlation was found to be higher in magnitude than phenotypic correlation. This may be due to modifying effects of environment on association of traits at genetic level (Johnson *et al.*, 1955b). Single plant yield showed significant positive correlation with plant height ($r_g=0.3266$, $r_p=0.3154$), pod length ($r_g=0.5659$, $r_p=0.5332$), number of clusters per plant ($r_g=0.6876$, $r_p=0.6793$), number of pods per plant ($r_g=0.9412$, $r_p=0.9365$), number of pods per cluster ($r_g=0.7170$, $r_p=0.7060$) and number of seeds per pod ($r_g=0.4877$, $r_p=0.4755$) at both genotypic and phenotypic level. Similar results were obtained by Manggoel *et al.*, 2012 in cowpea accessions at genotypic level. Significant negative association with yield was observed for pod width and hundred seed weight.

Knowledge on inter correlation between quantitative traits may facilitate breeders to decide the direction of selection on related traits for improvement. Traits *viz.*, number of cluster per plant exhibited significant positive inter-correlation with plant height, pod length, number of pods per plant and number of pods per cluster. Similarly, yield components *viz.*, number of pods per plant and number of pods per cluster showed positive significant inter correlation with plant height, pod length and number of seeds per pod respectively. Hence, selection based on six yield components *viz.*, number of cluster per plant, plant height, pod length, number of pods per plant, number of pods per cluster and number of seeds per pod would help to identify promising genotypes. It is suggested that the above mentioned traits shall be given importance while excising selection as it had exhibited significant direct association with yield and also proves to be promising yield contributing components.

Partitioning the genotypic correlation into direct and indirect effects by path analysis would provide idea on relative contribution of

each trait and its influence through other traits on yield. The results of path analyses were presented in Table 4. Four traits *viz.*, days to maturity (0.3314), number of pods per plant (1.0057), number of seeds per pod (0.2372) and hundred seed weight (0.1783) recorded positive and high direct effects on single plant yield. The results were in accordance with Reddy *et al.*, (2011) in greengram and Praveen *et al.*, (2011) in blackgram. Yield attributing characters like plant height, pod length, number of cluster per plant, number of pods per cluster and number of seeds per pod exhibited positive and high indirect effects on yield through number of pods per plant. Hundred seed weight exhibited positive and high direct effect but negatively correlated with yield. Hence, direct selection for the trait should be employed to remove the undesirable indirect effects. The residual effect (0.2017) is low which indicates the larger contribution of traits towards variability specifically with respect to yield. From correlation and path analysis, it is concluded that adopting selection techniques for the traits *viz.*, number of cluster per plant, plant height, pod length, number of pods per plant, number of pods per cluster and number of seeds per pod would be more rewarding in bringing yield improvement in horsegram since they were considered as major yield contributing traits.

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