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## Research Article

### Genetic variability, correlation studies, path coefficient analysis and genetic divergence in horsegram (*Macrotyloma uniflorum* (Lam.) Verdc.)

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#### Abstract

A field experiment was undertaken to evaluate the variability and performance of thirty horsegram genotypes collected from various regions of Kerala and outside for yield and yield attributing characters. Analysis of variance was carried out based on the recorded observations, and it showed significant differences among the 30 genotypes for all the fifteen characters studied. Most of the traits exhibited narrow differences between PCV and GCV except for seeds per pod, the number of primary branches per plant and yield per plant. Yield per plant was found to be significant and positively correlated to primary and the number of secondary branches per plant, nodes per plant, pod number per plant, seeds per pod and 100 seed weight both at phenotypic and genotypic levels. Path analysis revealed that pod number per plant, seeds per pod, nodes per plant, 100 seed weight and days to maturity were the major yield contributing characters owing to their favorable direct effect on yield per plant. Genetic diversity studies using Mahalanobis'  $D^2$  statistics assembled the 30 genotypes into eight clusters.

**Keywords:** Variability, heritability, path analysis, genetic divergence, horsegram

#### INTRODUCTION

Horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.], belonging to the family Fabaceae, is an under-exploited hardy pulse crop that has been widely adapted to extensive agricultural regimes of India. Apart from being a rich source of dietary proteins, it also possesses immense medicinal values which makes it a likely food source for generations to come. This crop also goes by the name of 'Dew crop', as it flourishes well during the winter season, even without any irrigation and mainly depends on the moisture provided by the dew fall. It is also raised as a green manure crop in many parts of the country because of its high potential for the immobilization of atmospheric nitrogen (Priyanka *et al.*, 2019). Being drought-hardy, horsegram not only improves the soil quality but also prevents soil erosion to a great extent. Largely mistaken as a minor pulse due to the entrenched biases surrounding

it, horsegram has received far less research compared to many other conventional pulse crops. Although its cultivation practices are relatively easy, not much work has been done to improve its genetic potential. Usually, the crop is cultivated in marginal lands, leading to lower productivity and low net returns for the farmer. Hence, focused scientific efforts like the development of high-yielding and climate-resilient varieties would help to maintain nutritional security in developing countries.

Germplasm serves as an indicator of the genetic richness of a country as it holds a major share of the most favorable genes in it. In any variety release programme, analyzing the existing variability is critical for the selection and identification of parental genotypes that can be used in the hybridization scheme. Hence, estimates of various genetic

parameters are essential for a better understanding of the nature and degree of variability present within a population and would thus be beneficial in determining appropriate selection techniques. Yield, being a complex trait, is driven by several polygenes which exhibit lower levels of heritability and thus direct selection for yield has a very restricted scope. As a result, the effectiveness of selection can be boosted by determining the association existing among yield and other plant characters which would serve as simple guides for spotting high yielders. In light of the above facts, the current study was performed to estimate the breeding value of the available genotypes of horsegram for different quantitative characters.

### MATERIALS AND METHODS

The present study was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, located at a latitude of 8°5' N and a longitude

of 76°9'E and at an altitude of 29 m above the mean sea level. The prevalent type of soil in the experimental site was found to be red loam of the Vellayani series, which is texturally classified as sandy clay loam. The experimental material consists of thirty genotypes of horsegram gathered from different regions of the state and outside (Table 1). They were subjected to evaluation in a randomized complete block design with three replications at a recommended spacing of 30 cm x 25 cm under optimum field conditions. A total of 25 plants were maintained in each experimental plot and five plants per plot were taken for recording observations on 15 yield contributing traits which include vegetative and flowering traits. Cultural practices as per recommendation were uniformly done in all the experimental plots to raise a successful crop. Genetic parameters, namely Genotypic and Phenotypic Coefficient of Variation (GCV & PCV) were estimated for each character in accordance with Sivasubramanian and

**Table 1. List of genotypes used for the study and their sources**

Genotypes	Name of genotype	Source
1	Vakalavalasa local	Andhra Pradesh
2	Chintada local	
3	Amudalavalasa local	
4	Nenmara local	Kerala
5	Thathamangalam local	
6	Agali local	
7	Chittur local	
8	Vadakarapalli local	
9	Kannanthara local	
10	Perumatti local	
11	Melarcodes local	
12	Palakkad local	
13	Nallepilly local	
14	Dharmapuri local	Tamil Nadu
15	Vanjangipeta local	Andhra Pradesh
16	Peruvamba local	Kerala
17	Attapadi local	
18	Panukuvalasa local	Andhra Pradesh
19	Pudur local	Tamil Nadu
20	Kozhinjampara local	Kerala
21	IC22762	NBPGR
22	IC19441	
23	IC15735	
24	IC19450	
25	IC22773	
26	IC19447	
27	IC22770	
28	IC19442	
29	IC19452	
30	IC22759	

Menon (1973) and they were categorized as low: values lower than 10%, moderate: 10% to 20% and high: values greater than 20%. Heritability ( $h^2$ ) was estimated in the broad sense as per the formula put forth by Burton (1952) and Johnson *et al.* (1955). The genetic advance was also worked out as proposed by Burton and De Vane (1953) and Johnson *et al.* (1955). Other genetic parameters such as correlation analysis (Falconer, 1964), path analysis (Dewey and Lu, 1959) and genetic divergence analysis (Rao, 1952) were also conducted following the procedure of the authors given.

## RESULTS AND DISCUSSION

Analysis of variance revealed that significant variation exists among the different genotypes included in the study for all the characters considered, which confirms that the material selected was quite variable (Table 2). The measures of PCV, GCV, heritability (broad sense) and genetic advance (GA) for yield and its contributing characters are represented in Table 3. As it is evident from the table, for all the traits the values of GCV were found to be smaller than their corresponding PCV values, which indicated a greater genotype x environment interaction. The narrow gap between PCV and GCV for certain characters *viz.*, days to 50 per cent flowering, days

to maturity, nodes per plant, pod number per plant, pod length, 100 seed weight, plant height and crop duration specified the minimum impact of the environment on the expression of such characters and hence their phenotypic values will be reliable for selection. These observations were supported by the conclusions made by Sood *et al.* (1994) and Prakash and Khanure (2000) based on their studies in horsegram. In this study, GCV values ranged from 5.57 per cent to 23.99 per cent with yield per plant recording the highest GCV followed by pod number per plant, while the lowest was for crude protein content. Khulbe *et al.* (2013) reported that, traits *viz.*, pod number per plant and yield per plant showed higher values for GCV and PCV in horsegram genotypes. The lower GCV values of crude protein have also been reported by Bhagwat (2015) in blackgram genotypes. This indicates a higher contribution of yield per plant and pod number per plant towards variability suggesting that parents selected based on these characters may be further utilized in various breeding programmes to obtain good segregants. Days to maturity and 50 per cent flowering, 100 seed weight, pod length, crop duration, crude protein, seeds per pod, nodes per plant and plant height recorded low to moderate GCV and PCV, indicating less scope for their improvement through selection. Nagaraja (1997),

**Table 2. Analysis of variance for the traits under study in Horsegram**

Source of Variation	df	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Replication	2	0.02	2.03	29.26*	15.51	31.81	30.36	10.71	0.01	0.10	0.01	78.05	0.45	5.84	5.43
Genotypes	29	0.57**	8.41*	18.40**	290.16**	322.93**	857.85**	975.70**	1.26**	0.47**	0.16**	632.10**	36.35**	309.03**	8.69**
Error	58	0.06	4.32	6.69	15.25	11.98	54.09	16.71	0.15	0.05	0.01	43.31	2.30	14.13	2.54

\*\* Significant at 1% level of probability, \* Significant at 5% level of probability

X1 Number of days to germination	X6 Nodes per plant	X11 Plant height
X2 Number of primary branches per plant	X7 Pod number per plant	X12 Yield per plant
X3 Number of secondary branches per plant	X8 Seeds per pod	X13 Crop duration
X4 Days to 50% flowering	X9 Pod length	X14 Crude protein

**Table 3. Estimates of genetic parameters for yield and yield contributing characters**

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GA (5%)
Number of days for germination	2.64	2.07 - 3.60	18.18	15.51	72.80	27.26
Number of primary branches per plant	9.11	5.60 - 12.47	26.17	12.82	23.99	12.93
Number of secondary branches per plant	13.54	10.53 - 18.93	24.04	14.59	36.84	18.24
Days to 50% flowering	65.66	46.33 - 80.67	15.54	14.30	84.73	27.12
Days to maturity	126.49	106.60 - 142.40	8.42	7.98	89.70	15.56
Nodes per plant	112.98	80.60 - 148.40	15.88	14.49	83.20	27.22
Pod number per plant	73.47	45.60 - 105.27	24.35	23.66	94.39	47.35
Seeds per pod	6.05	5.13 - 7.47	11.47	9.53	69.04	16.32
Pod length (cm)	5.12	4.32 - 5.68	8.69	7.43	73.19	13.10
100 seed weight (g)	3.23	2.76 - 3.68	7.35	6.97	89.85	13.61
Plant height (cm)	113.10	83.68 - 147.57	13.69	12.39	81.92	23.10
Yield per plant (g)	13.31	7.76 - 20.08	26.57	23.98	81.44	44.58
Crop duration (days)	138.65	121.40 - 153.47	7.42	6.89	86.06	13.16
Crude protein (%)	25.71	22.60 - 28.92	8.33	5.57	44.65	7.67

Nehru *et al.* (2000), Ram *et al.* (2005) and Priyanka *et al.* (2019) have reported similar findings in horsegram.

The strength of selection of each trait is based not only on the proportion of variability present but also on the degree to which that variability is being inherited. The estimates of heritability guide the plant breeder in the process of identification and selection of first-class genotypes from diversified genetic populations. However, heritability alone may fail to indicate the response to selection. Hence, estimates of heritability along with measures of genetic advance are known to be far more useful in the prediction of genetic gain under selection. In the current study, heritability was reported to be high for most of the characters and it ranged from 23.99 per cent for the number of primary branches per plant to 94.39 per cent for pod number per plant. High heritability estimates were observed for the characters *viz.*, pod number per plant, 100 seed weight, days to maturity, crop duration, days to 50 per cent flowering, nodes per plant, yield per plant and plant height. These findings are on par with the conclusions made by Sood *et al.* (1994), Tripathi (1999), Venkateswarlu (2000), Sahoo *et al.* (2010) and Varma *et al.* (2013) based on their research works in horsegram. The number of primary branches per plant showed low heritability, in line with the results acquired by Senapathi *et al.* (1998) and Durga (2012). Genetic advance as per cent of mean was observed to be high for pod number per plant followed by yield per plant. Higher values for

heritability coupled with high genetic advance expressed as per cent of mean was recorded for traits such as yield per plant, days to germination and 50 per cent flowering, nodes per plant, pod number and plant height. Sreekantaradhya *et al.* (1975) and Sahoo *et al.* (2010) have obtained parallel results in horsegram. This demonstrates that all the above characters are most likely governed by additive gene action and hence direct phenotypic selection may be effective.

Correlation analysis helps the plant breeder to understand the relative importance of different plant traits and provides a sufficient basis for selection. Correlation may be positive or negative based on the nature of the characters under study. In this study, genotypic and phenotypic correlation coefficients were worked out for 15 quantitative characters (**Table 4**). Characters under this study showed higher genotypic correlation coefficients compared to their phenotypic counterparts suggesting a strong association between them genetically and their phenotypic value is largely minimized by the pronounced interaction with the environment. Most of the component traits *viz.*, pod number per plant, the number of primary branches per plant, the number of secondary branches per plant, days to maturity, nodes per plant, seeds per pod and seed weight showed a strong positive correlation with yield per plant, which implies that an enhancement in any one of these traits will simultaneously bring amelioration in yield. Pod number per plant recorded the maximum positive significant correlation with yield per plant, number

**Table 4. Genotypic correlation of yield and yield contributing characters of horsegram**

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1													
X2	-0.059	1												
X3	0.359**	-0.175	1											
X4	0.326**	0.035	0.955**	1										
X5	0.137	-0.0593**	0.023	0.370**	1									
X6	0.215*	-0.506**	-0.066	0.419**	0.950**	1								
X7	0.360**	-0.022	0.864**	0.231**	0.285**	0.332**	1							
X8	0.934**	-0.030	0.524**	0.389**	0.209*	0.289**	0.402**	1						
X9	0.244*	0.302**	0.076	-0.232*	-0.469**	-0.456**	-0.056	-0.005	1					
X10	-0.067	0.401**	0.451**	0.126	-0.216*	-0.261*	0.078	-0.214*	0.251*	1				
X11	0.260*	-0.177	-0.218*	-0.051	0.205	0.131	-0.147	0.033	-0.113	0.039	1			
X12	0.276**	-0.148	0.957**	0.021**	0.356**	0.311**	0.900**	0.412**	-0.221*	-0.041	-0.188	1		
X13	0.221*	-0.515**	-0.087	0.472**	0.936**	0.013**	0.324**	0.275**	-0.403**	-0.302**	0.106	0.301**	1	
X14	-0.425**	-0.045	-0.114	-0.436**	-0.003	-0.092	-0.394**	-0.349**	0.209*	0.121	-0.230*	-0.374**	-0.105	1

\*\* Significant at 1% level of probability, \* significant at 5% level of probability

X1 Yield per plant

X2 Days to sprouting

X3 Number of primary branches per plant

X4 Number of secondary branches per plant

X5 Days to 50 % flowering

X6 Days to maturity

X7 Nodes per plant

X8 Pod number per plant

X9 Seeds per pod

X10 Pod length

X11 100 seed weight

X12 Plant height

X13 Crop duration

X14 Crude protein

of primary branches per plant and nodes per plant. These findings were in agreement with Savithamma (1994) and Poornima (2015). Crude protein content showed a negative correlation with a yield which suggests that a rise in yield per plant may reduce the protein content in the seeds marginally. Mello Filho *et al.* (2004) reported similar findings in soybean.

Partitioning of correlation coefficients into measures of direct and indirect effects of the component characters on yield can be achieved by path coefficient analysis. It discloses information about the cause and effect of association and interaction between two variables. Based on the genotypic correlation, nine yield components *viz.*, the number of primary branches per plant, the number of secondary branches per plant, days to maturity, nodes per plant, pod number per plant, seeds per pod, 100 seed weight, plant height and crude protein content had a strong association with yield and selected as independent characters for path analysis. This estimates the direct and indirect contribution of independent characters to dependent characters (Table 5). The highest positive direct effect on yield per plant showed by pod number per plant followed by seeds per pod, nodes per plant and 100 seed weight. Since all these characters were found to exhibit a significant positive correlation with yield, direct selection will definitely result in an improvement of yield in horsegram. This was in accordance with the study by Yarguntappa (1987) who reported that pod number per plant exerted a maximum direct and positive effect on yield per plant. Similar results were also reported by Prakash and Khanure (2000), Khulbe *et al.* (2013) and Priyanka *et al.* (2019) based on their field experiments in horsegram. Characters *viz.*, the number of primary branches per plant, the number of secondary branches per plant and plant height exhibited a high indirect effect on yield per plant

through nodes per plant. A low residual effect (0.049) was noticed, which specifies the contribution of the characters under the study in regard to variability.

The multivariate analysis with Mahalanobis  $D^2$  statistics is one of the best known techniques to measure genetic divergence. Knowledge on the nature and extent of genetic diversity within a population is essential for all improvement programmes in order to identify specific parents for realizing useful recombinants. The 30 genotypes selected for the present study were subjected to Mahalanobis  $D^2$  analysis based on 10 prominent characters such as yield per plant, the number of primary branches per plant, the number of secondary branches per plant, days to maturity, nodes per plant, pod number per plant, seeds per pod, 100-seed weight, plant height and crude protein. Using Tochers' method of clustering, the thirty genotypes were grouped into eight clusters (Table 7). Out of these, cluster I was the largest with twelve genotypes, cluster II with six genotypes, cluster III with five genotypes, cluster IV and cluster V with two genotypes and clusters VI, VII and VIII were solitary clusters. Based on the total  $D^2$  values, the average inter-cluster and intra-cluster distances were calculated and the results are presented in Table 6. The highest inter-cluster distance was recorded between clusters V and VIII (481.99), resulting in maximum divergence, followed by clusters IV and V (448.12). The distance between clusters is a measure of the degree of diversification. The highest intra-cluster distance was noticed for cluster V (16.18) followed by cluster I (15.27), which showed that the genotypes present in the same cluster exhibit significant variability among themselves. When the relative contribution of each character towards divergence was calculated (Table 8), it was observed that yield per plant (21.38) contributed the maximum percentage towards genetic diversity followed by the

**Table 5. Direct and indirect effects of different characters on yield**

	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genotypic correlation for yield per plant
X1	<b>0.1934</b>	-0.1689	-0.0015	0.5539	1.0234	0.0582	-0.1217	-0.2490	0.0327	0.359**
X2	0.1847	<b>-0.1768</b>	0.0098	0.7892	0.7605	-0.1780	-0.0284	-0.2654	0.1247	0.326**
X3	-0.0127	-0.0742	<b>0.0234</b>	0.2125	0.5643	-0.3505	0.0730	-0.0808	0.0264	0.215*
X4	0.1672	-0.2177	0.0078	<b>0.6409</b>	0.7857	-0.0427	-0.0821	-0.2341	0.1128	0.360**
X5	0.1013	-0.0688	0.0068	0.2578	<b>1.9535</b>	-0.0039	0.0183	-0.1072	0.0998	0.934**
X6	0.0147	0.0410	-0.0107	-0.0356	-0.0100	<b>0.7683</b>	-0.0629	0.0574	-0.0597	0.244*
X7	-0.0422	0.0090	0.0031	-0.0942	0.0641	-0.0865	<b>0.5585</b>	0.0490	0.0658	0.260*
X8	0.1852	-0.1805	0.0073	0.5769	0.8056	-0.1694	-0.1053	<b>-0.2600</b>	0.1068	0.276**
X9	-0.0221	0.0771	-0.0022	-0.2527	-0.6814	0.1604	-0.1285	0.0971	<b>-0.2860</b>	-0.425**

\*\* - Significant at 1% level of probability, \* - significant at 5% level of probability

R = 0.04972, Diagonal values represent the direct effects of different plant characters on yield per plant

X1 Number of primary branches per plant

X4 Nodes per plant

X7 100 seed weight

X2 Number of secondary branches per plant

X5 Pod number per plant

X8 Plant height

X3 Days to maturity

X6 Seeds per pod

X9 Crude protein

**Table 6. Average intra and inter-cluster distance among eight clusters**

Cluster	I	II	III	IV	V	VI	VII	VIII
I	15.27	29.45	58.05	126.54	129.83	47.46	40.08	132.36
II		4.70	118.28	223.65	62.55	117.02	34.54	243.14
III			8.96	31.47	314.48	21.04	109.81	40.42
IV				11.73	448.12	33.15	226.52	26.97
V					16.18	279.06	135.22	481.99
VI						0.00	110.66	31.34
VII							0.00	194.05
VIII								0.00

**Table 7. List of genotypes included in different clusters**

Cluster Number	Number of genotypes	Name of genotypes
I	12	Agali local, Panukuvalasa local, IC22759, IC22762, Vakalavalasa local, Nenmara local, Palakkad local, Thathamangalam local, Chintada local, IC19452, Amudalavalasa local, IC19447
II	6	IC19441, IC19450, Melarcode local, Chittur local, Dharmapuri local, IC22770
III	5	Peruvamba local, Pudur local, Kannanthara local, IC19442, Kozhinjampara local
IV	2	IC15735, IC22773
V	2	Nallepilly local, Attapadi local
VI	1	Vadakarapalli local
VII	1	Perumatti local
VIII	1	Vanjangipeta local

**Table 8. Relative contribution of each character to divergence**

S. No.	Character	Contribution (%)
1	Yield per plant	21.38
2	Number of primary branches per plant	18.85
3	Number of secondary branches per plant	8.74
4	Days to maturity	17.01
5	Nodes per plant	10.34
6	Pod number per plant	13.56
7	Seeds per pod	4.37
8	100 seed weight	3.68
9	Plant height	1.38
10	Crude protein	0.69
	TOTAL	100

number of primary branches per plant (18.85), days to maturity (17.01), and pod number per plant (13.56). This was in accordance with the findings of Dogra (2004) and Kalia and Dogra (2007) who also reported that yield gave the maximum contribution towards genetic diversity.

Cluster VI exhibited high mean values for characters viz., pod number per plant, plant height, the number of primary branches per plant and the number of secondary branches per plant, while cluster I have high mean

values for yield per plant and seeds per pod (**Table 9**). Cluster VIII had the highest average number of pods per plant and maximum 100 seed weight. Days to maturity which contributed 17.01 per cent for divergence exhibited high cluster means in cluster VII and crude protein had a high mean value in cluster II. These results implied that the selection of genotypes with high mean values for a particular trait can be done and they can be employed in further crop improvement programmes. These were in accordance with the findings of Neelima *et al.* (2021).

Table 9. Cluster mean of yield and yield contributing characters

Cluster Number	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
I	14.686	9.46	13.92	126.15	107.28	77.24	6.29	3.20	115.54	25.23
II	10.939	8.69	11.12	122.64	100.92	64.57	6.10	3.18	108.71	27.39
III	12.050	7.58	11.98	127.41	96.75	65.67	5.92	3.28	94.45	26.06
IV	14.640	8.92	14.47	118.90	117.49	81.44	5.67	3.19	107.55	26.09
V	13.385	8.85	16.80	133.53	133.52	79.77	5.57	3.30	140.02	24.34
VI	14.90	12.47	18.93	134.07	141.13	92.93	5.40	3.26	140.8	26.53
VII	11.83	9.78	12.33	136.07	104.27	71.43	5.60	3.19	119.9	22.60
VIII	14.54	11.97	18.70	132.57	148.40	74.87	6.27	3.39	126.17	23.93

X1 Yield per plant (g)

X2 Number of primary branches per plant

X3 Number of secondary branches per plant

X4 Days to maturity

X5 Nodes per plant

X6 Pod number per plant

X7 Seeds per pod

X8 100 seed weight (g)

X9 Plant height (cm)

X10 Crude protein (%)

The above study revealed the presence of wide variability among the thirty horsegram genotypes for all the traits studied. The selection for traits viz., nodes per plant, pod number per plant, seeds per pod, and 100 seed weight will be easy and would be useful in any further breeding programme for improving seed yield in horsegram. Also, the superior genotypes identified in the present study can be utilized in crop improvement programmes to develop high yielding varieties.

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