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Screening of Genetic Variability for Yield and its Components in Horse Gram [*Macrotyloma uniflorum* (Lam). Verdc]. Local Germplasm

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Abstract

A investigation was done to estimate the extent of genetic variability for seed yield and ten quantitative traits in 44 genotypes of Horse gram. For all of the traits, the analysis of variance revealed a significant difference between genotypes, indicating a high degree of variability. For all of the characters, the genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV). Most of the traits between GCV and PCV had the smallest differences, indicating a lower predominance of environment in the expression of these characters. As a result, breeders could undertake direct selection based on phenotypic values of the traits. Seed yield plant^{-1}, number of clusters plant^{-1} and number of pods plant^{-1} all had high genotypic and phenotypic coefficients of variation. Protein content followed by days to 50% flowering, days to maturity, seed yield plant^{-1}, number of pods plant^{-1}, plant height, number of clusters plant^{-1}, 1000 seed weight, number of primary branches plant^{-1} and pod length all had high estimations of heredity in the broad sense. Number of pods plant^{-1} had the maximum heritability (broad) coupled with high genetic advance as per cent of mean followed by number of clusters plant^{-1}, days to maturity, plant height and days to 50% flowering. As a result, these characters are mostly controlled by additive gene action, and hence characters can be improved through selection.

Key words : Genetic Advance. Genetic Variability, Heritability, Horse gram.

Arid legumes form very important source of food and nutrients, rich in protein for human beings especially in the dry land regions. Horse gram (*Macrotyloma uniflorum* (Lam.) Verdc) is one among them which is an important component in the dry land crop production system, due to its ability to withstand drought with minimum management. Although it grows under a diverse types of soil and climatic conditions but it is well identify for its hardiness, adaptability to poor soil and wide climatic conditions. Like other pulses it plays important role as food and fodder (dual purpose), as green manure crop, as good cover crop in controlling soil erosion, enhancing soil fertility and having ability of fixing atmospheric nitrogen into the soil. It is usually grown as catch crop for late *Kharif* or with the rains after a prolonged drought conditions and aberrant weather conditions.

Africa is the primary source of origin, while India is the secondary source of origin (Dana, 1976). The chromosome evolution of *Dolichos* is believed to have progressed in two directions; one group is having 20 small chromosomes (*D. biflorus, D. boumani* and *D. axillaries*) and other having 20 large chromosomes (*D. glabrescence, D. lignosus* and *D. argentinus*). Horse gram is mostly grown in the Indian states of Karnataka, Andhra Pradesh, Orrisa, Tamil Nadu, Madhya Pradesh, Chhattisgarh, Bihar, West Bengal and Jharkhand, as well as in the foothills of Uttaranchal and Himachal Pradesh. It is also grown in other nations such as Sri Lanka, Malaysia, and the West Indies.

In any crop improvement programme, information on genetic diversity, heritability and genetic progress is important for developing effective selection schemes. On Horse gram, a little amount of work of this kind has been done previously. Hence, the current research was carried out to investigate genetic variability, heritability, and genetic progress in horse gram.

Materials and Methods

The experiment was carried out on 44 horse gram local germplasm samples were collected from the Maharashtra (districts of Aurangabad, Ahmednagar, Solapur, Satara, Sangali, Jalgaon, Pune, Dhule, and Nandurbar) (Table 2). At the Department of Botany, College of Agriculture, Dhule, the experiment was set up in RBD with three replications (M.S.). A recommended package of practices and procedures was followed to establish a good and robust crop stand, with a spacing of 30 cm between rows and 10 cm between plants. Data are recorded and collected on eleven yield and yield contributing traits *viz*., days to 50 per cent flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of cluster plant^{-1}, pod length (cm), number of seeds pod^{-1}, 1000 seed weight, number of pods plant^{-1}, seed yield plant^{-1} and protein content (%).

Statistical analysis was performed on the mean of five plants. The data for distinct traits were statistically examined for significance using Panse and Sukhatme's analysis of variance technique (1985). With three replications, the adapted design was Randomized Block Design (RBD). Using the "F" Test, the significance of the mean sum of square for each character was compared to the corresponding error degrees of freedom (Fisher and Yates,1967). According to Burton and De Vane (1953) components of variances were utilized to determine genetic parameters such as phenotypic and genotypic coefficients of variation (PCV and GCV). Allard's (1960) formula was used to calculate heritability in the broad sense and genetic advance which was expressed as a percentage of mean was done bythe formula given by Burton (1955). WINDOSTAT program was utilized for the statistical analysis.

Results and Discussion

For all of the characters, analysis of variance revealed substantial variations between genotypes. The most important characters in studies of genetic variability were seed yield plant^{-1}, number of pods plant^{-1}, number of clusters plant^{-1}, days to maturity, plant height, and days to 50% flowering, which all had high phenotypic and genotypic coefficients of variation, heritability and genetic advance as percent of mean. Simple selection can be used to improve these characters, and hybridization followed by selection in early generations for these characters can be used to improve these characters in horse gram (Table 1). It demonstrates that the presence of variability and material selection are appropriate.

The nature and extent of variability in such populations influence the improvement of economic characteristics such as yield through selection. The phenotypic expression of a complex trait such as yield, on the other hand,

Table 1. ANOVA for twelve characters in Horse gram

Traits	**MSS**		
	Replication	**Treatment**	**Error**
Days to 50 per cent flowering	0.1	10866.21**	129.39
Days to maturity	49.5	17773.77**	292.5
Plant height (cm)	1.9	14562.48**	474.42
No. of primary branches plant^{-1}	2.19	42.64**	7.94
No. of cluster plant^{-1}	5.13	26359.68**	1063.03
Pod length	0.058	7.22**	1.72
No. seed pod^{-1}	0.0177	14.47**	4.06
1000 Seed weight	0.0094	408.16**	22.74
No. of pods plant^{-1}	13.76	26998.58**	854.2
Seed yield plant^{-1}	0.5	742.97**	22.99
Protein content	0.13	323.32**	1.6

*, ** : 5% and 1% level of significance, respectively

is a combination of genotype, environment, and their interplay. This highlights the importance of using proper statistical approaches to partition overall variability into heritable and non-heritable components.

The potential to improve any crop plant is largely determined by the extent of genetic variability. The genotypic and environmental components of phenotypic variability displayed by a genotype or a collection of genotypes in any species can be separated. Because the genotypic component is the heritable component of total variability, its magnitude for yield and component traits influence the breeders' selection tactics.

The genotypic coefficient of variation (GCV) estimations for all the characters were lower than the phenotypic coefficient of variation (PCV), indicating that the traits were less influenced by the environment. Therefore, selection for the improvement of these traits. Lad *et al*. (1999), Bhadait (2005), Joshi *et al*. (2007), Singhal *et al*. (2010), Latha *et al*. (2013) and Vijay Kumar et al. (2016) also reported similar result, indicating that the characters were less influenced by the environment. Therefore, selection for the improvement of these traits (Table 2).

Seed yield plant^{-1}, number of clusters plant^{-1} and number of pods plant^{-1} all had high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV). This is in conformity with the results of Dobhal and Rana (1994), Lad *et al*. (1999), Venkateshwarlu (2000), Kalia and Dogra (2007) and Kulbe *et al*. (2013) and medium magnitude of GCV and PCV was found in plant height, days to 50 per cent flowering, number of primary branches plant and days to maturity. The lowest genotypic coefficient of variation and phenotypic coefficient of variation recorded for pod length, number of seeds pod, 1000 seed

Table 2. Forty four horse gram genotype used in present investigation

Genotype	Source
DHLH-1	Soygaon-2 (Aurangabad)
DHLH-2	Soygaon-1(Aurangabad)
DHLH-3	Satara -1
DHLH-4	Satara-2
DHLH-5	Mohol-1 (Solapur)
DHLH-6	Mohol-2 (Solapur)
DHLH-7	Newasa-1 (Ahmednagar)
DHLH-8	Newasa-2 (Ahmednagar)
DHLH-9	Nangaon-1 (Nashik)
DHLH-10	Nangaon-2 (Nashik)
DHLH-11	Rahuri (Ahmednagar)
DHLH-12	Nandurbar-1
DHLH-13	Nandurbar-2
DHLH-14	Penur (Solapur)
DHLH-15	Akulkheda (Jalgaon)
DHLH-16	Dhule
DHLH-17	Niphad-1 (Nashik)
DHLH-18	Niphad-2 (Nashik)
DHLH-19	Shingare (Ahmednagar)
DHLH-20 (Ahmednagar)	Dhanore-2 (Rahuri)
DHLH-21 (Ahmednagar)	Dhanore-1 (Rahuri)
DHLH-22	Sakri-1 (Dhule)
DHLH-23	Sakri-2 (Dhule)
DHLH-24	Pimpalgaon (Nashik)
DHLH-25	Chikhali (Jalgaon)
DHLH-26	Sakri-3 (Dhule)
DHLH-27	Khatgaon (Solapur)
DHLH-28	Dhule
DHLH-29	Amalner (Jalgaon)
DHLH-30	Akole (Ahmednagar)
DHLH-31	Shirur-1 (Pune)
DHLH-32	Shirur-2 (Pune)
DHLH-33	Parner-1 (Ahmednagar)
DHLH-34	Parner-2 (Ahmednagar)
DHLH-35	Nandurbar-3
DHLH-36	Nandurbar-4
DHLH-37	Sangali-1
DHLH-38 (PhuleSakas)	Solapur
DHLH-39	Deolali (Rahuri) (Ahmednagar)
DHLH-40	Sangmner (Rahuri) (Ahmednagar)
DHLH-41	Yewala (Nashik)
DHLH-42	Junnar-1 (Pune)
DHLH-43	Junnar-2 (Pune)
DHLH-44	Surgana (Nashik)

weight and protein content. This is in conformity with result of Lad *et al*. (1999), Kulbe *et al*. (2013).

The presence of less environmental impact and the prevalence of additive gene action in their expression is revealed by high heritability combined with high genetic advance (Panse, 1957). Lower genetic advance values indicate a narrow range of variability and a high G x E interaction (non additive gene action). Seed yield per plant had the highest heritability as a percentage of mean in the present study, followed by number of clusters plant^{-1}, number of pods plant^{-1}, plant height, days to 50% flowering, and days to maturity, indicating that these characters are governed by additive genes and that phenotypic selection for these characters may be effective. As a result, placing a direct selection emphasis on these traits in horse gram should increase seed yield. Similar results are in conformity with results of Agrawal and Kang (1976), Shrikantradheya *et al*. (1975), Shivshankar *et al*. (1977), Ganeshian (1980), Suraiya *et al*. (1988), Samal and Senapati (1997), Joshi *et al*. (2007), Raina *et al*. (2007), Kulbe *et al*. (2013) and Priyanka *et al*. (2019).

For the number of primary branches, pod length, 1000 seed weight, seed yield plant^{-1} and protein content, high heritability was seen with low genetic advance, indicating a preponderance of non additive gene action and that selection for these traits may not be rewarding. Patil and Deshmukh (1985) indicated same result for protein content

The phenotypic coefficient of variation (GCV) in combination with heritable estimates would give a more accurate picture of the amount of genetic advance that can be predicted from phenotypic selection (Burton,1953). It is suggested that genetic gain be taken into account with heritability estimations (Johnson *et al*., 1955). Heritability estimates combined with genetic advance are usually more useful in projecting selection gain than heritability estimates alone (Table 3).

In conclusion, the genotypic make-up of the material picked differed, as demonstrated by significant differences in all of the quantitative traits evaluated. For all of the traits, the phenotypic coefficients of variation estimate was somewhat greater than the genotypic coefficients of variation, indicating that there was little environmental influence on their expression. As a result of the estimates of genetic parameters such as genotypic coefficient of variation, heritability, and genetic advance as

Table 3. Specifications of genetic variability for the traits in Horse gram

Ch. no.	Traits	General mean	σ2g	σ2p	σ2e	GCV (%)	PCV (%)	ECV (%)	h2 (BS%)	GA	GA as per cent of mean
1	Days to 50 per cent flowering	75.55	124.84	127.85	3.00	14.78	14.96	2.29	97.65	22.74	30.10
2	Days to maturity	131.65	203.27	210.07	6.80	10.82	11.00	1.98	96.76	28.89	21.94
3	Plant height (cm)	70.72	163.81	174.84	11.03	18.09	18.69	4.69	93.69	25.52	36.08
4	No. of primary branches plant-1	5.78	0.40	0.58	0.18	10.97	13.25	7.42	68.59	1.08	18.72
5	No. Cluster plant-1	67.68	294.14	318.86	24.72	25.33	26.38	7.34	92.25	33.93	50.13
6	Pod length (cm)	4.68	0.06	0.10	0.04	5.40	6.88	4.27	61.46	0.40	8.72
7	No. of seed pod-1	4.31	0.21	0.21	0.09	8.06	10.76	7.12	56.14	0.53	12.44
8	1000 seed weight (g)	24.82	4.48	5.01	0.52	8.52	9.01	2.92	89.44	4.12	16.61
9	No. of pods plant-1	79.11	304.00	323.86	19.86	22.03	22.74	5.63	93.87	34.79	43.98
10	Seed yield plant-1 (g)	8.54	8.37	8.90	0.53	33.87	34.94	8.56	94.00	5.77	67.66
11	Protein content (%)	21.63	3.74	3.77	0.03	8.93	8.98	0.89	99.01	3.96	18.32

a percent of mean are combined, the seed yield plant^{-1}, number of pods plant^{-1}, number of clusters plant^{-1}, days to maturity, plant height, and days to 50% flowering, is most important factor. Hybridization followed by selection in early generations for these characters would give the way for improvement these characters in horse gram.

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