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Research Note

Assessment of genetic diversity in Horse gram (*Dolichos uniflorus*)

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Abstract
Twenty three horse gram accessions were studied during spring seasons of 2008-09 and 2010-11. The results indicated significant differences among the 23 accessions for all characters studied, indicating the presence of sufficient genetic variation. Mahalanobis D^2 statistics grouped all the 23 cultivars of horse gram into seven clusters. Cluster I had 11 genotypes, Cluster II had 7 genotypes while clusters III, IV, V, VI and VII contributed as solitary germplasms. Among the seed yield components, test weight (8.7 %) followed by seed yield per plant (5.5 %) and pod length (2.4 %) contributed maximum towards the divergence. Among seed quality parameters, seedling dry weight (50.99 %) contributed the maximum to the genetic divergence. The maximum intra cluster distance ranged from 0 (clusters III, IV, V, VI and VII) to 8.15 (cluster II). The maximum inter cluster distance (24.89) was noticed between cluster V (HG 18) and cluster VII (AK 38) indicating that the genotypes included in these clusters had maximum divergence and may be used as promising parents for hybridization programme to obtain better segregants in hose gram.

Key words: Horse gram, Genetic diversity, yield

Horsegram (*Dolichos uniflorus* L.) is a quantitative character influenced by a number of yield contributing traits. The selection of desirable types should therefore be based on yield as well as on other yield components. Information on mutual association between yield and yield components is necessary for efficient utilization of the genetic stock in crop improvement program. For any planned breeding programs aimed to improve grain yield potential of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability. This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Vast scope lies for genetic improvement of the horse gram through genetic diversity. Keeping this in view, present study was undertaken to understand the diversity in different accessions of horsegram for assessment and creation of diverse lines for future use in the breeding programme.

A total of 23 horse gram accessions including released varieties (PLM 1, PLM 2 and AK 38 by ANGRAU), locally cultivated varieties and germplasm collections procured from RARS, Palem formed the experimental material for the present study. All accessions were sown during the early spring seasons of 2008-09 and 2010-11 at Seed Research & Technology Centre, Rajendranagar, Hyderabad in a randomized complete block design in three replications. The plot size was 1.2 x 4 m^2 and plants were spaced 30 cm apart and with 10 cm between plants within row. All the recommended agronomic practices were followed. The qualitative traits that were studied include stem, leaf, pod and seed morphological characters and the observations were recorded on five randomly selected plants. The quantitative traits that were observed from five randomly selected plants of each replication include plant height (cm), primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, pod length (cm), seed yield per plant (g), and test weight (g). The seeds of all accessions after harvesting and drying were tested for laboratory germination (paper towel) as per the International Seed Testing Association Rules (ISTA, 1985). The final count was recorded at 10th day and expressed in percentage. Ten normal seedlings were selected at random in each replication for recording seedling length in centimetres (cm) and the same seedlings were oven dried at 80 ºC for 17 h and weighed (g) for dry weights. The seeding vigour index I (SVI I) were calculated by multiplying the germination percentage with seedling length (Abdul-Baki and Anderson, 1973).

Phenotypic variance (VP) and genotypic variance (VG) were determined by formulae proposed by Brewbaker, 1964. Broad sense heritability was calculated using the formula proposed by Mahmud and Kramer, 1951. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PGV) were estimated by the formula suggested by Burton, 1952. The genetic advance (GA) was calculated according to Allard, 1962. Mahalanobis D^2 technique (Mahalanobis, 1936) was used to study the genetic diversity and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

Variance due to genotypes for all the fourteen traits was significant. The data on range, phenotypic and genotypic variances, phenotypic and genotypic coefficient of variations (PCV and GCV), heritability and genetic advance are presented in the Table 1. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. Maximum difference between PCV and GCV was noticed for primary branches per plant indicating maximum influence of environment while the minimum is noticed for test weight. Similarly high disparities between GCV and PCV for number of branches per plant were reported by Samal and Senapathi (1997) in horse gram. A perusal of coefficient of variability indicates that PCV was quite higher for pods per plant (27.47 %) followed by secondary branches per plant (23.31 %) and seed yield per plant (21.49 %).

The highest GCV was observed for pods per plant (20.96) followed by seed yield per plant (17.22) and very low GCV estimates was observed for pod length (3.79) and primary branches per plant (3.91). High heritability (64.2) coupled with high GCV (17.22) and high genetic advance as per cent mean (28.54) for seed yield indicated low environmental influence and high transmission index. Test weight exhibited the highest heritability estimate of 80.0 followed by seedling vigour index I (78.6), leaf width (77.8) and seedling length (75.3). Selection for these characters is likely to be effective whereas selection for primary branches per plant the least heritable trait (8.6) is found to be ineffective. This is in contrast to the findings of Dobhal and Rana (1994) who reported high heritability for clusters per plant, pods per plant and seed yield per plot. The genetic advance as per cent of mean was high for pods per plant (33.12) and seed yield per plant (28.54) indicating that phenotypic selection for the improvement of these characters may be effective.

On the basis of D^2 values, 23 genotypes were grouped into 7 clusters indicating wide diversity in the experimental material for majority of the characters (Table 2). Cluster I had the largest number of genotypes (11) followed by cluster II with 7 genotypes, while remaining all clusters possessed one genotype in each. Cluster I alone with 11 genotypes indicated that majority of genotypes under study had narrow genetic diversity among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity. However, the unidirectional selection potential for one particular trait or a group of linked traits in several places may produce similar phenotypes which can be aggregated into one cluster irrespective of their geographic origin (Jethava, 1996).

The highest inter cluster distance was observed between genotypes of cluster V and cluster VII (24.89) followed by cluster V and VI (19.67) (Table 3). These clusters are quite divergent from each other and the genotypes belonging to these clusters can be used as parents for hybridization programme as crosses between genotypes belonging to the clusters with maximum inter cluster distance, may give better recombinants (Bhatt, 1970). Gohil and Pandya (2008) also suggested that for creating variability and developing the best selection criteria, a large number of divergent lines, instead of few, should be used in the hybridization. Therefore, use of HG 18 and AK 38 accessions in the further breeding programme would lead to transgressive segregants. These results are in conformity with the findings of Lal (2001) and Jayalakshmi and Ronald (2011). Gohil and Pandya (2008) have also pointed out in *Salicornia brachiata* Roxb (a non traditional oilseed) that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability. Minimum distance between clusters I and VI indicated close genetic relation between these two cluster and selection of parents from these two clusters should be avoided.

The maximum cluster mean for number of pods was recorded in cluster V (139.05) and cluster VI (131.88) and for seed yield in clusters VI (18.77) and cluster VII (17.97). The maximum value for plant height was recorded in Cluster III (67.91) and for germination in cluster V (99.88). Cluster IV for 100- seed weight (3.81) and cluster VII for seedling vigour index I (2670.71) recorded higher values (Table 4).

The results on the contribution of individual traits towards total divergence suggested that the seedling dry weight (50.99 %) contributed highest for divergence followed by seedling length (16.60 %), test weight and seedling vigour index I (8.70 %). Among the seed yield components, test weight (8.70 %) followed by seed yield per plant (5.53 %) and pod length (2.37 %) contributed the maximum divergence. Among seed quality parameters, seedling dry weight (50.99 %) contributed the maximum to the genetic divergence. The characters contributing maximum diversity can be given more emphasis for the purpose of fixing priority of parents in hybridization program.

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Table 1. Estimates of variability, heritability and genetic advance in horsegram

Character	Mean	Genotypic coefficient of variance (%)	Phenotypic coefficient of variance (%)	Heritability (%)	Genetic advance	Genetic advancement as % of mean
Leaf length (cm)	5.40	6.68	9.07	54.2	0.55	10.17
Leaf width (cm)	3.58	10.45	11.85	77.8	0.68	19.08
Plant height (cm)	60.37	4.09	10.30	15.8	2.03	3.36
Primary branches per plant	8.87	3.91	13.34	8.6	0.21	2.37
Secondary branches per plant	6.93	16.77	23.31	51.7	1.73	24.96
Pods per plant	102.36	20.96	27.47	58.2	33.90	33.12
Seeds per pod	5.73	4.94	6.05	66.7	0.48	8.34
Pod length (cm)	5.28	3.79	5.01	57.1	0.31	5.93
Seed yield per plant (g)	13.88	17.22	21.49	64.2	3.96	28.54
Test weight (g)	3.21	6.23	6.97	80.0	0.37	11.54
Germination (%)	94.18	4.61	5.63	66.9	7.35	7.80
Seedling length (cm)	24.63	7.82	9.01	75.3	3.46	14.04
Seedling dry weight (g)	0.42	9.82	12.93	57.6	0.06	15.43
Seedling vigour index	2299.37	10.20	11.50	78.6	430.19	18.71

Table 2. Distribution of 23 horse gram genotypes in different clusters based on D^2 statistics

Clusters	**No. of genotypes**	**Genotypes**
Cluster I	11	HG32, HG24, PALEM 1, HG52, HG58, HG63, HG75, HG50, HG72, HG49, HG11
Cluster II	7	HG54, HG38, PALEM 2, HG41, HG14, HG46, HG17
Cluster III	1	HG59
Cluster IV	1	HG15
Cluster V	1	HG18
Cluster VI	1	HG35
Cluster VII	1	AK 38

Table 3. Average intra (diagonal) and inter-cluster D^2 values in horsegram

Clusters	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**
Cluster I	7.20	11.45	9.64	10.02	18.78	8.96	11.95
Cluster II		8.15	9.69	12.48	11.08	12.59	17.09
Cluster III			0.00	11.89	14.92	13.32	15.84
Cluster IV				0.00	18.57	10.80	12.94
Cluster V					0.00	19.67	24.89
Cluster VI						0.00	12.90
Cluster VII							0.00

Table 4. Cluster means and per cent contribution for various yield and yield attributing characters and seed quality characters in horse gram

Character	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Per cent contribution**
Leaf length (cm)	5.47	5.27	5.13	5.18	5.10	5.13	6.13	0.40
Leaf width (cm)	3.77	3.38	3.06	3.59	3.37	3.46	3.69	0.40
Plant height (cm)	61.15	58.62	67.91	60.63	61.09	59.03	56.99	0.40
No. of primary branches	8.61	9.11	9.10	8.98	10.75	7.93	8.90	0.00
No. of secondary branches	6.61	7.04	9.80	5.48	7.38	7.47	7.27	0.40
Pods per plant	88.06	110.57	96.15	117.07	139.05	131.88	127.45	1.58
Seeds per pod	5.77	5.75	6.15	5.20	6.05	5.83	4.75	0.79
Pod length (cm)	5.33	5.16	5.20	5.16	5.41	5.75	5.30	2.37
Seed yield per plant (g)	13.40	14.06	11.58	11.72	13.58	18.77	17.97	5.53
Test weight (g)	3.24	3.08	3.22	3.81	3.13	3.14	3.33	8.70
Germination (%)	91.86	96.69	98.38	99.50	99.88	83.23	97.90	3.16
Seedling length (cm)	25.10	24.18	26.87	22.02	24.51	20.80	27.03	16.60
Seedling dry weight (g)	0.43	0.39	0.45	0.47	0.35	0.55	0.46	50.99
Seedling vigour index	2274.89	2323.55	2590.27	2190.76	2447.73	1697.26	2670.71	8.70