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Genetic diversity among selected genotypes of M_4 generation in horsegram

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ABSTRACT

Effect of different doses of gamma rays (5, 10, 15, 20, 25, 30, 35 and 40) in three varieties of horsegram *viz.*, 'AK-21', 'AK-42' and 'Maru-K-1' was studied under field conditions at the Main Pulses Research Station, S. D. Agricultural University, Sardarkrushinagar during summer, 2004 to *kharif*, 2005. In all, eleven clusters were formed. Cluster I (34), followed by cluster IV (12), cluster V (4) and cluster VI (4) were found to be the largest. The highest inter-cluster distance was observed between cluster VI and cluster X. It was observed that the genotypes were clustered irrespective of their eco-geographical regions. Test weight was the main contributor towards the total divergence. Yield per plant, number of seeds per pod, pod length, days to maturity, plant height, days to 50% flowering and number of pods per plant had moderate contribution towards total divergence.

Key words: Cluster, Gamma rays, Genetic divergence, Horsegram

Horsegram (*Macrotyloma uniflorum* Lam. verdc, *Dolichos biflorus*) is well known for its versatility to perform well under adverse edaphic and climatic conditions. It is a hardy grain legume with an ability to withstand protracted droughts. It performs well in almost all types of soils, except highly alkaline soils. The grains may be utilized in multifarious ways ranging from whole boiled seeds as *dal* to grind flour mixed with main calory sources like wheat flour. The seeds have an immense medicinal value and work like panacea for those suffering from kidney stone which is the most prevalent problem in arid and semi arid areas due to nagging poor quality of potent water. Besides food, feed and medicinal uses, the crop has immense pertinence in sustaining and enhancing soil fertility by checking erosion and fixation of atmospheric nitrogen. In south India, the crop is especially grown as a preparatory crop in newly reclaimed lands to improve the soil fertility and organic matter status (Sen and Bhowal 1959).

Genetic diversity is a basic criterion to the crop plants whether through natural selection or by directed plant breeding. In plant breeding, genetic diversity plays an important role because hybrid between lines of diverse origin generally displays a greater heterosis than those between closely related parents. D^2 analysis (Mahalanobis 1936) is an extreme tool in quantifying the degree of divergence among the biological populations at genotypic level to assess the relative contributions of different components to the total divergence.

MATERIALS AND METHODS

Seeds (250g) of three cultivars of horsegram *viz.*, 'AK 21', 'AK 42' and 'Maru K-1' were obtained from the germplasm pool maintained at the Main Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar and were treated with different doses of gamma rays at the Bhabha Atomic Research Centre (BARC), Trombay with gamma rays intensity of 1.8 kR per minute. The doses applied were 0, 5, 10, 15, 20, 25, 30, 35 and 40 kR in all the three varieties, thus, making 27 treatments.

The mutated seeds were grown during *summer*, 2004 to *kharif* 2005. The M_1 was raised following proper package of practices in single replication. From each treatment in M_1 generation, 25 normal appearing plants were randomly selected to provide material for M_2 generation up to 20 kR. M_2 generation was raised to assess induced polygenic variability and to score the types of macro-mutations and their frequency. The M_2 and M_3 were raised in Compact Family Block Design with three replications. 25 seeds from each selected plants in M_1 were sown in a row for each replication. The selected 25 plants from each treatment in M_1 generation became families in M_2 generation. The row-to-row spacing was kept 45 cm and plant-to-plant 15 cm. Similarly M_3 generation was sown in Compact Family Block Design. M_4 generation was raised in Randomized Block Design with three replications. The selected 58 lines that yielded higher than respective checks in M_3 generation were selected and sown for their superiority in M_4 generation along with respective checks.

Transformation of original means of various characters (X_1's) to uncorrelated variables (Y_1's) was carried out by pivotal condensation as the common dispersion matrix by computer. This made D^2 value as a simple sum of squares of differences in transformed values for various characters. Grouping of the genotypes in different clusters was done by using Tocher's method (Rao 1952). The inter-cluster distance was calculated by measuring the distance between clusters I and II, I and III, II and III, and so on. Likewise, one by one all the clusters were taken and their distances from each other were calculated.

RESULTS AND DISCUSSION

Plant breeders are always interested to assess the genetic diversity among the germplasm/varieties/advanced breeding material available with them, so as to utilize them in the breeding programme because genetically diverse parents are likely to produce high heterotic effects (Griffing and

Lindston 1954). The distantly related parents within the same species when utilized in cross breeding programme are likely to produce a wider spectrum of variability.

To a plant breeder single character is not of much importance as the combined merit of a number of desirable traits becomes more important, when he is concerned with a complex trait like yield per plant. Hence, for improving yield, selection of parents based on number of characters having quantitative divergence is required which can be fulfilled by D^2 statistic developed by Mahalanobis (1936). In the present study, D^2 statistic estimated in 61 genotypes of horsegram isolated from M_3 generation (58 mutants + 3 checks) on the basis of their *per se* performance for nine characters showed that generalized distance (D) between two populations varied from 0.00 to 11.04.

Clustering of 61 genotypes was carried out following Tocher's method (Rao 1952). Over all, eleven clusters were observed (Table 1). Cluster I, followed by cluster IV, cluster V and cluster VI were found to be the largest with 34, 12, 4 and 4 genotypes, respectively. Seven more clusters, each having single genotype, were observed. Genetic drift and selection in different environments might result in greater diversity than geographical distance. Moreover, free exchange of seed material along different geographical regions changes the character constellation associated with particular region. Absence of parallelism between genetic diversity and geographical origin was reported in upland cotton and castor (Bhatt and Reddy 1987). Similar conclusion was derived by Ganeshaiah (1982). The maximum inter-cluster distance (D = 11.04) was observed between clusters X and VI, followed by clusters X and II (D = 9.86) and clusters X and V (D = 8.68) (Table 2). Large distances between clusters (inter-cluster) were reported by Balan *et al*. (1992) and Patil *et al.* (1993). High heterotic combinations are obtained when the genotypes of distantly placed clusters are inter-crossed. In the present investigation, genotypes of cluster X, if crossed with those of cluster VI, might give high heterosis. Similar results may be obtained by crossing cluster X and cluster II and cluster X and cluster V.

Cluster VII depicted the lowest mean values for days to 50% flowering and plant height, while cluster III depicted the lowest mean value for days to maturity. Cluster X showed highest mean values for number of effective branches per plant and test weight. Similarly, cluster XI for number of pods per plant, cluster VIII for pod length, cluster IX for number of seeds per pod and cluster III for yield per plant exhibited the highest mean values (Table 3). Inter crossing of genotypes among these clusters will induce variability for the respective traits.

Table 1. The distribution of 61 genotypes of horsegram to different clusters on the basis of D^2 statistics

Cluster	Number of genotypes	Genotypes
I	34	AK-42 15 kR 20, MK-1 15 kR 10, AK-42 5 kR 10, MK-1 15 kR 13, AK-21 15 kR 14, AK-42 10 kR 5, AK-42 20 kR 12, MK-1 15 kR 19, MK-1 5 kR 17, AK-21 20 kR 15, AK-21 5 kR 13, MK-1 20 kR 4, MK-1 20 kR 11, AK-42 20 kR 23, AK-21 20 kR 3, AK-42 20 kR 1, AK-42 control, AK-42 5 kR 8, MK-1 15 kR 7, AK-42 15 kR 6, MK-1 5 kR 7, AK-21 5 kR 20, AK-21 5 kR 22, AK-42 15 kR 23, MK-1 15 kR 2, MK-1 5 kR 21, AK-21 15 kR 5, MK-1 20 kR 16, AK-21 20 kR 17, AK-42 5 kR 3, AK-21 5 kR 4, MK-1 5 kR 13, MK-1 15 kR 4, MK-1 15 kR 9
II	1	MK-1 10 kR 10
III	1	AK-21 10 kR 12
IV	12	AK-21 10 kR 9, MK-1 10 kR 17, AK-21 10 kR 8, MK-1 5 kR 22, AK-21 10 kR 20, AK-21 10 kR 17, MK-1 20 kR 18, AK-42 10 kR 2, AK-21 10 kR 4, AK-21 10 kR 6, AK-21 20 kR 23, MK-1 10 kR 19
V	4	AK-21 control, MK-1 control, MK-1 15 kR 23, AK-21 15 kR 12
VI	4	AK-42 10 kR 14, MK-1 10 kR 8, AK-42 10 kR 7, AK-42 5 kR 4
VII	1	AK-42 5 kR 24
VIII	1	AK-42 15 kR 25
IX	1	AK-21 5 kR 11
X	1	AK-21 15 kR 2
XI	1	MK-1 5 kR 2

Table 2. Average intra and inter-cluster (D) values for 61 genotypes of horsegram

Cluster	1	2	3	4	5	6	7	8	9	10	11
1	2.79	3.40	3.81	4.54	3.69	4.76	3.85	3.71	3.93	7.68	5.56
2		0.00	5.72	6.53	3.96	3.46	5.04	4.99	4.52	9.86	6.57
3			0.00	3.02	5.14	6.79	3.77	4.67	4.41	5.56	5.38
4				3.00	5.27	7.58	4.18	4.34	5.06	4.93	5.40
5					3.45	5.25	4.87	4.29	5.59	8.68	7.13
6						4.17	6.16	5.55	5.85	11.04	7.93
7							0.00	4.76	2.83	7.07	3.60
8								0.00	4.51	6.96	6.24
9									0.00	7.11	3.34
10										0.00	6.43
11											0.00

Table 3. Cluster means for different characters of 61 genotypes of horsegram

Cluster Number	Number of genotypes	Days to 50% flowering (no)	Plant height (cm)	Effective branches/ plant (no)	Pods/ plant (no)	Pod Length (cm)	Seeds/ pod (no)	Days to maturity (no)	Test weight (g)	Yield/ plant (g)
I	34	57.04	58.91	3.09	38.23	4.03	4.84	105.50	3.49	7.39
II	1	59.45	58.80	2.83	40.59	4.08	5.00	105.92	3.31	8.07
III	1	55.44	56.53	2.89	38.84	3.64	5.38	102.56	3.69	8.37
IV	12	56.11	57.58	2.97	37.91	4.00	4.61	107.18	3.76	6.98
V	4	57.67	53.73	3.15	36.27	3.75	4.26	110.28	3.45	6.72
VI	4	54.67	60.59	2.82	39.94	4.11	4.70	104.79	3.26	7.55
VII	1	54.00	48.74	3.00	43.42	3.87	4.89	107.00	3.62	6.85
VIII	1	55.22	57.49	2.92	31.13	5.00	3.93	105.78	3.57	5.20
IX	1	56.00	53.09	2.83	35.65	4.68	5.44	103.33	3.55	6.23
X	1	59.22	62.22	3.21	29.89	4.70	4.92	104.11	4.02	5.56
XI	1	58.00	61.73	2.58	44.89	4.37	5.00	105.56	3.71	6.21

The results revealed that test weight was the main contributor towards the total divergence (Table 4). Similar results were obtained by Ramakrishnan *et al*. (1979) in horsegram and Renganayaki and Rangasamy (1991) in green gram. Yield per plant, number of seeds per pod, pod length, days to maturity, plant height, days to 50% flowering and number of pods per plant had moderate contribution towards total divergence, while number of effective branches per plant had least contribution to the total divergence.

The clustering pattern could be utilized for identifying the best cross combinations in generating variability with respect to various traits. Superior genotypes for hybridization programme can also be selected on the basis of inter-cluster distance and cluster means. In the present investigation, the significant correlation in positive direction with yield per plant was observed by days to 50% flowering, number of effective branches per plant and number of pods per plant in 'AK-21'; number of effective branches per plant, number of pods per plant, and number of seeds per pod in 'AK-42' and days to 50% flowering, days to maturity, number of pods per plant, pod length and number of seeds per pod in 'MK-1'. Maximum cluster mean was observed for yield per plant (cluster III), number of pods per plant (cluster XI) and number of seeds per pod (cluster IX). Therefore, for creating wide spectrum of variability and improving yield, the genotypes included in cluster III, cluster XI and cluster IX should be inter crossed.

Table 4. Per cent contribution of each character towards the total divergence

Sr. No.	Character	Number of times character ranked first	Contribution (%)
1	Days to 50% flowering (no)	94	5.14
2	Plant height (cm)	109	5.96
3	Effective branches/plant (no)	20	1.09
4	Pods/plant (no)	90	4.92
5	Pod length (cm)	122	6.67
6	Seeds/pod (no)	166	9.07
7	Days to maturity (no)	111	6.07
8	Test weight (g)	937	51.20
9	Yield/plant (g)	181	9.89

The foregoing discussion clearly demonstrates that the genetic variability induced by physical mutagen both at morphological and quantitative levels in majority of the character broadens the scope of selection for desired characters and plant type for future breeding programme. Mutation breeding could not perform miracles but still it was very successful in opening new horizons for a crop like horsegram, which is strictly self pollinated and crossing is very difficult due to tiny structure of flower.

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