Int.J.Curr.Microbiol.App.Sci (2021) *10*(09): 291-300

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 10 Number 09 (2021)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2021.1009.034

Genetic Divergence (D^2) Evaluation in Horsegram [*Macrotyloma uniflorum* (L) Verdcout] Genotypes

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Keywords

Horsegram, cluster analysis, divergence, germplasm

Article Info

Accepted:
15 August 2021
Available Online:
10 September 2021

A B S T R A C T

The experiment was performed at Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, Jagdalpur, Chhattisgarh. A total of 56germplasm lines and 1 check variety of horsegram were assessed for 10 quantitative traits during *kharif*2018.Genotypes were grouped into eight clusters. Clusters VI had maximum intra cluster distance while inter cluster distance was maximum between cluster VI and cluster VIII. Cluster III and cluster VIII had highest mean values for seed yield per plant characters. The characters *viz*., pods per plant followed by days to maturity and seed yield per plant were main contribution to total divergence. Based on the result genotypes belonging to clusters II, III and VIII are recommended for hybridization, as these genotypes showed good performance for seed yield and belong to the diverse clusters.

Introduction

Horsegram [*Macrotyloma uniflorum* (L) Verdcourt] belonging to Family: Leguminosae, Sub-family: Faboidae, Tribe: Phaseoleae, Sub-tribe: Phaseolinae, Genus: *Macrotyloma*, Species: *uniflorum*. *Macrotyloma uniflorum* (L) Verdcourt synonyms are *Dolichos uniflorus* and *Dolichos biflorus* with chromosome number of 2n=2x=20, 22, 24. Genus *Macrotyloma* consist about twenty five species; most of them are mainly present in Africa. Within *Macrotyloma uniflorum* (L) Verdcout four varieties have been identified *viz*., var. *uniflorum*, *benadirianum*, *stenocarpum* and *verrucosum* (Uma Rani *et al.*, 2013). It is an under exploited arid legume crop. It is an important pulse crop as seeds are rich in protein and consumed in majority by poorest section of the society. It is an important component in the dryland crop production

system due to its ability to withstand drought with minimum management. It is commonly known as kulthi and hirwa or harwa in Bastar Region. It is an annual succulent herb, slender, downy, slightly twining branching, springing from the base of the plant, semi-erect, low growing habit with 60-120 cm height; leaves are trifoliate with 2.5 to 5.0 cm in length. Stipules are one cm long and ovate lanceolate. Peduncles are short, bisexuals, bracteate, pedicellate, zygomorphic and complete. Calyx are downy teeth lanceolate, corolla arc light yellow, petals are five, standard longer than wings, stamens diadelphos (9+1), filaments are alternately short and long anthers, introse, uniform diversified. Gynoecium is with superior ovary. Style file from terminal, curved, stigma capitate and hairy. Pods are linear, recurned beaked with 5-7 seeds. Seeds are normal flattened 3-6 mm long, black, light red, brown or mottled, testa skinny with small hilum. Horsegram is a self fertilized crop, matures in 3 to 4.5 months. The tap root produces a branched root system with smooth, rounded nodules. Nodules contains nitrogen fixing bacteria (Kumar and Vittal, 2007). During twelfth plan (2012-2015), the total area under horsegram was 2.32 lakh hectares and production was 1.05 lakh tonnes respectively. With regard of area and production, Karnataka is on the first position on all India basis sharing 26.72% and 25.71% respectively followed by Odisha sharing 19.46% area and 15.48% production and Chhattisgarh is in third position sharing 19.29% area and13.29% production. The highest productivity was noted in the state of Bihar (959 kg/ha) followed by W.B. (796 kg/ha) and Jharkhand (603 kg/ha) (Anon., 2015-16). In Chhattisgarh during 2017-2018 area, production and productivity under crop was 47.62 ha, 16.37 MT, 344 kg/ha (Anon., 2017-18).

All the varieties developed to date are mainly by single plant selection from locals. There is greater need to increase the yield and quality of this crop by breeding while understanding the genetic makeup of this crop. Hence, it is essential to generate new variability through hybridization. By germplasm exploration superior germplasm's can be identified from these local varieties which can be ultimately used for developing superior lines in breeding programme.

The present study was taken up to evaluate the germplasm of horsegram for genetic divergence and selection of genetically divergent parents from the available germplasm before taking up hybridization programme for evolving better heterotic response for further breeding programme.

Materials and Methods

The present experiment entitled "Genetic Divergence (D^2) Evaluation in Horsegram [*Macrotyloma uniflorum* (L) Verdcout] Genotypes" was performed at "Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, (Jagdalpur), Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh)" located at N 19°5'35'' longitude E 81°57'37'' latitude and at an altitude ranging from 530 to 850 meters above mean sea level (MSL) with an annual rainfall 1400 mm. The experimental material comprised of fifty six horse gram genotypes along with the check variety Indira kulthi-1. The experimental material was planted in a Randomized Complete Block Design with three replications during *kharif* 2018. Each genotype was planted in three rows of 4 m length × 1 m width having 30 ×10 cm spacing between rows and plants. The observations were recorded on five randomly selected plants per replication for each accession. The analysis of variance for different characters was carried out using the mean data through method given by Panse and Sukhatme (1967).

The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tocher's method as detailed by Rao, 1952. The genotypes were grouped into different clusters, inter and intra cluster distances and mean performances for characters were also computed. Each character was ranked on the basis of values in all the combination of genotype for estimation of contribution of individual characters towards divergence.

Results and Discussion

Analysis of variance

Analysis of variance was performed for ten quantitative characters including yield and yield attributing traits of fifty seven genotypes. From the analysis of variance it was observed that mean sum of squares due to genotypes were significant for all characters at 5% level of significance under study thus exhibiting the presence of considerable genetic variability for all the traits in the experimental material. The results found were presented in Table 1. Significant genetic variation between horsegram genotypes for different yield attributing traits has been reported earlier also by Chahota *et al.,* (2005), Durga (2012), Gomashe *et al.,* (2018) and Priyanka *et al.,* (2019).

Genetic Divergence

Multivariate analysis was done utilising Mahalanobis D^2 statistic. Rao (1952) used D^2 statistics technique for the estimation of genetic diversity among germplasm lines. It is used to measure the degree of diversification and also determines relative portion of each component trait to total divergence. This technique says that, if distance between clusters of genotypes is large, there will be more genetically diversity and if small distance exists then genotypes are less divergent from each other. So, genotypes falling under different cluster will be more divergent from each other corresponding to those falling in the same cluster. Genotypes belonging to different clusters can be used for the hybridization programme.

Clustering of Genotypes

Mahalanobis D^2 statistics divided all the 57 cultivars of horsegram into eight clusters (Table 2 and Fig. 1). The cluster's strength varied from single genotype to twenty six genotypes. Fifty seven genotypes had been clustered into eight clusters on the basis of assessed values of D^2statistics. Clustering pattern of germplasm lines of horse gram are represented in Table 2and through dendogram in Fig.1. Among the eight clusters formed, cluster II was found to be largest group consisting of twenty six genotypes followed by cluster I having twenty one genotypes, cluster III, IV, V and VI having two genotypes each and cluster VII and VIII having single genotype. The distribution pattern of genotypes confirmed the existence of diversity among the genotypes considered.

Intra and Inter-cluster distances

The basic theme behind formation of clusters is to get the intra and inter cluster distances. These distances are used as index for parents with diverse origin. The intra and inter cluster values are means derived from D^2 values of cluster elements. It is assumed that the statistical distance (D) is the index of genetic diversity. Among the eight clusters formed from the fifty seven horsegram genotypes, the uppermost intra cluster distance was found in cluster VI (47.973) trailed by V (34.334), I (32.428), II (32.291), IV (28.870) and III (16.680). Cluster VII (0.000) and VIII (0.000) have nil intra cluster distance. Maximum inter cluster distance was noticed between cluster

VI and VIII (372.038) followed by cluster II and VI (328.092) and cluster IV and VIII (259.401),which indicated that the genotypes grouped in these clusters were highly divergent from each other. Table. 3 and Fig. 2 represents the average D^2 values of intra and inter cluster distances of horsegram germplasm under study. Genotypes included in a particular cluster indicated their close relationship among themselves as compared to the other clusters. Therefore, it could be expected that genotypes within a cluster were less genetically diverge with each other, and were diverse from the accessions belonging to other clusters.

As the D^2 values represent the index of genetic diversity among the cluster, it would be more appropriate to make cross between genotypes separated by high estimates of statistical distance (Parhe *et al.,* 2014). Selecting parents from the maximum divergent clusters are expected to manifest maximum heterosis in crossing and wide variability in genetic architecture (Chowdhary *et al.,* 2002 and Kumar *et al.,* 2016).

Cluster mean value for different characters

Table 4.8 represents the comparison of cluster means for different traits. The results obtained from cluster means for different characters showed frequent variation present among clusters categorised according to D^2 analysis. Range of means made it conceivable to know the characters effecting divergence. Cluster mean for different traits revealed that the magnitude of differences among the mean of the traits for clusters was significant. The early days to 50% flowering genotypes are present in Cluster VIII (44.333) followed by cluster II (45.359) and cluster I (45.476). The early maturing genotypes are present in cluster VIII (84.000) followed by cluster II (85.641) and I (85.698). The maximum plant heights were found in cluster V (57.667 cm) followed by cluster II (57.122 cm) and IV (55.867cm). The total number of primary branches per plant was found high in Cluster V (7.333) followed by cluster III (6.833) and cluster II (6.825).

The number of pods per plant was found high in Cluster III (56.012) followed by cluster VIII (53.497) and cluster VII (53.320). The petiole length was highest in Cluster VII (4.667 cm) while cluster IV (3.940 cm) exhibited lowest petiole length.

The maximum pod length was observed in cluster I (4.552 cm) followed by cluster II (4.395cm) and VI (4.342 cm). The number of seed per pod was highest in cluster III and VII (5.000) followed by cluster II (4.615) and I (4.238). Character test weight (1000 seeds) was highest in Cluster V (29.993 g) trailed by cluster II (26.204 g) and I (26.086 g). The seed yield per plant was observed maximum in cluster III (11.767) followed by cluster VIII (11.00 g) and VII (10.960 g).

Contribution of characters towards genetic divergence

The contribution of the characters towards the genetic divergence is presented in Table 5 and Fig. 3. Out of the ten traits assessed, pods per plant contributed maximum towards diversity (42.776%), trailed by days to maturity (18.493%), seed yield per plant (13.597%), test weight (7.707%), plant height (6.869%), days to 50 per cent flowering (4.148%), pod length (2.066%), petiole length (1.684%), primary branches per plant (1.390%) and number of seeds per pod (1.272%) showed least contribution towards genetic divergence.

Geetha *et al.,* (2011) observed that seed yield, total number of pods per plant and number of branches per plant while Sahoo *et al.,* (2010) reported that days to maturity followed by days to flowering contributed most to divergence.

Table.1 Analysis of variance for seed yield and seed yield attributing traits in horsegramgermplasm lines

Source of variation	Degree of freedom	DFF	DM	PH (cm)	PBPP	PPP	PeL (cm)	PL (cm)	SPP	SYPP (g)	TW (g)
Replication	2	19.702	10.251	34.014	0.155	8.855	3.25	1.09	1.754	2.029	0.531
Treatment	56	17.076*	58.539*	132.352*	1.449*	160.639*	0.714*	0.892*	1.231*	18.327*	6.412*
Error	112	2.404	2.388	16.605	0.720	2.988	0.401	0.295	0.433	1.023	0.649
S.Em.±	-	0.895	0.892	0.895	0.490	0.998	0.366	0.314	0.380	0.584	0.465
CV (%)	-	3.369	1.770	3.369	12.886	3.652	14.739	12.370	15.123	11.375	3.086
CD (5%)	-	2.512	2.504	2.512	1.375	2.800	1.026	0.880	1.066	1.639	1.305

*Significant at 5%level of significance

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, PBPP= Number of primary branches per plant, PPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, SPP= Number of seeds per pod, SYPP= Seed yield per plant, TW= Test weight.

Table.2 Clustering array of genotypes of horsegram based on D^2 analysis

Cluster no.	No. of genotypes	Name of genotypes
I	21	SGHG 8, SGHG 9, SGHG 71, SGHG 28, SGHG 58, SGHG 60, SGHG 67, SGHG 39, SGHG 40, SGHG 68, SGHG 10, SGHG 47, SGHG 62, SGHG 75, SGHG 15, SGHG 5, SGHG 37, SGHG 24, SGHG 91, SGHG 59, SGHG 74.
II	26	SGHG 51, SGHG 88, SGHG 29, SGHG 48, SGHG 92, SGHG 69, SGHG 38, SGHG 36, SGHG 73, SGHG 26, SGHG 46, SGHG 6, SGHG 17, SGHG 14, SGHG 66, SGHG 78, SGHG 63, SGHG 32, SGHG 31, SGHG 13, SGHG 81, SGHG 52, SGHG 23, SGHG 72, SGHG 35, SGHG 2.
III	2	SGHG 50, SGHG 53
IV	2	SGHG 54, SGHG 55
V	2	SGHG 21, SGHG 79
VI	2	SGHG 56, SGHG 90
VII	1	Indira kulthi-1
VIII	1	SGHG 27

Table.3 Average intra and inter cluster distances among germplasm lines of horsegram for yield and yield related traits

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**32.428**	115.162	168.483	104.355	67.776	168.839	166.864	119.874
Cluster II		**32.291**	93.594	227.683	103.899	328.092	107.867	49.707
Cluster III			**16.68**	140.258	150.964	233.724	59.15	117.715
Cluster IV				**28.87**	121.065	66.185	167.384	259.401
Cluster V					**34.334**	197.159	156.238	136.953
Cluster VI						**47.973**	167.822	372.038
Cluster VII							**0**	146.259
Cluster VIII								**0**

Table.4 Cluster means of germplasm lines of horse gram for yield and yield related traits

Cluster	DFF	DM	PH (cm)	PBPP	PPP	PeL (cm)	PL (cm)	SPP	TW (g)	SYPP (g)
Cluster I	45.476	85.698	51.295	6.347	40.679	4.288	4.552	4.238	26.086	6.852
Cluster II	45.359	85.641	57.122	6.825	53.288	4.336	4.395	4.615	26.204	10.755
Cluster III	45.667	98.167	53.433	6.833	56.012	4.067	4.245	5.000	25.237	11.767
Cluster IV	46.167	98.000	55.867	6.167	40.200	3.940	3.950	3.500	25.373	6.325
Cluster V	48.500	89.000	57.667	7.333	42.618	4.060	3.688	3.500	29.933	7.785
Cluster VI	54.500	99.667	48.433	5.567	37.062	4.385	4.342	3.500	24.570	5.512
Cluster VII	54.667	96.333	48.200	6.733	53.320	4.667	4.220	5.000	24.270	10.960
Cluster VIII	44.333	84.000	38.000	6.200	53.497	4.547	3.820	4.000	25.983	11.000

DFF= Days to 50 % flowering, DM= Days to maturity, PH= Plant height, PBPP= Number of primary branches per plant, PPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, SPP= Number of seeds per pod, SYPP= Seed yield per plant, TW= Test weight.

Table.5 Contribution of characters towards genetic divergence

Characters	Contribution (%)
Number of pods per plant	42.776%
Days to maturity	18.493%
Seed yield per plant	13.597%
Test weight	7.707%
Plant height	6.869%
Days to 50 per cent flowering	4.148%
Pod length	2.066%
Petiole length	1.684%
Number of primary branches per plant	1.390%
Number of seeds per pod	1.272%

Fig.1 Dendogram describing the distribution of horsegram genotypes

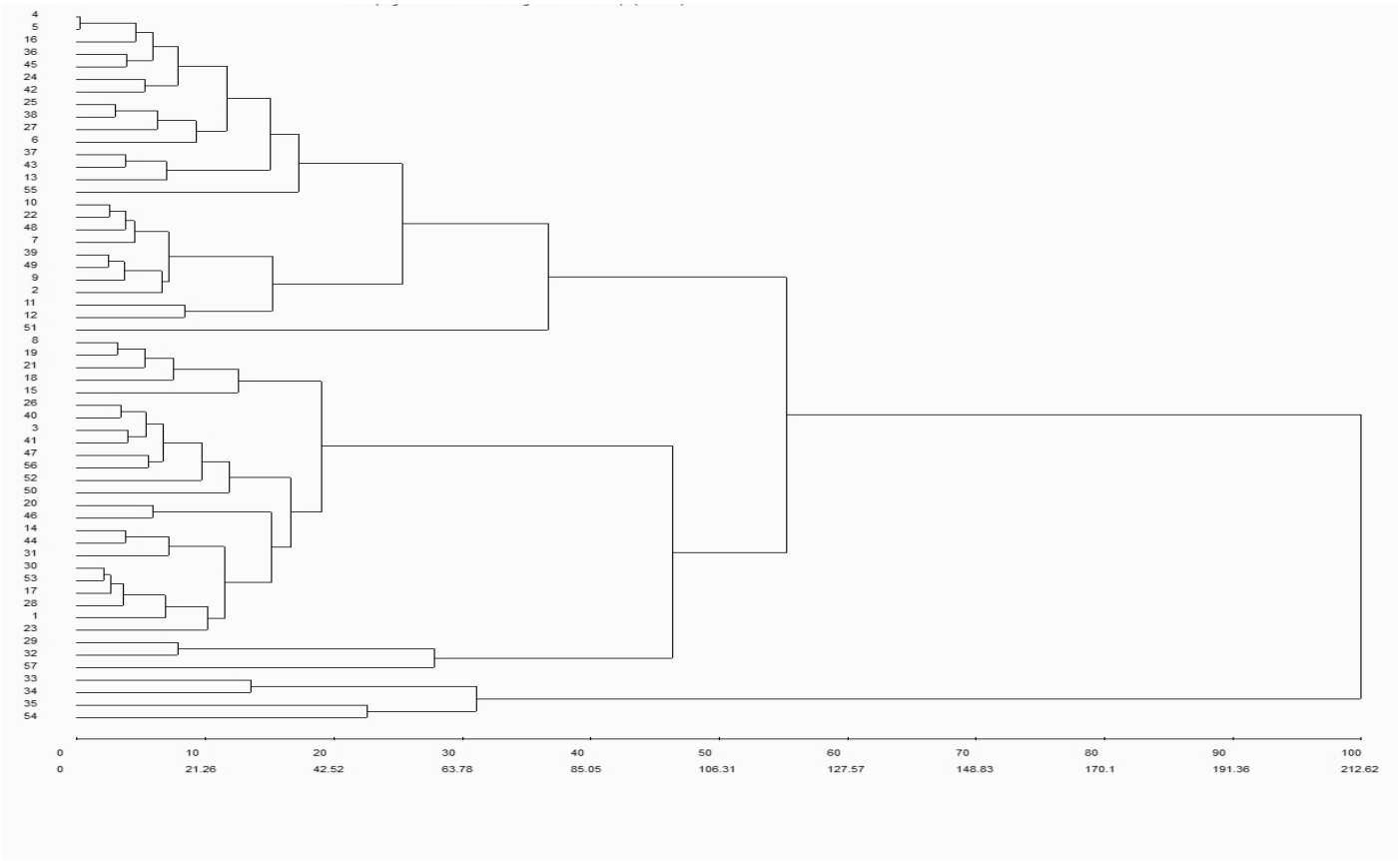


Fig.2 Average intra and inter cluster distances among germplasm lines of horsegram for yield and yield related trait

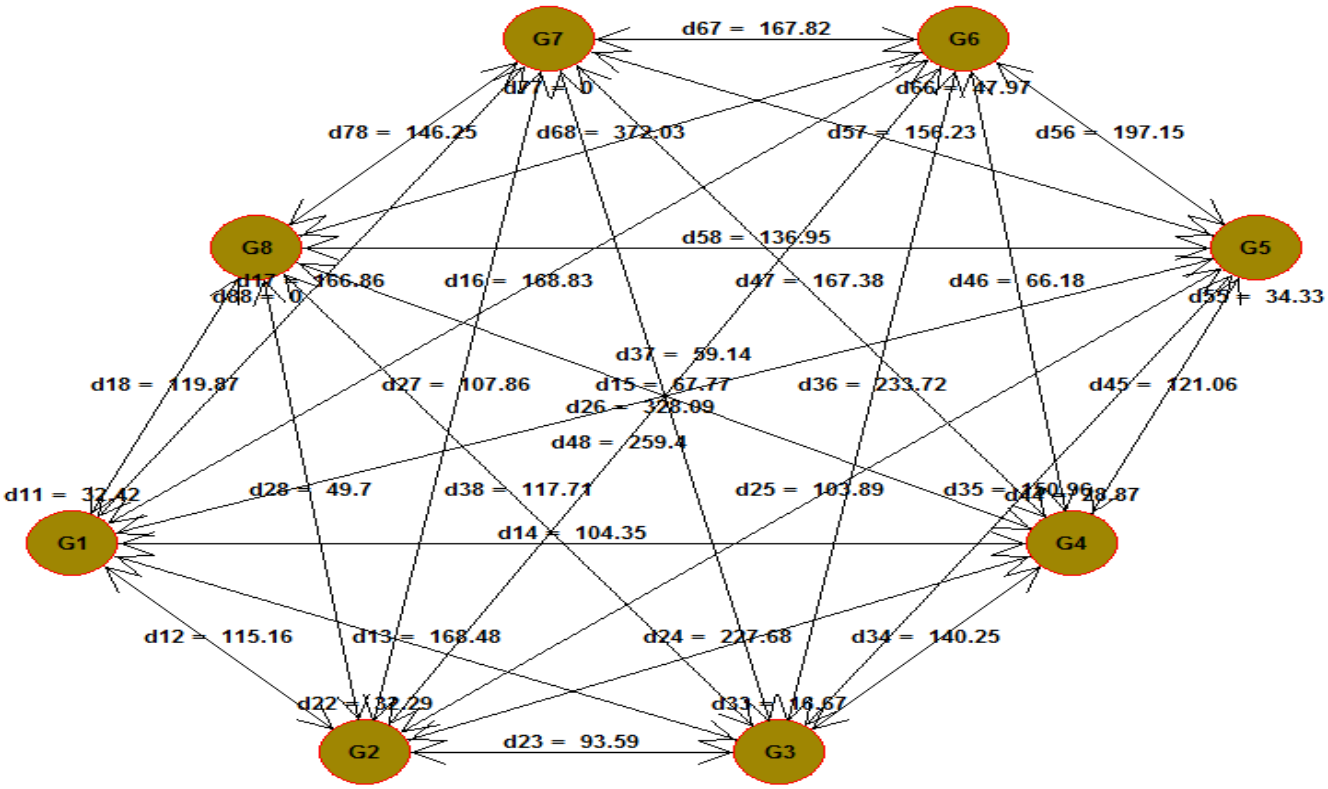
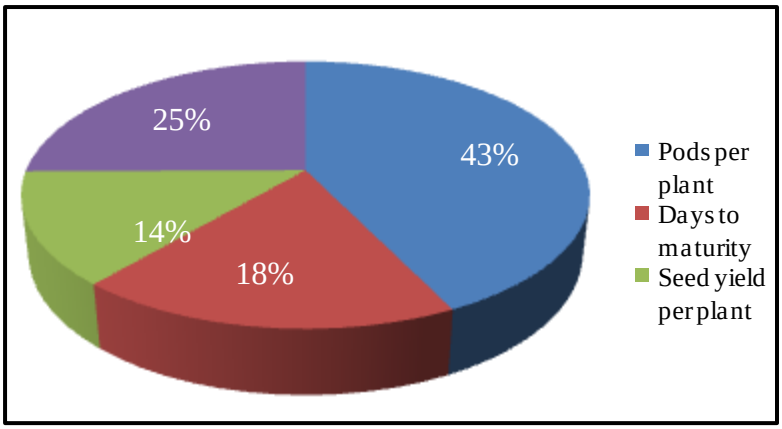


Fig.3 Percent contribution of characters towards genetic divergence



The knowledge of genetic diversity helps in the tagging of germplasm, identification of gene stock and establishment of core collections Upadhyaya *et al.*, (2007).

Fifty seven genotypes of horsegram had been grouped into eight clusters, maximum intra cluster distance was found in cluster VI. Maximum inter cluster distance was found

between cluster VI and VIII. Cluster mean values obtained through D^2 analysis revealed cluster III as most promising for the trait seed yield per plant. The character pods per plant funded maximum towards genetic divergence followed by days to maturity and seed yield per plant. As, clusters VI and VIII exhibited higher genetic diversity and thus genotypes of these cluster may be used for inter varietal hybridization programme for getting higher yielding recombinants. The promising genotypes identified can be used as donors for respective characters and breeders can use them in their breeding programmes for their transfer into the important agronomic bases. The inter-relationship among seed yield and most of the other traits was significant and positive suggesting indirect selection based on component traits would help in improving the seed yield. Further, it may be concluded that selection of genotypes from different diverse groups and their judicious utilization in hybridization programme would increase the probability to obtain transgressive segregants.

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How to cite this article:

Rakesh Singh, J. L. Salam and Mahendra. 2021. Genetic Divergence (D^2) Evaluation in Horsegram [*Macrotyloma uniflorum* (L) Verdcout] Genotypes. *Int.J.Curr.Microbiol.App.Sci.* 10(09): 291-300. doi: https://doi.org/10.20546/ijcmas.2021.1009.034