



Study on genetic diversity analysis for quantitative traits in black gram (*Vigna mungo* (L.) hepper.)

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Abstract

The presence of sufficient genetic variability, the knowledge of nature of association among different characters and relative contribution of different characters to yield is a prerequisite to any breeding programme. The aim of the present study was to estimate genetic parameters of 13 yield attributing traits in 36 Blackgram cultivars with a view to select better yield attributes in chickpea. P-1 (2.86g) was found to be superior for seed yield per plant among 36 genotypes followed by PLU-144 (2.80g), KU-96-4 (2.800g) and PUSA URD (2.6g). The higher value of phenotypic co-efficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated that there was an influence of the environment. Among the 13 quantitative characters, high estimates of GCV and PCV were recorded for harvest index (32.66, 33.65), biological yield (27.28, 28.41), number of clusters per plant (23.99, 25.08) and number of primary branches per plant (22.19, 23.13). The present investigation high heritability coupled with high genetic advance was observed in harvest index (65.30, 94.20%), biological yield (53.98, 92.30%), number of clusters per plant (47.28, 91.50%), primary branches per plant (43.86, 92.00%), seed index (39.01, 90.00%), number of pods per plant (35.60, 84.30%) and seed yield per plant (34.18, 81.60%). Respectively suggesting that there was preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection. Hence selection of these characters can bring enhancement in chickpea production and productivity. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The present investigation further revealed that genotypes belonging to cluster II have maximum intra cluster distance and can improve the yield potential. As maximum inter cluster distance was notice between cluster IV and V and cluster III and IV crosses involving genotypes from these clusters would give wider and desirable recombination's. Therefore, genotypes present in these clusters are suggested to provide a broad spectrum of variability and may be used as parent for future hybridization programme to develop desirable genotypes.

Keywords: blackgram, D^2 , analysis, genetic diversity and cluster

Introduction

Blackgram (*Vigna mungo* (L.) Hepper), is an annual leguminous crop belongs to the family Fabaceae and sub-family Papilionaceae with a chromosome number of $2n=22$ (Dana, 1980) and originated from the Indian continent (De Candolle, 1882, Vavilov, 1926 and Zuckovskji, 1962). It is popularly known as urd bean, urd or mash, is one of the important grain legumes, and is excellent source of easily digestible good quality proteins. It is important self-pollinating diploid grain legume (Naga *et al.* 2006) domesticated from *V.mungo* var. *silvestris* (Lukoki *et al.* 1980). It is widely cultivated in the Indian sub- continent and two are lesse extent in the Thailand, Australia, and other Asian and South Pacific countries (Poehlman, 1991). The area of traditional cultivation of urad bean is confined tp South Asia and adjacent areas including India, Pakistan, Afghanistan, Bangladesh, and Myanmar.

It is an economically important legume crop in Asia, widely cultivated on marginal lands with low inputs during khari, rabi, and summer seasons. A seed of blackgram is the most important product which is consumed in the form of dal (whole or split, husked and unhusked) or parched. The most popular south Indian dishes such as Idli and Dosa have blackgram as their main ingredient. The urad flour is used in making papad and vada. Sprouted seeds are edible and also prescribed as medicine for internal and external paralysis, rheumatism, and nervous problems.

Black gram is an erect, fast growing annual herbaceous legume reaching 30-100 cm in height. It has a well-developed taproot and its stem is diffusely branched from the base. The leaves are trifoliolate with ovate leaflets 4-10 cm long, 2-7 cm wide. It contains 4-10 ellipsoid black or mottled seeds. This is one of the most important short-duration legume crop utilized in the food, fodder, soil conservation, integrated farming system, reclaiming of degraded pastures, and symbiotic nitrogen fixation. It is still cultivated on marginal lands under rainfed conditions and faces terminal drought which affects by its productivity to its great extent.

Black gram is the fourth important pulse crop in India which holds about 13 percent of the total pulse area and contributing about 10 percent of the total pulse production. It is grown in various agro-ecological conditions and cropping systems with diverse agricultural practices (Chauhan *et al.* 2008) [4]. In India, Black gram is grown on 44.93 lakh hectares area with a production of 29.26 tonnes and 651 kg/ha productivity (Directorate of Economics and Statistics, 2018-2019). It is mostly grown in Andhra Pradesh, Uttar Pradesh, Maharashtra, Tamil Nadu, Rajasthan, Orissa and Bihar. Systematic and well-planned work on amelioration of Blackgram was started from mid-sixties when the Indian Council of Agriculture Research (ICAR) launched a co-ordinated pulse improvement scheme. Improvement of yield from the prime objective of

breeding in any crop species and Blackgram is no exception to that. The knowledge of variability, direction, magnitude of the association between various traits is essential for a plant breeder to boost the yield levels.

Yield is a polygenic complex character, depends on number of component characters, which are quantitatively inherited. As such, before launching any breeding programme a through knowledge on the nature and magnitude of genetic variability and extent of association between yield and other components is very essential. Genetic variation among traits is important for breeding and selecting desirable types on other hand heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the offspring and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression. While genetic advance aids in exercising the necessary selection pressure. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Murty and Arunachalam, 1966 and Ram and Panwar, 1970). It also permits to select the genetically diverged parents which can produce new recombinants with desirable traits when they are crossed together. Joshi and Dhawan (1966) reported that genetic diversity was very much important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops. They also inferred that Mahalanobis's D^2 statistics was a powerful tool for choosing parents for hybridization aiming at hybrid improvement.

Materials and methods

The experiment materials for the present investigation comprised of us genotype to divergence studies D^2 statistic. Thirty six black gram germplasm including check were sown on 23rd February, 2021 at department of Genetics and Plant Breeding, SHUATS, Prayagraj. The experiment was laid in Randomized Complete Block Design (RBD) with three replications. The experimental plot size 4.5 m width and length 37.5 m. inter row spacing was kept 30cm and plant to plant spacing was 10cm. The recommended crop practices were followed for raise a healthy crop. Data for 13 quantitative traits were recorded viz., Days to 50% flowering, days to maturity, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per cluster, Number of seeds per pod, Number of pods per plant, pod length, Biological yield per plant (g), 100-Seed weight (g), Harvest index(%), Seed yield per plant(g). D^2 statistic and Tocher's method was used for Assessment of genetic divergence and the genotype was grouped into different clusters.

The days to 50% flowering and days to maturity were accounted on a plot basis and rest of the characters was documented from random sample of five plants in each plot from all the three replications. The recommended agronomical practices and crop protection measures were followed during the crop growth period. Biometrical analysis were followed to estimate Analysis of variance (ANOVA) Fisher and Yates (1936), Genotypic and Phenotypic Co-efficient of Variation (Burton and De vane, 1952), heritability in broad sense (Lush, 1940), genetic

advance (Johnson *et al.*, 1955) and D^2 analysis (Mahalanobis (1936)^[10].

Results and discussion

The analysis of variance revealed significant differences among the genotypes for all the characters under study (Table 1). Thus, it indicated considerable amount of genetic variability among thirty six black gram germplasm. Similar, results has been reported by

Estimation of genetic parameters

Estimation of genetic parameters, helps to explore important traits during the selection for improving yield of black gram. Heritability, Genotypic Co-efficient of variation (GCV), Phenotypic Co-efficient of variation (PCV), Genetic Advance (GA), Genetic Advance as percentage of mean GA(%) for all the yield contributing traits are shown in Table 2. PCV was higher than the corresponding GCV for all the characters indicating that there was an influence of the environment. Highest PCV and GCV were observed for Biological Yield Per Plant (28.400 and 27.281) followed by harvest index (33.651 and 32.660), Number of clusters Per Plant (25.08 and 23.992), Number of Primary branches Per Plant (23.137 and 22.197) in Table 2. High GCV for harvest index (32.660), Number of clusters per plant (23.99), Biological yield per plant (27.281), number of primary branches per plant (22.197) were also earlier reported. Similar results were reported by Where, as moderate PCV and GCV were recorded for 100-seed weight (20.901 and 19.897), Where as the lowest PCV and GCV were observed for Days to maturity (3.618 and 1.802), days to 50% flowering (4.985, 2.413), pod length (6.643, 3.832), number of pods per cluster (10.679, 7.928), plant height (10.702, 6.664).

The high estimates of GCV and PCV for these traits suggested the possibility of yield improvement through selection of these characters. With the help of GCV alone, it is not possible to determine the extent of variation that is heritability. Hence, the knowledge of heritability helps the plant breeders in prediction. The genetic advance for quantitative traits aids in exercising necessary selection procedure. The traits studied performed high heritability ranging from (75.4% to 97%). Among the traits studied the highest heritability was recorded by Days to maturity (97.340%) followed by days to 50% flowering (96.50%), harvest index (94.2%), biological yield per plant (92.3%), Number Of primary branches Per Plant (92.0%), 100-seed weight (90.6%) (Table 2). Similar, results were been reported by. The high heritability values of the considerable traits in the present study indicated that these characters were less influenced by the environment and thus helps in effective selection of the traits based on the phenotypic expression by adopting simple selection method and suggested the scope of genetic improvement.

The genetic advance as percent of mean was higher for Biological yield per plant (53.983), harvest index (65.300), Number of clusters per plant (47.280), Number of primary branches per plant (43.869), number of Pods per plant (35.6), 100-seed weight (39.0), seed yield per plant (34.1) indicating that direct selection for these traits would be effective for the yield improvement similar findings related to high genetic advance as percent of mean for various traits have been reported by the characters having high heritability coupled with high genetic advance generally indicates that

heritability is more due to additive gene effect and advocated the use of high estimates of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection high heritability coupled with high genetic advance as percent mean was observed for harvest index, biological yield per plant, number of primary branches per plant. So direct selection of these characters based on phenotypic expression by simple selection method would be effective due to accumulation of more additive genes leading to further improvement.

Genetic divergence analysis was carried out by calculating D^2 values from the means of 36 genotypes of black gram for 13 quantitative characters. The genotypes were grouped into 6 clusters [Table-3]. Among 6 clusters, cluster -1 maximum numbers of 20 genotypes followed by cluster -2 with minimum number of genotypes (12), cluster -3, cluster -4, cluster -5 and cluster-6 with 1 genotypes. The dendrogram depicting the clustering pattern was depicted in figure -. The pattern of clustering indicates presence of significant amount of variability. The inter and intra cluster D^2 value are presented in [Table-4] in the present study, it is indicated that the inter cluster distance were greater than intra cluster distances which shows considerable amount of genetic diversity existed among genotype. Intra cluster distance ranged from 0.00 to 31.47. Cluster -2 recorded the maximum cluster distance of 31.47 followed clusters- 6, 5, 4,3, 1 (0.00 to 30.25.respectively. Three solitary cluster with no intra cluster value. The uniqueness of these genotypes placed then separately. The highest inter cluster distance was found between cluster 4 and 5 (247.68), cluster 3 and 4 (237.4) cluster 3 and 6 (194.60) which was followed by cluster 5 and 6 (166.85) and cluster 2 and 3 (140.30) indicates wide divergence among the genotypes of these clusters. The magnitude of heterosis depends largely on the degree of genetic diversity in the parental lines. There for the genotypes from these diverse clusters could be used in the hybridization to get broad spectrum of genetic variability in the segregating generation. Genetic constitution of genotype in one cluster were in close proximity with the genotypes in the other cluster of pair. It was observed on the basis of least inter cluster distance which is found between cluster 3 and 5 (29.24). Hence genotypes from these clusters may not be useful. This result is supported by other research findings in black gram. The relative contribution of each character towards divergence was represented in the [Table-6] seed yield per plant (21.5)

contributed maximum towards genetic divergence followed by biological yield per plant (19.84), 100-seed weight (17.14) and harvest index (12.81). The contribution of plant height (3), number of seeds per pod (4), days to 50% flowering (2), number of primary branches per plant (2), days to maturity (1) and number of clusters per plant (9) respectively.

The cluster contributing maximum to the divergence should be given more importance for the purpose of further selection and the choice of parents for hybridization. The cluster mean values were estimated over genotype for thirteen quantitative characters in black gram related to yield, which revealed that a wide range of variation [Table-5]. Minimum days to 50% flowering was observed in genotype of cluster 6 followed by cluster 2. Maximum days of 50% flowering was recorded by cluster 3. Maximum Days to 50% maturity was recorded by cluster3 followed by cluster 4. The highest mean for number of clusters per plant was recorded by cluster 4 and cluster 2. Cluster 4 recorded the highest mean for Number of Pods per plant followed by cluster 6. Cluster 6 recorded the highest mean for pod length, seed yield per plant Cluster 6 recorded the highest mean, 100 seed weight highest mean value recorded for cluster 5. Plant height, number of primary branches per plant, number of pods per plant, pod length, number of pods per cluster, number of seeds per pod recorded highest mean value for cluster 6, Hence the genotypes in cluster were high yielding.

Table 1: Analysis of variance (ANOVA) Among 36 black gram genotypes for 13 quantitative traits

Sl.No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	35	70
1	Days to 50% flowering	17.8450	11.402*	5.939
2	Days to maturity	19.2310	12.345**	6.398
3	Plant height (cm)	5.3750	3.452*	1.792
4	Primary branches per plant	0.170	0.701**	0.057
5	Number of pods per plant	3.3940	9.563**	1.134
6	Pod length (cm)	0.1530	0.106*	0.062
7	Number of clusters per plant	0.6710	2.198**	0.224
8	Number of pods per cluster	0.44**	0.132*	0.075
9	Harvest index (%)	40.5350	347.545**	35.153
10	100 seed weight (g)	00	2.129**	0
11	Seed yield (g)	0.2790	0.529**	0.093
12	Number of seeds per pod	0.2170	0.507**	0.208
13	Biological yield (g)	3.1270	13.136**	1.044

*,** indicate significant at 5% and 1% level

Table 2: Metersstes of components of variance and genetic parameters for 13 quantitative characters in blackgram germplasm

Genetic Parameters													
	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Number of pods per plant	Pod length (cm)	Number of clusters per plant	Number of pods per cluster	Harves t index (%)	100 seed weight (g)	Seed yield (g)	Number of seeds per pod	Biological yield (g)
GCV	2.414	1.773	5.851	21.571	18.243	3.248	22.533	5.909	31.281	20.232	17.336	6.103	26.481
PCV	4.983	3.646	12.045	24.252	21.615	7.376	26.088	13.066	36.178	20.236	22.216	10.71	29.712
h ² (Broad Sense)	23.466	23.652	23.597	79.115	71.237	19.394	74.605	20.455	74.761	99.961	60.893	32.474	79.435
Genetic Advancement 5%	1.347	1.41	0.744	0.849	2.914	0.111	1.443	0.129	18.176	1.735	0.612	0.371	3.686
Gen.Adv as % of Mean 5%	2.409	1.776	5.855	39.525	31.719	2.947	40.094	5.506	55.718	41.67	27.868	7.165	48.62

GCV:Genotypic coefficient of variation, PCV:Phenotypic coefficient of variation, h² : heritability, GA : Genitic advance

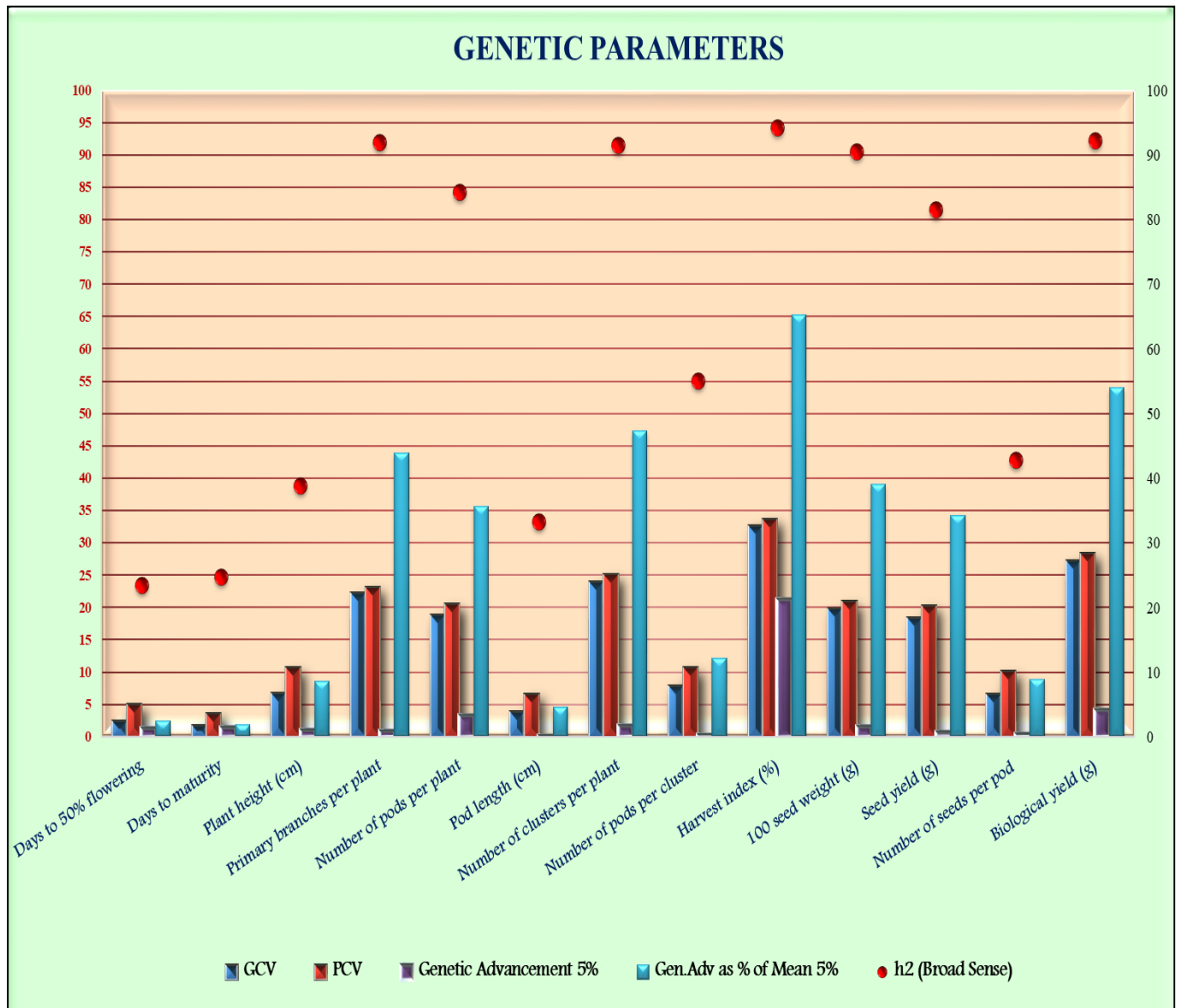


Fig 1: Histogram depicting GCV, PCV, Genetic advance and Heritability for 13 quantitative characters of Blackgram genotypes.

Table 3: Distribution of genotypes into different clusters based on torcher method

Sl.No	Cluster number	number of genotypes	Genotypes Includes
1	I	20	No-7386-15,ku-88-9-1, Ng-2119, Vbn-4, Ku-303, Kkm-4,ndu-5-7, Azad-3, Plu-99-2, Bh-82-2, Ku-96-8, Np-16, Ipu-81-1, P-1, Ic-456048, Lbg-11, Lbg-719, Pusa Urd, Plu-144, Plu-99-10
2	II	12	Azad-1, Ku-302, Plu-708, Plu-19, Ku-48, Ic-240-183, Lbg-623, Ipu-95-13, Vbn-5, No-7368-15, Pdv-103,ku=96-4
3	III	1	Azad - 2
4	IV	1	Pu-31
5	V	1	Plu-302
6	VI	1	SHEKHAR-2

Table 4: Interr and intra cluster distances

Cluster Distances						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	30.25	81.80	63.49	132.54	50.19	81.11
Cluster 2		31.47	140.30	75.10	147.59	63.34
Cluster 3			0.00	237.70	29.24	194.60
Cluster 4				0.00	247.68	72.95
Cluster 5					0.00	166.85
Cluster 6						0.00

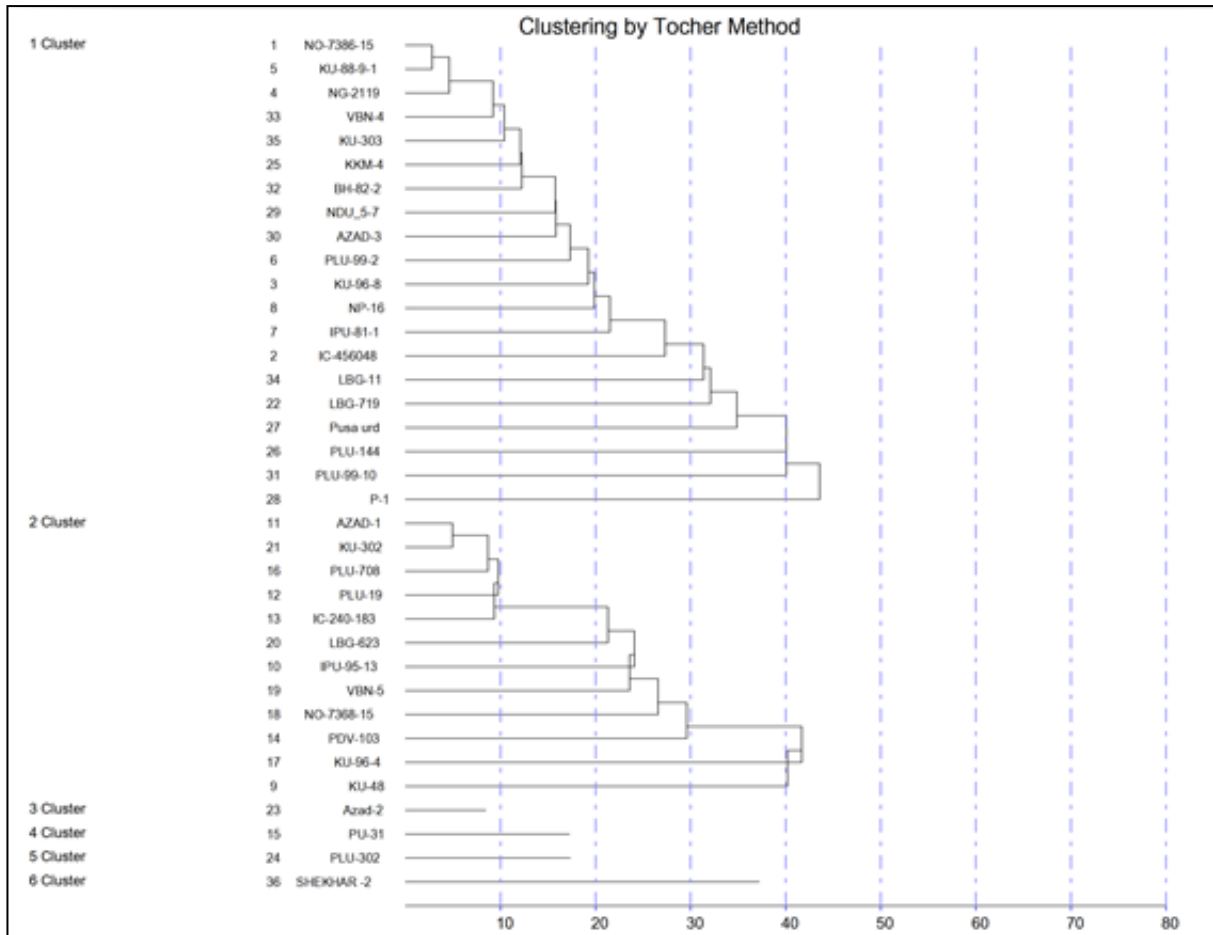


Fig 2: Dendrogram showing clustering pattern of Genotypes

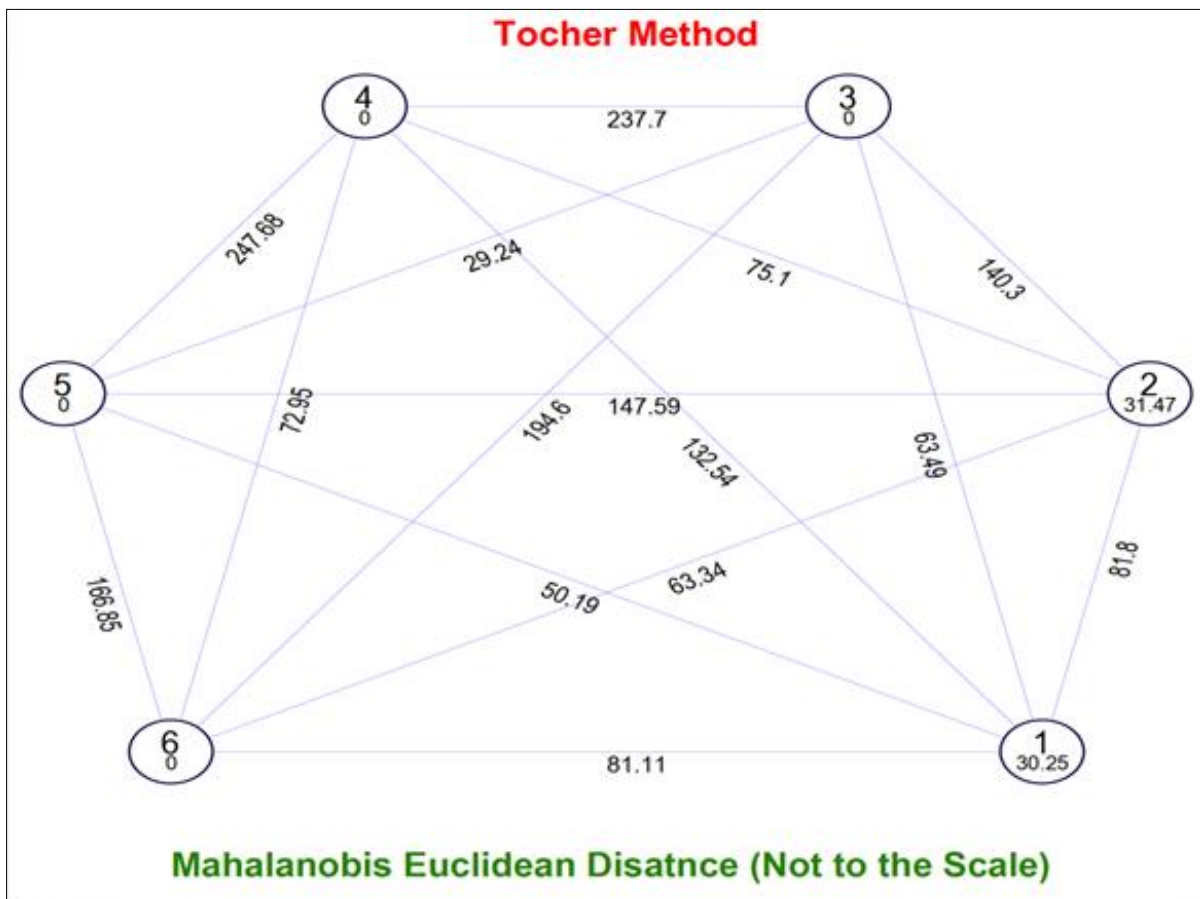


Fig 3: Histogram showing relative position of clusters and inter and intra cluster

Table 5: Clusterr mean value performance of 13 quantitative traits by torcher method

Cluster Means : Tocher's Method													
	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Number of pods per plant	Pod length (cm)	Number of clusters per plant	Number of pods per cluster	Harvest index (%)	100 seed weight (g)	Seed yield (g)	Number of seeds per pod	Biological yield (g)
Cluster 1	56.25	79.60	12.44	1.88	9.74	3.71	3.31	2.33	25.52	4.30	2.26	4.99	9.02
Cluster 2	55.94	79.36	12.88	2.58	8.39	3.81	3.89	2.35	45.36	4.00	2.17	5.55	5.27
Cluster 3	57.33	81.67	13.10	1.26	5.80	3.49	2.40	2.00	20.29	3.00	1.47	4.91	8.00
Cluster 4	56.00	81.00	13.30	2.80	11.33	3.64	6.60	2.60	45.35	3.00	2.07	4.99	5.67
Cluster 5	54.67	80.33	12.60	1.53	6.86	3.54	2.60	2.00	15.18	5.00	1.27	4.08	9.53
Cluster 6	48.33	71.33	16.67	3.07	10.86	4.37	3.87	3.13	38.83	4.90	2.97	5.93	7.60

Table 6: Percent contribution of different Characters of genetic diversity in Blackgram genotypes

Sl.No	Source	Contribution %	Times ranked 1st
1	Days to 50% flowering	2	12.5
2	Days to maturity	1	6.25
3	Plant height (cm)	3	18.75
4	Primary branches per plant	2	12.5
5	Number of pods per plant	3.65	22.8125
6	Pod length (cm)	3.25	20.3125
7	Number of clusters per plant	9	56.25
8	Number of pods per cluster	0.63	3.9375
9	Harvest index (%)	12.81	80.0625
10	100 seed weight (g)	17.14	107.125
11	Seed yield (g)	21.5	134.375
12	Number of seeds per pod	4	25
13	Biological yield (g)	19.84	124

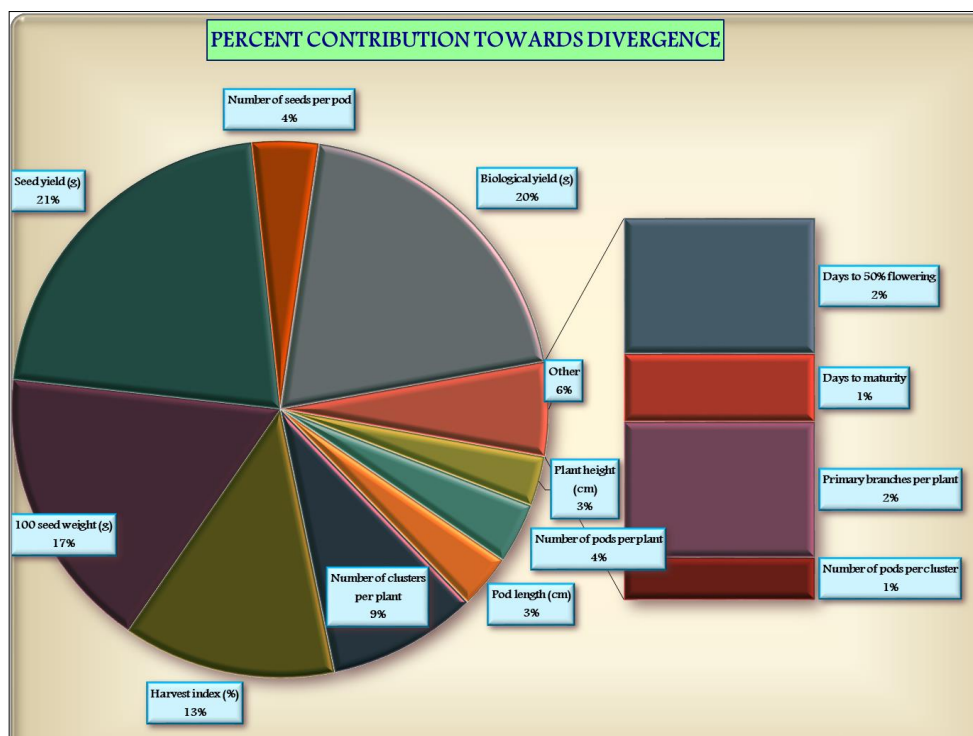


Fig 4: Percentage contribution towards divergence

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