Original Research Article

STUDY ON GENETIC DIVERSITY IN BLACK GRAM (*Vigna mungo* L. hepper)

ABSTRACT

The present study ~~consists~~ carried out ~~of~~ with45 black gram genotypes including one check variety were ~~evaluated~~ conductedat~~he~~Field Experimentation Centre of the Department of Genetics and Plant Breeding, to studygeneticvariability,heritability,geneticadvance,correlationandpathcoefficientfor13quantitative characters. The experiment was conducted by using Randomized Block Designwith three replications during*Kharif, 2022.*Genotype SNTP- 02 (7.44 gms), PL-416 (7.35 gms), AKU-13-15 (7.26 gms), PLU -1016 (7.22gms), KC- 153 (7.21gms) were found to be superior in seed yield per plant. High GCV AND PCV were observed in Number of primary branches, Number of clusters per plant ~~&~~andNumber of pods per plant. Moderate PCV and GCV were observed in Number of pods per plants (43.04), Biological yield (33.77), Seed Yield per plant (30.282), Harvest index (25.4), Low PCV and GCV for Days to 50% pod setting (6.24) DivergenceanalysisfollowingMahalanobis(1936)D^2analysishasrevealedpresenceofsubstantialamount of genetic diversity among the genotypes. These 45 genotypes were grouped into 6clusters by following Tocher's method. Cluster I contain 19genotypes, while the cluster II, III, IV, V, VI were Monogenotypic. The maximum inter clusterdistance was observed betweenClusterV andI (76.71)and minimum betweenclusterIVandII (81.02). Variance of cluster meansrevealed that Seed yield per plant, biological yield, harvest index had a maximum contribution towards divergence in the presentmaterial.Thus,thesegenotypespresentintheseclustersprovideabroadspectrumofvariabilityinsegregationandmaybeusedasparentsinthefuturehybridizationprogramme todevelop desirable genotypes forgrain yield improvement inBlack gramgenotypes.

Keywords:GCV,PCV,Variability,Heritability,GeneticDivergence

INTRODUCTION

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I suggest the following structure:
1. First, set the context of the study
2. Justify the importance of this study
3. then highlight the problematic or research questions the authors are addressing
4. state the objective clearly and precisely

~~Pulses, also known as grain legumes,~~Grain legumes are a great gift from nature and a significant addition to a diet that mostly consists of cereal. In Asia, they represent the main source of protein. They play a crucial role in Indian agriculture. They play a key role in food and are a crucial and important source of dietary protein, especially for the Indian subcontinent's largely vegetarian population. Pulses have roughly three times the amount of high-quality protein found in cereals, making them a more affordable source of protein to combat human protein deficiency. They may be used as fodder and concentrates in cattle husbandry and are especially helpful in treating protein deficiency. Pulses have unique qualities that make them particularly useful in various cropping systems.

Blackgram (*Vignamungo* (L.) Hepper), also known as urd-bean, udand dal, or urad in India, is a short-lived, self-pollinating, diploid (2n=2x=22), grain legume crop belonging to the family Leguminosae with a small genome size of 574Mbp (**Gupta and Gopalakrishna*et al.*, 2015**). It is significant from the perspective of global food and nutritional security. It is a good pulse crop because it does better in every season. The seeds are incredibly nutrient-dense, containing 24–26% protein, 60% carbohydrates, 1.5%

fat, minerals, amino acids, and vitamins. Additionally, it provides a significant amount of lysine for vegetarians and is a fair source of vitamins like thiamine, niacin, and riboflavin, as well as the essential minerals iron and phosphorus. So it is commonly referred to as "poor man's meat". Blackgram is grown as a mixed crop, cash crop, sequential crop besides growing as sole crop under residual moisture conditions, either after the harvest of rice after the harvest of other summer crops under semi irrigated and dry land condition (**Parveen***etal*., 2011). It is still cultivated on marginal lands under rainfed conditions and faces terminal drought which affects its productivity to a great extent. It is mainly grown for human consumption and also used as fodder for cattle and green manure for soil fertility.

Blackgram is consumed in the form of 'dal' (whole or split husked and unhusked) or parched. It is the chief constituent of 'papad' and also of bark (special balls) which makes a delicious curry. Seeds are used in the preparation of many popular dishes. Blackgram differs from other pulses in its peculiarity of attaining some mucilaginous pasty character, when ground up with watt. Blackgram has been distributed mainly in tropical to subtropical countries where it is grown in Kharif and summer reason. It is utilized in various ways where seeds are consumed as source of protein, vitamins and minerals, while plant parts are used as fodder. It is cooked for consumption with roti and rice and also used in making pastes for several south Indian dishes like idly, dosa, vada etc. With a production of 2.42 million tonnes and a ~~productivity~~ yield of 615 kg ha^{-1}, India leads the world with an area of 37.2 lakhsha^{-1}~~/ha~~ (Directorate of Economics and Statistics, 2019-2020). It is primarily grown in Maharashtra, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Tamil Nadu, Rajasthan, and Karnataka, among other agro-climatic zones of the nation. Blackgram is grown on 7.01 lakh hectares in Uttar Pradesh, where it produces 2.3 lakh tonnes at a productivity of 553 kg per hectare. Blackgram originated in the Indian subcontinent, claims Vavilov. It is suitable for dry land farming and is typically grown as an intercrop with other crops because it is a drought-resistant crop. In terms of area and importance, blackgram is the second-most important pulse crop in India.

The physiological expression and genetic potential of the crop are greatly influenced by the weather conditions, which have a significant impact on crop growth. It is well known that the availability of specific optimum rainfall, solar radiation, temperature, soil moisture, heat units, etc. during different stages of crop growth determines the yield from any given crop or variety. Despite the fact that this crop is more crucial from a nutritional standpoint, there hasn't been a noticeable increase in area or production between 1950–1951 and 2009–2010. To meet domestic demand, India imports about two lakh tons of pulses from other nations each year. The demand for grains and legumes is growing in tandem with the increase in global population, and agriculture. Due to the low availability of pulse grains in India (36 g/day/capita versus the minimum requirement of 80 g/day/capita) and the need to maintain the protein-to-calorie ratio in the diet, pulse production is necessary. ~~the~~ Theprimary limitations of blackgram genetic Lack of genetic diversity that can be exploited, lack of ideotypes that are appropriate for various cropping systems, a poor harvest index, susceptibility to biotic and abiotic stresses, and lack of access to high-quality seeds of improved varieties are all factors that need improvement. It is primarily the result of a few parents who have a high degree of relatedness being used repeatedly in crossing programs (**Jayamani** and **Sathya**, **2013**). The degree and type of genetic variability present in traits that contribute to yield heavily influences the success of yield improvement (**Johnson*etal*., 1955**).

MATERIAL~~S~~ AND METHODS

~~**3.5.1**~~ The experimental material~~s~~(Table 1) for the present study was procuredfrom ~~Dr. G.M LAL from~~ Department of Genetics and Plant Breeding, SHUATSduring*kharif*-2022**.** ~~listof genotypes, used in thepresentstudy~~ Forty-fiveblack gramgenotypes aregrowninRandomizedBlockDesign(RBD)withthreereplications during*kharif*-2022.~~DesignofExperiment is RBD in 3 replications~~ The recommended dosesof fertilizers N: P:K @ 20:40:40 kg/ha were applied. The fulldose of P_2O_5 and K_2O and nitrogen were applied as

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Comment [H2]: What do you mean by productivity?
NB: Kg per hectare is the yield and not productivity

Comment [H3]: Your background is well developed but not focus on your study interest. Most of the information's in this part must deal with the variation or diversity within your research material.
Additionally, you do not give the sources of your assertions. Only three references quoted, It is not very reliable when you do not give sources for verification if need be.

Comment [H4]: Sources ????

Comment [H5]: You can not give figures without giving sources

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basal dose at the time ofsowing. The observations were recorded on plot basis for days to 50% flowering, days tophysiologicalmaturityand seed yield per plot. For the restof the charactersthe datawasrecorded onfiverandomly selected plantsfromeachgenotype ineach replication leavingfirst two border rows from all the four sides in order to avoid sampling error. The characters recorded were ~~**QuantitativeTraits**~~

Daysto 50%flowering,Days to 50% pod setting,Days to maturity,Plant height, Number of primary branches per plant, Number of clusters per plant,Number of pod per plant,Pod length, Numberofseedsperpod, Biologicalyieldperplant,Harvestindex**,**Seedindex**,** seedyieldperplant.Data were subjected to analysis of Mahalanobis’ D2-statistics (Mahalanobis, 1936), and intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985). Clustering of genotypes was done by using Tocher’s method (Rao, 1952). The cluster distance was estimated by the formula given by Singh and Chaudhary (1977).

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Table:1Listofexperimentalmaterial(45blackgramgermplasm)

1	**PLU-856**	**11**	**AKU-13-15**	**21**	**AZAD-1**	**31**	**SNTP-02**	**41**	**PKGV-03**
2	**TLU-328**	**12**	**VBN-08**	**22**	**PLU-103**	**32**	**DH-85-5**	**42**	**PU-11-14**
3	**LBG-648**	**13**	**PL-416**	**23**	**PDU-1**	**33**	**LBG-628**	**43**	**PKRU-03**
4	**BGP-21-28**	**14**	**TBG-104**	**24**	**IPU-94-1**	**34**	**IPU-94-2**	**44**	**IC-106-176**
5	**KU-96-14**	**15**	**PLU-547**	**25**	**PLU-570**	**35**	**T9**	**45**	**SEKHAR2(check)**
6	**JU-2**	**16**	**IPU-99-18**	**26**	**KU-321**	**36**	**TU-99-2**		
7	**PLU-1016**	**17**	**DH-85-2**	**27**	**TLU-32-6**	**37**	**IPU-99-16**		
8	**KC-153**	**18**	**VBN-11-16**	**28**	**UH-85-2**	**38**	**AKU-14-02**		
9	**ADT-3**	**19**	**PLU-302**	**29**	**PLU-708**	**39**	**BG-369**		
10	**PLU-86-C**	**20**	**PU-31**	**30**	**LBG-623**	**40**	**IPU-99**		

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RESULTS AND DISCUSSIONS

The analysis of variance revealed significant differences among all the 13 charactersunder study at 1% level of significance. This indicates that the presence of significantly higheramount of genetic variabilityamong the genotypes present in the investigation for all the yieldrelatedcharacters studied.So, there was a sample scope for selection of promising lines from the present gene pool foryield and its components. The presence of large amount of variability might be due to diversesourceofmaterials takenaswell asenvironmental influenceaffectingthe phenotype.The PCV was higher than the GCV for all the characters under study which indicated that the environmental factors influencing the characters studied. The present findings are in accordance with the findings of **Panigrahi***et al.***(2014)**, **Deepshikha***et al.***(2014),Priyanka***et al.* **(2016)** and **Gowsalya***et al.***(2016).** ~~high~~ Highestimates of heritability coupled with high genetic advance as percent of mean was observed respectively for number of cluster per plant (98.301% and 105.841%), number of primary branches (98.01.% and 113.665%), number of pods per plant (97.423% and 86.365%), biological yield (95.837% and 66.687%), seed yield per plant (93.37% and 58.287~~%),~~ %) andplant height (94.93%, 356.517%).~~, respectively~~ Thissuggesting that there was preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection. The findings are in agreement with the results of Aftab*etal*. (2018), Kuralarasan*et al*. (2017),Gowsalya et al. (2016) and Singh*et al.* (2014).Geneticdivergencein45genotypesofblack gramwasmeasuredbyfollowingMahalanobis's D^2 statistic. The diversity available in the crop decides the success of anycrop improvement programme with manifested objectives. Assessment of divergence in thegermplasm is pre-requisite to know the spectrum of diversity. Clustering of genotypesfollowingtheTocher'smethodasdescribedbyRao(1952)ledtoformationof~~SIX~~sixclusters. ~~In the present investigation, 0 genotypes of BLACK GRAM were studied for their geneticdiversity by multivariate analysis as per Mahalanobis D^2 statistic (1936) with respect toelevenimportant quantitativecharacters.~~Tocher's method (Rao,1952) was used for grouping of genotypes using thepairs of combinations of D^2 values. 40 genotypes were grouped in to six clusters. Cluster I was biggest and consisted of 35 genotypes. All remaining clusters *viz.*clusterII,III,IV, V andVIweresolitary, with onegenotype in each of theseclusters.

Comment [H10]: This must be specified in your methodology before

Comment [H11]: This sentence is very poorly expressed. It needs to be reworded entirely

Comment [H12]: What do you mean by simple selection ??????????

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IntraandInterClusterDistances

Intra and inter cluster distance values have been presented in Table 1. Intracluster distance was ranged from zero (cluster IV and VI) to 761.71 (cluster I).Thehighestintraclusterdistancewasrecordedinclusterl(761.71)followedbycluster IV. The high

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intra cluster distance values revealed the presenceof genetic diversity between the genotypes grouped together in those clusters. Hence,thereis a lotof scopefor exchangeof genes amonggenotypes within theseclusters.

From the inter cluster distance values of the six clusters, the highest divergenceoccurred between cluster III and V (441.63) subsequently between cluster I and IV(465.11), cluster III and IV (177.82), cluster I and VI (221.34), cluster I and III(392.43),cluster I and III (135.97). Suggesting that the crosses involving genotypes from theseclusters would give desirable recombination. From the closest inter cluster distance itwas concluded that these genotypes were not very distant but couldn’t be groupedtogetherbasedonstudiedtraits.Severalauthorshavesuggestedthatthecrossingbetween the genotypes of clusters with highinter cluster would yield good segregantsfor selection~~.~~(Panigrahi*et al.*,~~(~~2020). The intercluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accessions. The intra cluster distance ranged from 0.00 to 7.65 and the inter cluster distance ranged from 3.10 to 15.07, indicating that the selected genotypes were highlydivergent. Minimum intra cluster distance had been recorded with cluster XII (0.00) due to the presence of solitary accession followed by cluster I (2.32) and cluster III (2.74).The data revealed that considerable differences existed among the clusters for most ofthe characters. The cluster IV showed the highest mean values for five characters *viz*. Days to 50% flowering, Days to 50% pod setting Days to maturity Plant height, Number of primary branches, Number of clusters per plant, Number of pods per plant. The cluster I exhibited lowest mean for Pod Length, Number of seeds per pod, Seed index, Harvest index, Biological yield, Seed yield per plant from the results, it was noticed that cluster VI (SNTP - 02) performed bettermeans in Harvest index, Biological yield, Seed yield per plant but no cluster contained at least one genotype with all desirable characters, whicheliminated the possibility of directly selecting one genotype for immediate use. Therefore,hybridization programme between the selected genotypes from diverse clusters is essential tocombineall the targeted traitsto improvephenotypicperformance.~~PercentContributionofVariousCharacterstowardsDivergence.~~

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The per cent contribution of thirteen characters studied towards total divergencehas been presented in Table 1. Data revealed that, seed yield per plant had contributedhighest(21.00%)forgeneticdivergenceandsubsequentlybybiological yield(14.54%), harvest index (10.21 %), number of pod per plant (9.81%), number ofclusters (8.46%),plantheight(6.53%),Days to maturity (4.00%).

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CONCLUSION

From the present research, it is concluded that Analysis of Variance showed significant variation to all the characters. among 45 genotypes, SNTP-02(7.44) and PL -416 (7.353), genotypes were found to be superior for grain yield per hill over the check (SEKHAR – 2). High to moderate estimates of GCV, PCV, high heritability coupled with high genetic advance as percent mean were recorded for Number of cluster per plant, number of pod per plant, number of primary branches indicating predominance of additive gene effects and possibilities of effective selection for the improvement of the characters. Cluster V and I (761.71), cluster IV and I (465.1) had high inter cluster distances~~,~~ were most diverse from each other and hybridization between genotypes present in these clusters provide a broad spectrum of variability in segregation these genotypes may be used as parents in the future hybridization programme to develop desirable genotypes for seed yield Improvement in black gram.

Table 2AnalysisofVariancefor13quantitativecharacters of45 black gram genotypes

Sr.No.	Source	Replication	Treatment	Error
	Degreesoffreedom	**2**	**44**	**88**
1	**Days to 50% flowering**	3.8220	20.885**	7.686
2	**Days to 50% pod setting**	7.2670	16.248**	8.721
3	**Days to maturity**	4.4220	169.1**	20.127
4	**Plant height (cm)**	1.2520	637.413**	11.149
5	**Number of primary branches**	0.7360	55.615**	0.374
6	**Number of clusters per plant**	0.6130	46.649**	0.267
7	**Number of pods per plant**	0.3440	170.663**	1.492
8	**Pod Length (cm)**	0.0990	0.178**	0.08
9	**Number of seeds per pod**	0.0020	1.393**	0.163
10	**Seed index (g)**	0.0010	0.956**	0.06
11	**Harvest index (%)**	1.3790	165.028**	11.747
12	**Biological yield (g)**	0.5860	114.962**	1.641
13	**Seed yield per plant (g)**	0.090	8.099**	0.187

Table 3Meanperformanceof45Blackgramgenotypesfor13quantitativeparametersduring*Kharif*-2022.

Sl. No.	Genotypes	Days to 50% flowering (days)	Days to 50% pod setting (days)	Days to maturity (days)	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Pod Length (cm)	Number of seeds per pod	Seed index (g)	Harvest index (%)	Biological yield (g)	Seed yield per plant (g)
1	PLU – 856	43	49	59.667	61.733	12.333	12.33	25.333	4.047	6	4.6	26.167	23.363	6.113
2	TLU – 328	42	53	65	56.42	11.267	7.8	17.4	4.04	6.133	4.1	28.133	23.027	6.473
3	LBG – 648	47.333	54	62	60.133	8.067	3.533	8.197	4.107	5.6	5.097	28.053	23.193	6.5
4	BGP - 21- 28	46	51	62.667	46.81	11.4	13.867	32.333	4.273	6.467	3.5	31.35	22.88	7.17
5	KU – 96- 14	46.333	52.667	63.333	61.533	15.467	13.337	41.933	4.347	5.6	5.2	31.023	21.19	6.573
6	JU - 2	45	54	65.667	62.693	12.537	9.933	20.867	4.06	6.133	4.3	28.44	24.43	6.947
7	PLU - 1016	46.333	54	59.667	81.333	12.533	11.4	12.933	3.687	5.733	5.4	26.82	26.92	7.22
8	KC – 153	43	54	63.667	55.797	14.003	16.067	25	4.293	6.533	4.797	30.99	23.28	7.213
9	ADT – 3	48	53.667	64.333	68.137	15.267	16	24.2	3.97	5.8	4.5	28.443	24.967	7.077
10	PLU – 86 - C	44	50	61.667	57.447	10.867	12	20.667	4.273	6.467	4.9	28.83	23.833	6.873
11	AKU – 13- 15	47.667	52.667	64.333	65.597	12.537	12	24.6	3.82	6	4.297	29.88	24.893	7.26
12	VBN -08	43.333	54.333	75	31.437	3.933	3.863	12.533	4.04	4.7	3.583	26.617	13.127	3.46
13	PL – 416	48	53.333	64.667	66.2	13.003	11.933	34.2	4.22	6	4.703	29.787	24.69	7.353
14	TBG – 104	41	54	81.333	35.22	3.6	3.667	10.6	3.62	4.267	3.923	20.4	14.633	2.973
15	PLU – 547	43	48.667	63	72.463	12.533	11.6	16.4	4.213	6.133	4.3	27.807	26.33	7.313
16	IPU – 99 – 18	43.667	55.667	77.333	37.2	4.367	4.733	14.467	3.577	5.503	4.037	18.043	17.593	3.163
17	DH – 85 - 2	47.667	52.333	61	83.07	9.467	12.133	22.067	4.013	6.133	4.603	27.513	26.74	7.357
18	VBN – 11- 16	44.667	56	77	35.03	3.8	3.967	11.6	3.703	5.433	3.847	30.257	10.433	3.16
19	PLU – 302	48.333	52.333	61	59.737	8.067	5.333	13.13	4.293	5.6	3.9	26.937	21.707	5.847
20	PU - 31	45	56.667	75.333	35.513	3.4	3.667	11.6	4.053	4.5	3.96	54.34	8.4	4.577

Sl. No.	Genotypes	Days to 50% flowering (days)	Days to 50% pod setting (days)	Days to maturity (days)	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Pod Length (cm)	Number of seeds per pod	Seed index (g)	Harvest index (%)	Biological yield (g)	Seed yield per plant (g)
21	AZAD - 1	44.667	50.333	61.667	65.8	7.467	5.867	13.13	3.77	5.933	3.703	24.487	24.1	5.907
22	PLU – 103	41	54.333	76.333	40.473	3.267	4.133	20.47	4.017	6.067	3.893	49.123	12.567	6.157
23	PDU – 1	48.333	53.667	65.667	62.533	12.6	11.203	33.4	3.993	6.133	4.3	30.677	23.973	7.353
24	IPU – 94 – 1	45.667	57.667	77.667	38.803	2.967	4.567	13.433	3.573	4.467	3.917	38.97	9.64	3.757
25	PLU – 570	49.333	55.667	68	64.8	7.6	7.133	15.6	4.283	6	4.897	27.063	24.603	6.613
26	KU – 321	43.667	54.333	80	36.58	3.333	3.667	9.4	4.04	4.5	3.773	31.41	8.72	2.74
27	TLU – 32 – 6	47.667	54	65	34.8	9.467	8.733	15.4	4.18	6	5.1	34.64	18.457	6.39
28	UH – 85 – 2	47	59	82	34.563	2.767	4.667	11.667	3.763	5.5	3.747	49.437	7.7	3.773
29	PLU – 708	46.333	52.333	69.333	74.803	12.467	9.267	15.533	3.897	5.867	3.7	23.96	27.02	6.473
30	LBG – 623	44	54	78	37.477	3.433	4.367	14.4	3.56	5.533	3.747	26.61	10.367	2.753
31	SNTP – 02	40	50	62	50.86	4.733	10.133	25.2	4.033	6.2	6.1	37.313	19.94	7.44
32	DH – 85 – 2	45.333	57.333	76.667	41.783	4.063	6.6	20.43	4.267	6.267	3.843	37.24	17.593	6.537
33	LBG – 628	41	52	63	56.273	9.333	10.533	17.6	4.12	6	4.897	31.163	21.17	6.597
34	IPU – 94 – 2	38.667	53.333	80	39.243	3.967	4.4	12.467	4	5.467	3.847	34.337	14.633	5.03
35	T9	45	52	67	67.513	8.867	9.867	19.6	3.953	6.267	3.9	26.743	24.92	6.66
36	TU – 99 – 2	42.667	55.333	80	40.69	3.397	3.267	11.467	3.71	4.467	3.947	46.953	9.42	4.403
37	IPU – 99 – 16	44	51	67	59.133	11.73	10.933	21.933	4.113	6.133	4.097	32.56	20.71	6.743

Sl. No.	Genotypes	Days to 50% flowering (days)	Days to 50% pod setting (days)	Days to maturity (days)	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Pod Length (cm)	Number of seeds per pod	Seed index (g)	Harvest index (%)	Biological yield (g)	Seed yield per plant (g)
38	AKU – 14 – 02	44.667	56	82	39.09	3.767	2.9	10.4	3.767	5.5	3.87	37.74	8.667	3.22
39	BG – 369	42	53	64	61.413	13.533	7.13	23.733	4.17	6.4	4.497	33.89	20.79	7.047
40	IPU – 99	40.667	53.667	77	37.217	3.53	3.437	9.4	3.607	4.533	3.94	21.99	12.567	2.753
41	PKGV – 03	41	52.333	78	36.517	2.73	4.3	12.467	3.82	4.563	3.843	33.527	10.627	3.533
42	PU – 11 – 14	41.667	55.667	76	40.843	3.3	5.367	10.537	4.173	4.433	3.877	34.037	15.417	4.747
43	PKRU – 03	41.667	53.667	73.333	35.467	2.867	2.933	11.633	3.8	4.467	3.763	28.07	13.63	3.823
44	IC – 106 – 176	47	59	77.667	38.2	3.033	3.433	12.5	3.543	4.87	3.783	25.707	14.633	3.76
45	SEKHAR – 2 (CHECK)	42.667	53	78	40.593	3.8	3.933	13.7	4.413	5.57	3.913	25.057	18.883	4.737
Mean		44.42	53.64	70.07	51.31	7.7	7.6	17.68	3.98	5.6	4.23	31.17	18.59	5.55
CV		6.24	5.51	6.4	6.51	7.94	6.8	6.91	7.11	7.21	5.8	11	6.89	7.8
SEm		1.6	1.71	2.59	1.93	0.35	0.3	0.71	0.16	0.23	0.14	1.98	0.74	0.25
CD at 5%		4.5	4.79	7.28	5.42	0.99	0.84	1.98	0.46	0.65	0.4	5.56	2.08	0.7
CD at 1%		5.96	6.35	9.64	7.18	1.31	1.11	2.63	0.61	0.87	0.53	7.37	2.75	0.93
Minimum		38.67	48.67	59.67	31.44	2.73	2.9	8.2	3.54	4.27	3.5	18.04	7.7	2.74
Maximum		49.33	59	82	83.07	15.47	16.07	41.93	4.41	6.53	6.1	54.34	27.02	7.44

Comment [H17]: Give the legend for the abbreviations in the table

Table4 Estimation ofvariabilityandgeneticparametersfor13 quantitative charactersinblack gramgermplasm for*kharif,2022*

Traits	GCV	PCV	h^2 (BroadSense)	GeneticAdvance 5%	Genetic Advance as % of(Mean5%)
Days to 50% flowering	4.722	7.826	36.404	2.607	5.869
Days to 50% pod setting	2.953	6.247	22.342	1.542	2.875
Days to maturity	10.057	11.923	71.159	12.245	17.477
Plant height (cm)	28.159	28.901	94.93	28.999	56.517
Number of primary branches	55.735	56.298	98.01	8.751	113.665
Number of clusters per plant	51.747	52.192	98.301	8.031	105.689
Number of pods per plant	42.476	43.034	97.423	15.269	86.365
Pod Length (cm)	4.521	8.43	28.76	0.199	4.994
Number of seeds per pod	11.442	13.523	71.591	1.116	19.944
Seed index (g)	12.91	14.155	83.189	1.027	24.257
Harvest index (%)	22.934	25.434	81.307	13.277	42.601
Biological yield (g)	33.068	33.778	95.837	12.395	66.687
Seed yield per plant (g)	29.282	30.304	93.37	3.233	58.287

Comment [H18]: Provide the legend for the abbreviations in the table

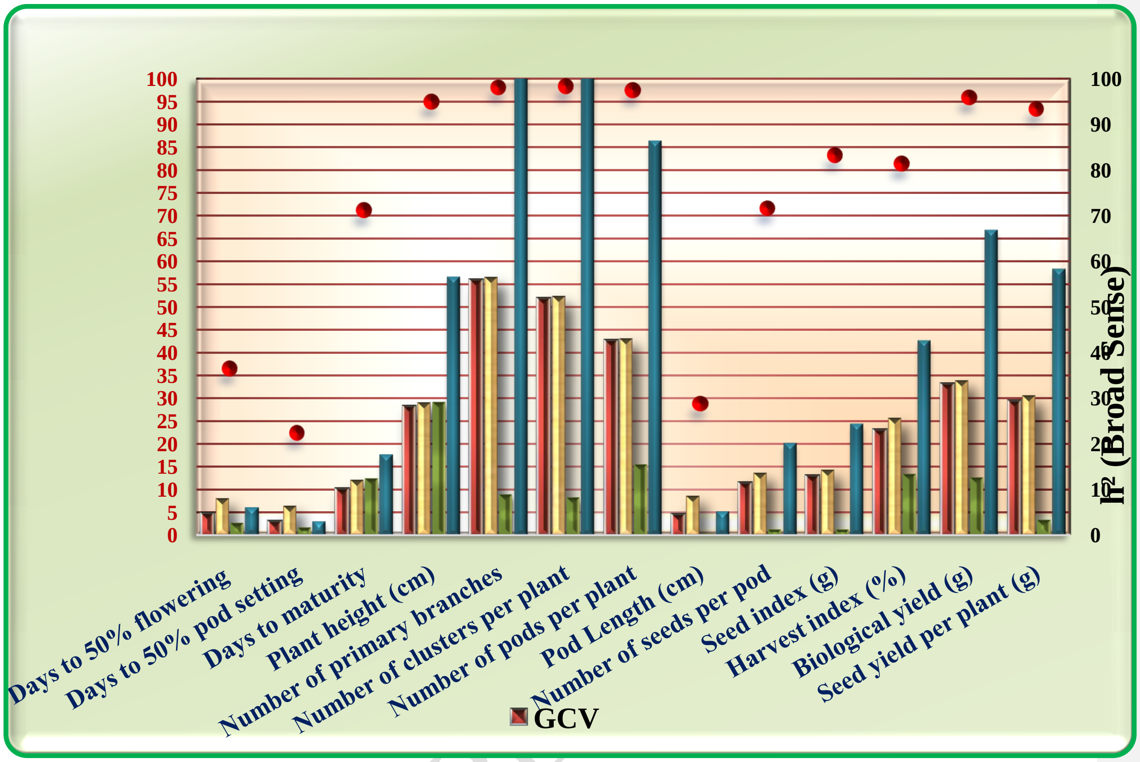

Fig.1. Histogram depicting GCV, PCV, Genetic advance and h^2 for quantitative characters of black gram genotype.

Table 5:Grouping of45 blackgramgenotypes based on D^{2}values

Cluster Group	No. ofgenotype	List of genotypes
1 Cluster	19	TBG - 104, IPU - 99, PKRU - 03, IC - 106 - 176, VBN -08, VBN - 11- 16, PKGV - 03, LBG - 623, KU - 321, IPU - 94 - 1, AKU - 14 - 02, IPU - 94 - 2, PU - 11 - 14, IPU - 99 - 18, SEKHAR - 2 (CHECK), TU - 99 - 2, UH - 85 - 2, PU - 31 &PLU - 103
2Cluster	15	PL - 416, PDU - 1, BGP - 21- 28, PLU - 856, AKU - 13- 15, IPU - 99 - 16, PLU - 86 -C, JU - 2, BG - 369, DH - 85 - 2, LBG - 628, T9, PLU- 547, TLU- 328 & PLU- 708
3Cluster	6	PLU- 302, AZAD - 1, PLU - 570, LBG - 648, TLU - 32 - 6 & DH - 85 - 5
4Cluster	1	PLU- 1016
5Cluster	3	KC - 153, ADT - 3 & KU - 96- 14
6Cluster	1	SNTP - 02

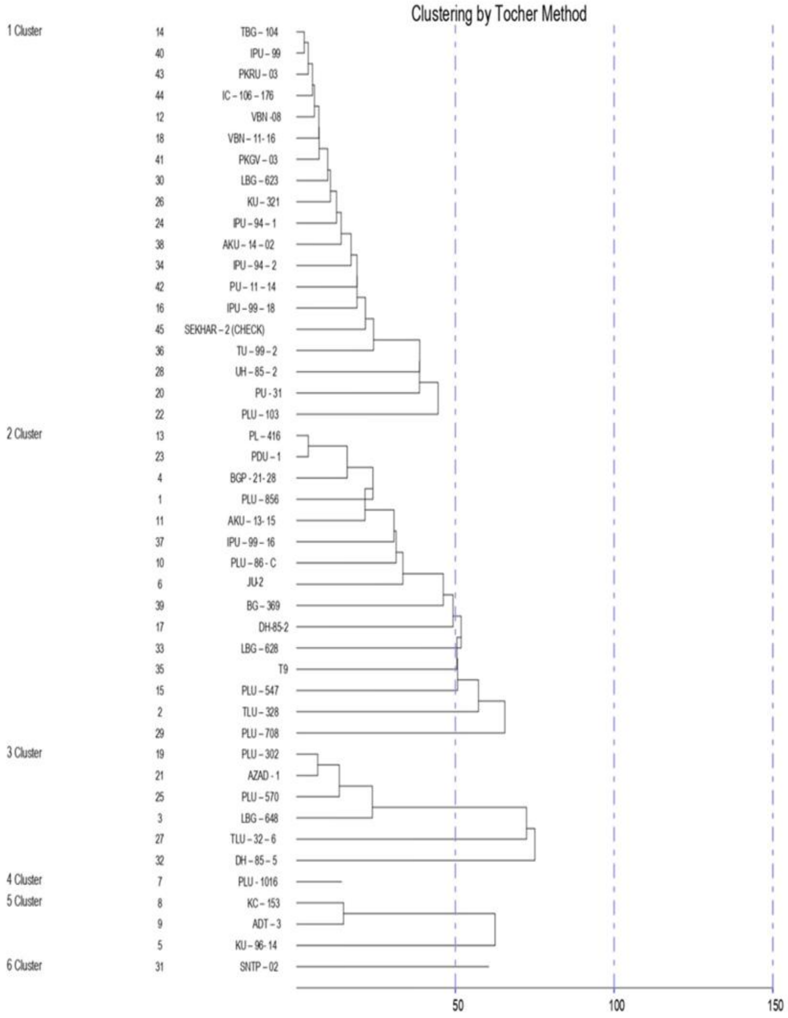

Fig. 2: Dendrogram depicting clustering of blackgram genotypes into 6 clusters

Table6:Averageintra and interclusterdistance(D^2)values forsix clusters in 45 black gramgenotypes

ClusterDistances						
	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6
Cluster1	24.83	392.43	135.97	465.11	761.71	221.34
Cluster2		51.99	164.36	81.02	137.12	140.76
Cluster3			63.68	177.82	441.63	120.26
Cluster4				0.00	207.00	222.20
Cluster5					67.46	307.01
Cluster6						0.00

Table7:MeanvaluesoftheSix clustersfor13charactersin black gramgenotypes

ClusterMeans:Tocher Method													
	Days to 50% flowering	**Days to 50% pod setting**	**Days to maturity**	**Plant height**	**Number of primary branches**	**Number of clusters per plant**	**Number of pods per plant**	**Pod Length**	**Number of seeds per pod**	**Seed index**	**Harvest index**	**Biological yield**	**Seed yield per plant**
Cluster1	43.14	55.16	78.00	37.38	3.43	3.96	12.35	3.83	4.97	3.85	33.30	12.19	3.82
Cluster2	44.87	51.87	64.24	63.61	11.63	10.84	23.04	4.08	6.15	4.31	29.13	23.92	6.92
Cluster3	47.11	53.94	65.72	54.51	7.45	6.20	14.31	4.15	5.90	4.42	29.74	21.61	6.30
Cluster4	46.33	54.00	59.67	81.33	12.53	11.40	12.93	3.69	5.73	5.40	26.82	26.92	7.22
Cluster5	45.78	53.44	63.78	61.82	14.91	15.13	30.38	4.20	5.98	4.83	30.15	23.15	6.95
Cluster6	40.00	50.00	62.00	50.86	4.73	10.13	25.20	4.03	6.20	6.10	37.31	19.94	7.44

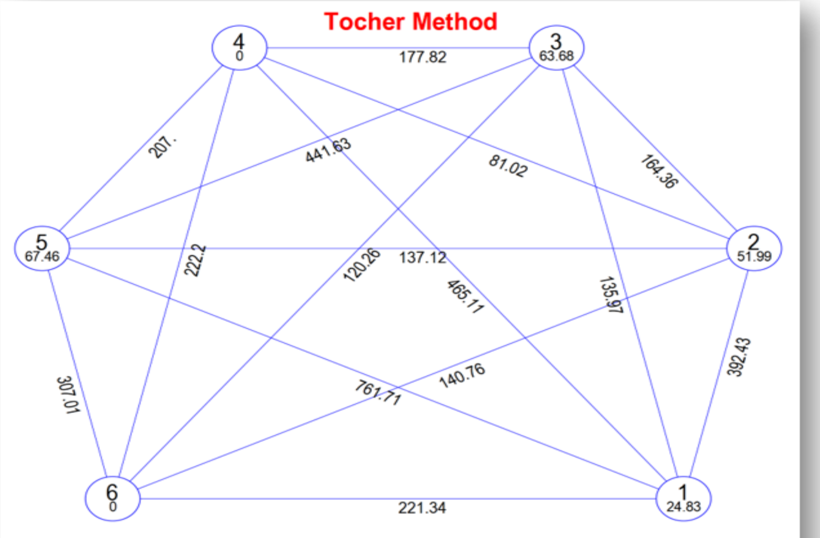

Fig. 3: Cluster diagram depicting intra and inter-cluster distances. (The figure is notexactlyto thescale)

Table 8: Per cent contribution towards divergence of 13 different characters ofblackgram genotypes

Sl.No.	Source	Contribution%	Timesranked1st
1	Days to 50% flowering	0.30	3
2	Days to 50% pod setting	4.92	49
3	Days to maturity	4.00	40
4	Plant height	6.53	65
5	Number of primary branches	5.76	57
6	Number of clusters per plant	8.45	84
7	Number of pods per plant	9.81	97

8	Pod length	2.30	23
9	Number of seeds per pod	6.54	65
10	Seed index	5.64	56
11	Harvest index	10.21	101
12	Biological yield	14.54	144
13	Seed yield per plant	21.00	208

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