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Divergence analysis of black gram (*Vigna mungo* L.) for grain yield and yield components

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ABSTRACT

Thirty-two black gram genotypes were evaluated using twelve quantitative and fifteen qualitative traits at Motilal Nehru National Institute of Technology (MNNIT), Allahabad, India to determine genetic divergence using important yield and yield contributing traits. The number of pods plant^{-1}, peduncle length, harvest index and biomass yield plant^{-1} are important traits affecting grain yield response in black gram. The quantitative traits like; pod length, number of pods plant^{-1}, 100-grain weight as well as qualitative traits like; stem pubescence, leaf pubescence, pod pubescence, pre mature pod colour and plant growth habit which have major contribution in the genetic divergence of black gram. The number of pods plant^{-1} is most important grain yield contributing and genetic divergence developing traits. The genotypes were classified into six clusters based on Euclidean distance. The genotypes belonging to cluster I, II and III were highly diverse than genotypes lies in cluster IV, V and VI. The genotypes IPU 99-176, UH 82-51, GE 154, IPU 99-3 and NG 2119 had good potential to develop high yielding transgressive segregants. The wide genetic diversity is present in black gram. The present study will be much helpful for selection of the parental lines to develop good grain yield producing black gram cultivar in accordance with changing climate.

Key words: Divergence, Hybridization, Grain, *Vigna*, Yield.

INTRODUCTION

Black gram (*Vigna mungo* L.) with chromosome number of 2n = 22 belonging to the family *Fabaceae*, is a self-pollinating and widely cultivated grain legume (Naga *et al.*, 2006). It is mainly cultivated in Asia since ancient times (Paroda and Thomas, 1987). In India, it is cultivated under wide agro-ecological zones. India is the largest producer and consumer of black gram. The annual production of black gram in India is 17.60 lakh tones from 32.60 lakh hectare with an average productivity of 534 kg/ha (Gupta, 2012). Black gram is the ultimate source of protein for vegetarian persons (Pandey *et al.,* 2016). India is the centre of origin of black gram (Vavilov, 1926). There is a wide genetic variability available among genotypes of black gram, providing a wide scope for future black gram improvement programs in India.

A precise assessment of the nature and extent of genetic variability for qualitative, quantitative traits and genetic diversity within the black gram genotype is necessary not only for better understanding of the pattern for varietal differentiation and evaluation but also assisting plant breeders in selecting appropriate materials for further genetic improvement of cultivation and effective management of black gram genetic resources (Shamim *et al.,* 2016). Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Inclusion of diverse parents in hybridization programme saves the purpose of combining desirable recombination (Jayamani and Sathya, 2013). Therefore, it is needed to characterization and divergence analysis of the available genotypes for modern crop improvement programs. The limited amount of black gram potential is utilized for varietal development programme, (Roy *et al.*, 2016). Only black gram genotype T9 is the most frequently used ancestor appearing in 64% of the varieties (Jayamani and Sathya, 2013). There are very little study performed on the extent of genetic variability and divergence analysis using diverse black gram genotypes (Ghafoor *et al.*, 2001). The present study was performed to investigate the extent of genetic diversity and grain yield components in black gram using agro-morphological traits.

MATERIALS AND METHODS

The thirty-two black gram genotypes were obtained from Indian Institute of Pulses Research (IIPR) Kanpur, India and evaluated for twenty-seven agro-morphological traits. All genotypes were evaluated at Biotechnology experimental field of Motilal Nehru National Institute of Technology (MNNIT) Allahabad, India (25.45^{o}N and 81.84^{o}E) during the wet season (July-October) 2014. The experiment was laid out in a randomized block design (RBD) with three replications. The row length was three meters, row to row

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and plant to plant spacing were maintained at 45×15 cm. All the recommended agronomic practice was followed to raise a good crop. The genotypes were characterized according to the descriptor of Indian Institute of Pulses (IIPR), Kanpur, India for black gram (PPV & FR India, 2007).

The one-way analysis of variance (ANOVA) was performed to determine the level of significance at $P \leq 0.01$ and $P \leq 0.05$ (Gomez and Gomez, 1984). The GCV and PCV for each quantitative traits were estimated according to Johnson *et al* (1955). The heritability and other variability parameters were estimated as per Burton and Devane (1953). Genotypic and phenotypic correlation coefficient was calculated following the method of Al-Jibouri *et al.*, (1958). The path analysis was performed as per the procedure suggested by Dewey and Lu (1959). The Euclidean^2 distance were estimated using formula suggested by Shfries and Sacks (1980). The hierarchical clustering of genotypes was performed on the basis of Euclidean^2 distance using Ward's minimum variance method (Ward, 1963). The data were analyzed using software Windostat version 9.2 developed by INDOSTAT services, Hyderabad, India.

RESULTS AND DISCUSSION

Analysis of variance: Analysis of variance (ANOVA) was carried out separately for each of the twelve quantitative characters recorded in the present investigation (Table 1). ANOVA revealed that calculated F-values due to thirty-two genotypes were highly significant for the twelve quantitative characters recorded in present investigation.

Estimation of variance components and genetic parameters for grain yield and yield contributing traits: The estimated variance components and genetic parameters for quantitative characters are presented in Table 2. In all observed cases PCV was higher than GCV indicates polygenic nature of characters under study and also the involvement of additive genes to control the characters, similar observations recorded by Gowda *et al* (1997) and Malik *et al* (2008). The broad sense heritability was estimated from 58.84-93.97% for different quantitative traits. The leading heritability was found in pod length, pods plant^{-1}, biomass yield plant^{-1}, grain yield plant^{-1} and 100-grain weight, indicates that these characters are negligible or low influenced by environment. High genetic advance occurs only due to additive gene action (Panse 1957). The high heritability estimates coupled with high genetic advance would be more useful than heritability alone for selection of best individual (Kishor *et al.*, 2008). The genetic advance as percent of mean was ranged from 9.83-58.78%. After consideration of both genetic heritability and genetic advance as percent of mean it was observed that number of pods plant^{-1}, biomass yield plant^{-1} and grain yield plant^{-1} is the appropriate traits for direct selection of individuals. These findings are comparable to the earlier findings reported by Veeramani *et al.*, (2005); Reni *et al.*, (2013); Panigrahi *et al.*, (2014) and Usharani *et al.*, (2016). The model descriptor state related to qualitative traits of black gram genotypes are present in Table 3. Among the qualitative traits the high level of variability was observed for plant growth habit, petiole colour, pod colour (immature), pod colour (mature) and seed colour.

Association analysis among grain yield components: The values of phenotypic and genotypic correlation coefficient among grain yield contributing traits are presented in Table 4. In the present investigation biomass yield plant^{-1}, number of pod^{-1}, peduncle length, leaf length, plant height, harvest index are significantly as well as positively associated with grain yield plant^{-1} at phenotypic and genotypic level, indicates that these characters has inherent relationship and simultaneous selection of these characters will be beneficial to improve grain yield. These findings are in agreement with the results reported by Ghafoor *et al.*, (2000); Shivade *et al.*, (2011); Panigrahi *et al.*, (2014); Mathivathna *et al.*, (2015) and Mehra *et al.*, (2016). The path coefficient analysis values for all studied characters are presented in Table 5. Biomass yield plant^{-1}, harvest index, number of pods plant^{-1}, leaf width and leaf length has more effect on grain

Table 1: Analysis of variance (ANOVA) for twelve quantitative characters in black gram.

Characters	Range of mean	Grand mean	SE (m)	CV (%)	CD (5%)	Mean sum of squares	Error mean sum of squares	F-Calculated
Days to 50% flowering	25.33-40.33	34.90	1.79	8.90	5.07	50.96	9.64	5.29**
Leaf length (cm)	8.35-12.28	10.12	0.22	3.83	0.63	2.12	0.15	14.12**
Leaf width (cm)	3.77-6.36	4.79	0.18	6.55	0.51	1.24	0.098	12.59**
Peduncle length (cm)	11.11-15.31	13.23	0.35	4.63	1.00	3.18	0.378	8.48**
Pod length (cm)	3.65-5.14	4.24	0.05	1.83	0.13	0.29	0.006	47.77**
Number of pods plant^{-1}	24.53-94.13	60.15	2.98	8.59	8.43	984.54	26.70	36.88**
Days to maturity	43.00-63.00	54.65	3.25	10.30	9.19	87.12	31.70	2.75**
Plant height (cm)	35.08-54.91	44.84	1.51	5.83	4.27	86.80	6.83	12.71**
100-grain weight (g)	4.12-5.62	4.93	0.08	2.78	0.22	0.400	0.019	21.30**
Biomass yield plant^{-1} (g)	64.71-145.15	98.35	4.10	7.22	11.59	1483.89	50.42	29.43**
Harvest index	17.43-29.73	24.72	0.01	8.42	0.034	0.00312	0.00043	7.20**

** Significant at 1% probability level.

Degree of freedom for treatments = 31; Degree of freedom for error = 62; Degree of freedom for replication = 2.

Table 2: Estimates of variance components and genetic parameters for different characters

Characters	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	h^2(%)	GA	GA(%) mean
Days to 50% flowering	23.409	13.773	9.636	13.87	10.64	58.84	5.86	16.8
Leaf length (cm)	0.807	0.657	0.15	8.88	8.01	81.39	1.51	14.88
Leaf width (cm)	0.479	0.38	0.098	14.45	12.88	79.44	1.13	23.65
Peduncle length (cm)	1.311	0.935	0.375	8.66	7.31	71.38	1.68	12.73
Pod length (cm)	0.099	0.093	0.006	7.43	7.2	93.97	0.61	14.39
Number of pods plant^{-1}	345.979	319.282	26.698	30.92	29.71	92.28	35.36	58.78
Days to maturity	50.17	18.474	31.697	12.96	7.87	36.82	5.37	9.83
Plant height (cm)	33.49	26.658	6.832	12.91	11.52	79.6	9.49	21.16
100-grain weight (g)	0.146	0.127	0.019	7.74	7.23	87.12	0.68	13.9
Biomass yield (g) plant^{-1}	528.243	477.825	50.419	23.37	22.23	90.46	42.83	43.55
Harvest index	0.001	0.001	0.005	14.75	12.11	67.4	0.05	20.48
Grain yield (g) plant^{-1}	38.407	33.821	4.586	25.58	24	88.06	11.24	46.4

σ^2p: Phenotypic variance σ^2g: Genotypic variance, σ^2e: Environmental variance, PCV: Phenotypic coefficient of variance, GCV: Genotypic coefficient of variance, h^2(%): Heritability percentage, GA: genetic advance, GA(%) mean: Genetic advance as percent of mean

Table 3: Estimates of variability parameters for fifteen qualitative characters in black gram

Character	Modal descriptor state	SD	CV (%)
Leaf colour	Green	5.5	28.20
Plant growth habit	Semi erect	26.38	46.56
Plant habit	Determinate	10.00	34.48
Stem colour	Purple with green	16.34	66.23
Stem pubescence	Absent	9.00	25.00
Leaflet (terminal) shape	Lanceolate	11.19	45.68
Leaf vein colour	Green	6.50	27.66
Leaf pubescence	Present	4.00	12.51
Petiole colour	Purple	4.00	13.51
Pod colour (Immature)	Dark green	27.25	88.52
Pod: pubesence	Present	26.47	47.27
Pod:colour of mature pod	Brown	13.91	58.78
Seed:colour	Black	11.84	58.46
Seed: shape	Oval	12.00	33.33
Seed:luster	Dull	12.50	19.01

yield plant^{-1} at phenotypic level. Grain yield plant^{-1} at genetic level is highly and positively influenced through number of pods plant^{-1} followed by harvest index, biomass yield plant^{-1}, peduncle length, days to flowering and pod length. The number of pods plant^{-1}, harvest index, biomass yield plant^{-1} and peduncle length has major direct effect on grain yield at phenotypic and genotypic level. The findings of present study are in accordance with the findings of Raika *et al.*, (2002), Chauhan *et al.*, (2007); Konda *et al.*, (2008); Shivade *et al.*, (2011); Mathivathana *et al.*, (2015) and Mehra *et al.*, (2016).

Principal components and cluster analyses: The principle components analysis (PCA) of thirty-two black gram genotypes on the basis of twenty-seven traits was performed (Table 6 & Fig 1). The result of PCA analysis indicates that all the genotypes used in this experiment except Shekhar 2 lies on a single quadrant indicates about the narrow genetic base of black gram. The Sol No2, LBG 623 and IPU 99-243 are placed together, GE 154 and IPU 25 have very close genetic similarity but these genotypes have much variability as compare to other genotypes.

A dendrogram was generated using Euclidean distance values among the genotypes to show the genetic relationships of the black gram genotypes studied (Table 7). The thirty-two genotypes were grouped in six major clusters I, II, III, IV, V and VI (Fig 2; Table 8). The cluster IV has maximum intra-cluster distance whereas minimum for Cluster I. The highest inter cluster distance recorded among cluster III and IV lowest for cluster I and V. The maximum transgressive segregants will be developed through hybridization of the genotypes belonging to cluster III with cluster IV because these are highly divergent, whereas minimum probability to obtain transgressive segregant with hybridization of cluster I and V.

Table 4: Phenotypic (P) and Genotypic (G) correlation coefficient among yield components in black gram (*Vigna mungo* L.).

Characters		Days to 50% flowering	leaf length	leaf width	Peduncle length	Pod length	Number of pods plant^{-1}	Days to maturity	Plant height	100-Grain weight	Biomass yieldplant^{-1}	Harvest index
leaf length	P	-0.0831										
	G	-0.0588										
leaf width	P	-0.1168	0.0786									
	G	-0.0464	0.0566									
Peduncle length	P	-0.0552	0.2041	0.3334								
	G	-0.1387	0.2292	0.3770*								
Pod length	P	-0.2743	0.2503	0.0686	0.0634							
	G	-0.3844*	0.3178	0.0474	0.0433							
Number of pods plant^{-1}	P	0.1257	0.4130*	0.1116	0.4281*	0.0218						
	G	0.1281	0.4820**	0.1438	0.4556**	0.0147						
Days to maturity	P	0.5181**	0.2631	-0.0242	0.0581	-0.2110	0.0765					
	G	0.6826**	-0.4160	0.0858	0.2554	-0.4270*	0.1437					
Plant height	P	-0.0377	0.1990	0.3128	0.3881*	-0.0134	0.5383**	0.0249				
	G	0.0223	0.2076	0.3295	0.4474*	-0.0162	0.5837**	0.1069				
100-Grain weight	P	-0.2292	0.1414	0.0179	0.1734	0.2129	0.0906	-0.2497	-0.0577			
	G	-0.2703	0.1903	0.0639	0.2301	0.2298	0.0803	-0.4004*	-0.0765			
Biomass yield plant^{-1}	P	-0.1175	0.3959*	0.1806	0.5029**	0.2666	0.8110**	-0.0776	0.5376**	0.2954		
	G	-0.1733	0.4463*	0.2156	0.5720**	0.2853	0.8520**	-0.1891	0.5919**	0.3183		
Harvest index	P	0.1553	0.3417	-0.1054	0.1106	-0.0334	0.1715	-0.1134	-0.1459	0.1100	-0.0749	
	G	0.2085	0.4449*	-0.2115	0.0736	-0.0377	0.2177	-0.0401	-0.1152	0.1810	-0.0556	
Grain yield plant^{-1}	P	-0.0252	0.5438**	0.1669	0.5289**	0.2239	0.8083**	-0.1121	0.4138*	0.3113	0.8385**	0.4279*
	G	-0.0822	0.6207**	0.1535	0.5550**	0.2485	0.8711**	-0.1640	0.4687**	0.3736*	0.8751**	0.4445*

*and ** significant at 5% and 1% probability levels, respectively.

Table 5: Path coefficient analysis showing direct and indirect effects of yield components on grain yield plant^{-1} in black gram (*Vigna mungo* L.) using phenotypic (P) and genotypic (G) correlations.

Characters		Days to 50% flowering	leaf length	leaf width	Peduncle length	Pod length	Number of pods plant^{-1}	Days to maturity	Plant height	100-Grain weight	Biomass yieldplant^{-1}	Harvest index
Days to 50% flowering	P	**-0.0033**	0.0003	0.0004	0.0002	0.0009	-0.0004	-0.0017	0.0001	0.0008	0.0004	-0.0005
	G	**0.1159**	-0.0068	-0.0054	-0.0161	0.0445	0.0148	0.0791	0.0026	-0.0313	-0.0201	0.0242
Leaf length	P	-0.0033	**0.0399**	0.0031	0.0082	0.0100	0.0165	-0.0105	0.0079	0.0056	0.0158	0.0136
	G	0.0088	**-0.1500**	-0.0085	-0.0344	-0.0477	-0.0723	0.0624	-0.0311	-0.0285	-0.0669	-0.0667
Leaf width	P	-0.0065	0.0044	**0.0558**	0.0186	0.0038	0.0062	-0.0013	0.0175	0.0010	0.0101	-0.0059
	G	-0.0022	0.0026	**0.0468**	0.0176	0.0022	0.0067	0.0040	0.0154	0.0030	0.0101	-0.0099
Peduncle length	P	-0.0018	0.0065	0.0107	**0.0320**	0.0020	0.0137	0.0019	0.0124	0.0055	0.0161	0.0035
	G	-0.0327	0.0540	0.0889	**0.2358**	0.0102	0.1074	0.0602	0.1055	0.0542	0.1348	0.0174
Pod length	P	-0.0040	0.0037	0.0010	0.0009	**0.0146**	0.0003	-0.0031	-0.0002	0.0031	0.0039	-0.0005
	G	-0.0421	0.0348	0.0052	0.0047	**0.1096**	0.0016	-0.0468	-0.0018	0.0252	0.0313	-0.0041
Number of pods plant^{-1}	P	0.0083	0.0273	0.0074	0.0283	0.0014	**0.0661**	0.0051	0.0356	0.0060	0.0536	0.0113
	G	0.0725	0.2726	0.0813	0.2577	0.0083	**0.5657**	0.0813	0.3302	0.0454	0.4820	0.1231
Days to maturity	P	0.0070	-0.0036	-0.0003	0.0008	-0.0029	0.0010	**0.0136**	0.0003	-0.0034	-0.0011	-0.0015
	G	-0.2219	0.1352	-0.0279	-0.0830	0.1388	-0.0467	**-0.3250**	-0.0348	0.1301	0.0615	0.0130
Plant height	P	0.0003	-0.0017	-0.0026	-0.0032	0.0001	-0.0045	-0.0002	**-0.0083**	0.0005	-0.0045	0.0012
	G	-0.0009	-0.0085	-0.0135	-0.0183	0.0007	-0.0239	-0.0044	**-0.0410**	0.0031	-0.0243	0.0047
100-Grain weight	P	-0.0028	0.0017	0.0002	0.0021	0.0026	0.0011	-0.0030	-0.0007	**0.0122**	0.0036	0.0013
	G	-0.0051	0.0036	0.0012	0.0043	0.0043	0.0015	-0.0075	-0.0014	**0.0188**	0.0060	0.0034
Biomass yield plant^{-1}	P	-0.0911	0.3069	0.1400	0.3898	0.2067	0.6288	-0.0601	0.4167	0.2290	**0.7753**	-0.0581
	G	-0.0486	0.1252	0.0605	0.1604	0.0800	0.2390	-0.0530	0.1660	0.0893	**0.2805**	-0.0156
Harvest index	P	0.0720	0.1583	-0.0488	0.0512	-0.0155	0.0795	-0.0526	-0.0676	0.0510	-0.0347	**0.4634**
	G	0.0741	0.1580	-0.0751	0.0261	-0.0134	0.0773	-0.0142	-0.0409	0.0643	-0.0197	**0.3551**
Grain yield plant^{-1}	P	-0.0252	0.5438	0.1669	0.5289	0.2239	0.8083	-0.1121	0.4138	0.3113	0.8385	0.4279
	G	-0.0822	0.6207	0.1535	0.5550	0.2485	0.8711	-0.1640	0.4687	0.3736	0.8751	0.4445

Residual effect (P) = 0.2193; Residual effect (G) = 0.0163; R^2 (P) = 0.9519; R^2 (G) = 0.9997.

Table 6: Contribution of agro-morphological characters in genetic divergence analysis.

Name of the characters	Number of times first	Contribution
Days of 50% Flowering	1.00	0.20 %
Leaf length	9.00	1.81 %
Leaf width	5.00	1.01 %
Peduncle length	5.00	1.01 %
Pod length	77.00	15.52 %
Number of pods plant^{-1}	43.00	8.67 %
Days of maturity	0.01	0.00 %
Plant height	2.00	0.40 %
100-grain weight	18.00	3.63 %
Biomass yield plant^{-1}	3.00	0.60 %
Harvest index	3.00	0.60 %
Grain yield plant^{-1}	3.00	0.60 %
Foliage: colour	0.01	0.00 %
Plant: growth habit	17.00	3.43 %
Plant: habit	0.01	0.00 %
Stem: colour	2.00	0.40 %
Stem: pubescence	151 .00	30.44 %
Leaflet (terminal) shape	7.00	1.41 %
Leaf vein colour	0.01	0.00 %
Leaf pubescence	72.00	14.52 %
Petiole: colour	0.01	0.00 %
Pod: colour (premature)	24.00	4.84 %
Pod: pubescence	45.00	9.07 %
Pod: colour (mature)	0.01	0.00 %
Seed: colour	9.00	1.81 %
Seed: luster	0.01	0.00 %
Seed: shape	0.01	0.00 %

On the basis of present study it was concluded that there is a wide genetic variability is present for each trait in black gram. The number of pods plant^{-1}, grain yield plant^{-1}, peduncle length and biomass yield plant^{-1} are most important characters. Therefore, the more emphasis should focus on these characters for selection of parental lines to improve black gram yield. There is a wide range of genetic diversity present in the investigated black gram genotypes. Qualitative traits have more importance than quantitative traits for divergence analysis of black gram. The PCA analysis suggests about the narrow genetic base of black gram, so it is needed to identify more suitable parental lines for development of high yielding abiotic and biotic stress tolerance lines. The genotypes IPU 99-176, UH 82-51, GE 154, IPU 99-3 and NG 2119 had good potential to develop high yielding, abiotic and biotic stress tolerant transgressive segregants. The key opportunities are available in black gram to develop new cultivar which has potential to tolerate changing climate conditions and able to produce good grain quality and quantity to overcome not only the protein malnutrition but also conquer the food problem through sustainable agricultural practices.

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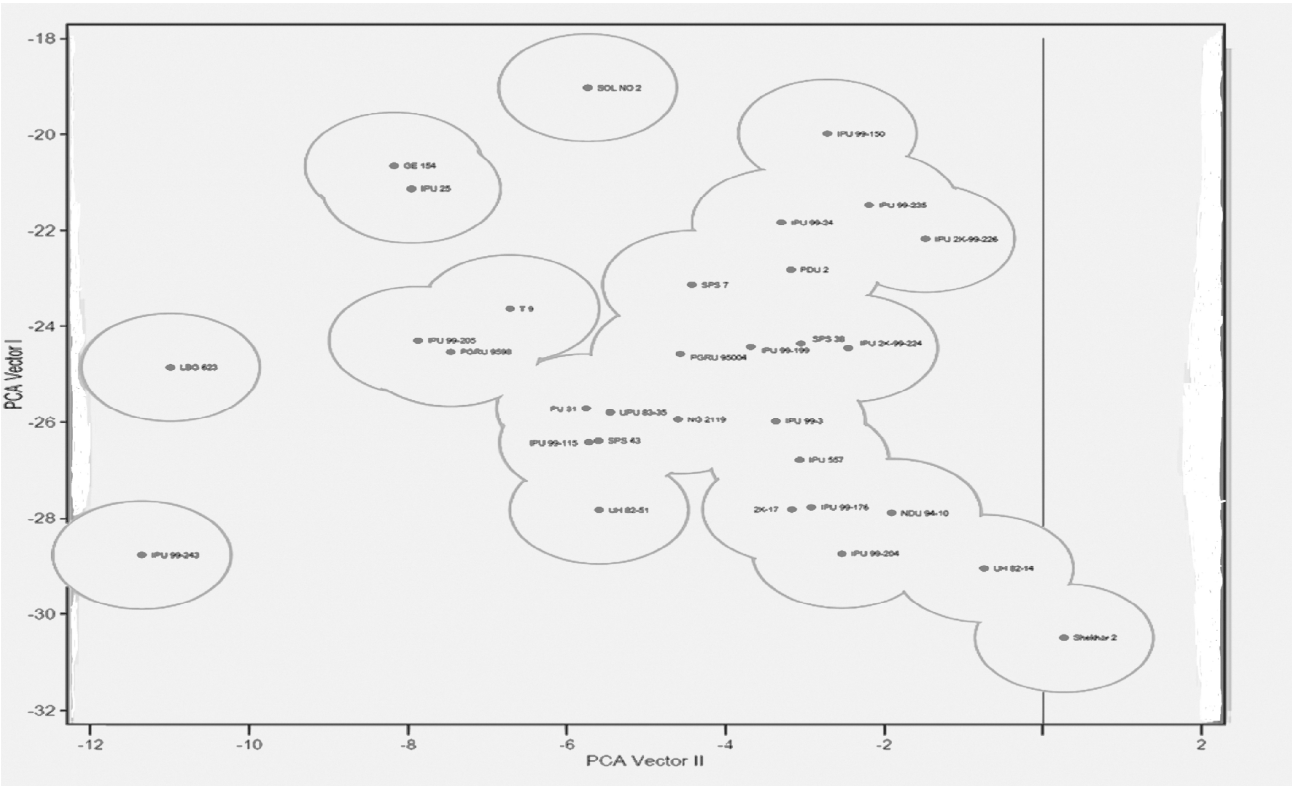

Fig 1: 2-D diagram of black gram (*Vigna mungo* L.) germplasm for first two PCs.

Table 7: Cluster distance: Eucledian² for twenty-seven morphological traits in thirty-two genotypes of black gram.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	54.579	141.504	132.145	359.903	121.037	124.456
Cluster II		89.986	220.369	583.742	218.168	264.754
Cluster III			84.992	574.868	283.030	211.813
Cluster IV				136.003	205.443	245.507
Cluster V					60.681	162.845
Cluster VI						98.529

Table 8: Cluster composition based on Eucledian² taxonomic distance for twenty-seven morphological traits in thirty-two genotypes of black gram.

Cluster name	Number of genotypes	Genotypes name
Cluster I	9	T9, IPU 99-205, PGRU 95004, PDU 2, PGRU 9598, LBG 623, PU 31, SPS 38, UPU 8335
Cluster II	2	IPU 2K 99-226, IPU 99-150,
Cluster III	3	SOL NO 2, IPU 25, GE 154
Cluster IV	2	Shekhar 2, UH 82-14
Cluster V	6	UH 82-51, IPU 99-204, IPU 2K-17, IPU 99-176, IPU 2K 99-224, NG 2119
Cluster VI	10	SPS 43, IPU 99-3, IPU 99-115, IPU 557, NDU 94-10, IPU99-243, IPU 99-24, IPU 99-235, SPS 7, IPU 99-199

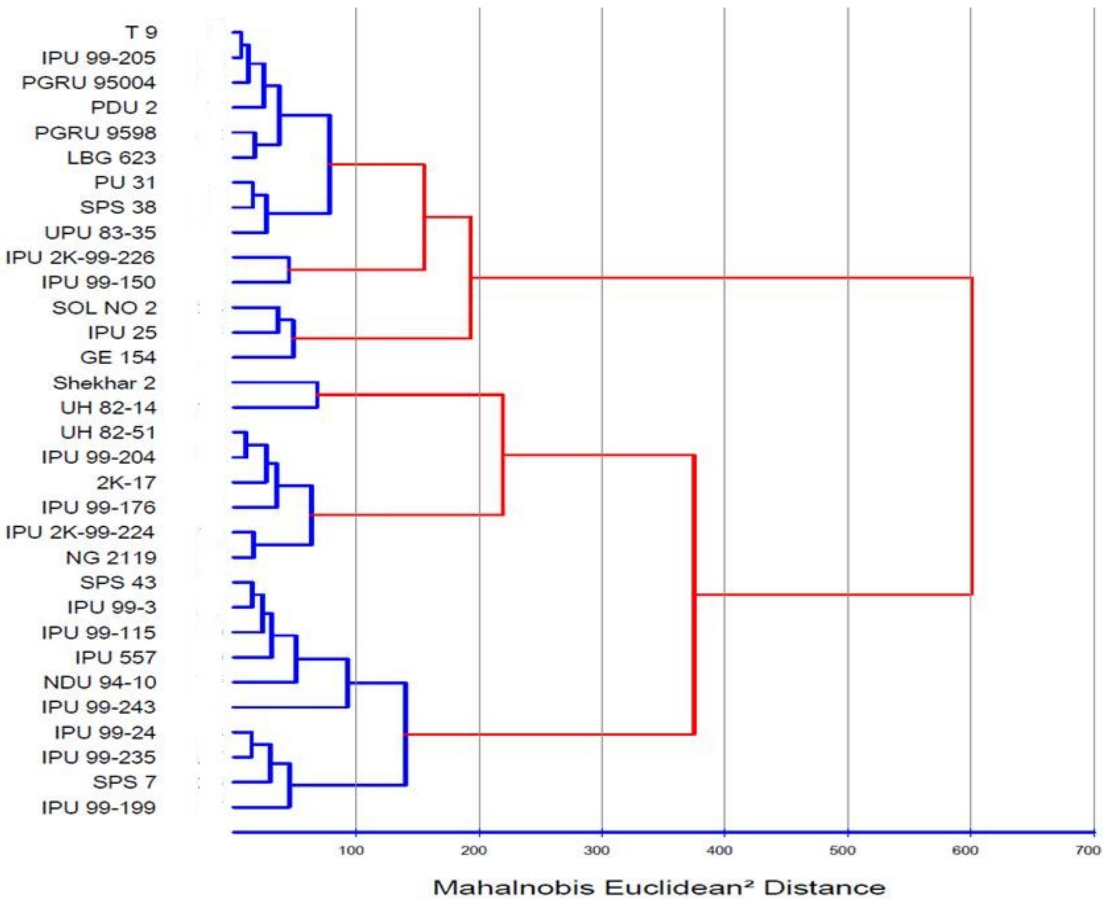

Fig 2: Cluster analysis of 32 black gram genotypes based on 27 morphological traits.

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