Original Research Article

“Principal Component Analysis and Traits Association in Blackgram (Vigna mungo (L.) Hepper)”

ABSTRACT

~~The present~~ This study investigation entitled **“Prinicipal Component Analysis and Traits Association in Blackgram (*Vigna mungo* (L.) Hepper)”** in the 23 genotypes of blackgram during *Zaid*-2021 at the research field, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, technology and Sciences, Prayagraj. LBG-645 is identified as high seed yielding per plant at Prayagraj agro-climatic condition. The analysis of variance for all the characters revealed that genotypes were highly significant except Harvest Index (%). Genotypes were highly significant at 5%, 1% level for all the characters, indicating presence of considerable amount of genetic variability in the parental material tested. The characters with high range estimates of GCV and PCV number of clusters per plant, number of pods per plant. heritability and genetic advance as % of mean values were high for Number of pods per plant. The seed yield per plant exhibited positive significant and correlation with Number of pods per plant at genotypic and phenotypic level. At genotypic and phenotypic path coefficient analysis revealed that number of pods per plant had greatest positive direct effect on seed yield per plant. Principal component (PC1) contributed maximum towards variability 22.808 % was correlated with Seed Index followed by, Plant height and Number of seeds per pod. The second principal component (PC2) accounted 21.410% per cent of total variance and it reflected positive loading of Days to 50% pod initiation, Days to 50% flowering, and Pod length whereas; the third principal component (PC3) accounted 15.642% per cent of total variance and positive loading of Harvest Index followed by Seed Index. Fourth principal component (PC4) contributed 11.325% of variability reflected loadings of Days to maturity followed by seed yield per plant. The fifth principal component (PC5) contributed 9.489% variability of seed yield per plant, followed by days to 50% flowering.

Keywords: Blackgram, Genetic Variability, Correlation, Path Analysis and Principal Component Analysis

1. 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 and originated from the Indian continent. It is popularly known as “urd bean, urd or mash”, is one of the important grain legumes, and is an excellent source of easily digestible good quality proteins. It is an important self-pollinating diploid grain legume [1], domesticated from V. mungo var. silvestris [2]. It is widely cultivated in the Indian subcontinent and two are lesser extent in Thailand, Australia, and other Asian and South Pacific countries [3]. The area of traditional cultivation of urad bean is confined to South Asia and adjacent areas including India, Pakistan, Afghanistan, Bangladesh, and Myanmar. It is an economically important grain legume crop in Asia, widely cultivated on marginal lands with low inputs during Kharif, rabi, and summer seasons. India produces around 32-33 lakhs tones of blackgram annually from above 50.31 lakh hectares of area, and an average productivity of 652 to 750 kg/hectare. (source: ICAR-Directorate of pulses development annual report, (2019-2020).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. Many south Indian dishes as dosa and idli have blackgram as the main ingredient. The urad flour is also used in making papad and Dahi-vada. Sprouted seeds are also eatable and prescribed as medicine for internal and external paralysis, rheumatism, and nervous problems

In-plant breeding, variability studies are important to establish the genetically divergent genotypes. Genetic diversity analysis can be used to identify the divergent genotypes and to utilize these genotypes to exploit heterosis. The genetically diverse parent is likely to produce not only heterotic effect but also desirable segregants useful for practicing selection. Correlation between different morphological parameters and yield components with yield gives an idea of growth and yield attributes, promotion of which helps in the realization of higher productivity. It splits the correlation into positive correlation and negative correlation. The traits that are showing a positive effect on yield are positively correlated towards yield and those characters that show a negative effect on yield are negatively correlated towards yield. The knowledge of the extent of existing genetic variability and character association is The problem of increasing the yield can be tackled effectively based on the performance of yield components and selection for closely related characters. Considering the potentiality of this crop, there is a need for improvement and to development of varieties suited to specific agro-ecological conditions and also for specific enduse. Thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement program. With limited variability, much cannot be achieved and the breeder will have to enrich the germplasm or he can resort to creating greater variability by hybridization, mutation, and polyploidy breeding. This investigation was undertaken to ascertain the magnitude and extent of genetic variability, correlation, and path coefficient analysis in blackgram.

Principal Component Analysis (PCA) describes the composition of variances and covariances through several linear combinations of the primary variables, without missing an important part of the original information. In another term, it is about obtaining a unique set of orthogonal axes where the data has the largest variance. Its main aim is to overcome the dimensionality of the problem. The reduction of dimensionality should be such that when dropping higher dimensions, the loss of data is minimum. Also, the interpretation of principal components can explain associations among variables that are not visible at first glance. It helps analyze the scattering of the observations and recognize the variables responsible for distribution. Information on correlation, path coefficients and principal component analysis is of much use to plant breeder for selection and breeding genotypes with increased yield potential correlation coefficients in general shows association among independent characteristics and the degree of linear relation between these characteristics.The main objective of this study is To rank genotypes and their traits based on principal component analysis.

2. Materials and methods

The present investigation was carried out during zaid-2021 comprising 23 genotypes of Blackgram [Vigna mungo (L.) Hepper] (Table.1) at the field experimentation centre, Department of Genetics and Plant Breeding, Naini agriculture institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P. during zaid-2021. All types of facilities necessary for cultivation of successful crop including field preparation, inputs and irrigation facilities were provided

The experiment was conducted in Randomized Block Design with three replications. The gross area of experiment was 149 m2 and cash plot size was 1×1 m spacing of 30 cm between rows and 10 cm between plants.

The observations were noted from 5 randomly selected plants for Days to 50% flowering, Plant height (cm), Number of primary branches, Days to 50% pod setting, Number of clusters per plant, Days to Maturity, Number of pods per plant, Number of Seed per pod, Pod length (cm), Biological yield per plant, 100 seed weight (Seed Index), Harvest index (%), Seed yield per plant (g)

The statistical analysis was subjected to basic statistics methods followed for Analysis of variance, (**Fisher, 1936)** Genetic variability (**Burton, 1952)**, Heritability (**Burton and Devane, 1953)**, Genetic advance (**Johnson et al 1955)**, Correlation coefficient analysis (**AI Jibouri et al., 1958)**, Path coefficient analysis (**Dewey and Lu, 1959**), Principal component analysis (**Kaiser, 1958)**.

2.1. LAYOUT DESCRIPTION

Crop : Black gram (*Vigna mungo* (L.) Hepper)
Family : Leguminacae
Season : *zaid*-2021
Design of Experiment : Randomized Block Design (RBD)
No. of. Genotypes : 23
No. of. Replications : 03
Planting distance : 30×10cm
Row to Row distance : 30
Plant to Plant distance : 10
Gross Cultivated Area : 149 m^2
Net Cultivated Area : 69 m^2
Fertilizer Dose : N: P: K @ 20:40:40 kg/ha

Table 1: List of blackgram genotypes used in present investigation:

Sl. No.	Genotypes	Sl. No.	Genotypes
1	PU-09-37	13	AKU-16-03
2	BGP-21-28	14	KU-96-7
3	ADT-3	15	LBG-20
4	KU-96-4	16	LBG-645
5	PLU-103	17	PDV-2
6	TBG-104	18	IC-240-183
7	CO-6	19	PDV-1103
8	VBN-6	20	PU-31
9	PLU-302	21	PLU-708
10	TLU-328	22	KU-48
11	IPU-95-13	23	SHEKHAR-2 (Check)
12	AZAD-1		

Source: Department of genetics and plant breeding SHUATS

3. RESULT AND DISCUSSION

3.1 Analysis of variance

Mean sum of squares data for 13 characters were subjected to analysis of variance for experimental design. The analysis of variance for different characters is presented in. The mean squares due to genotypes showed highly significant differences (α = 0.01) for all characters except Harvest Index which showed significant differences (α = 0.05) indicating the presence of substantial amount of genetic variability among the Blackgram genotypes (Table 2). Provide genetic reasons to support your claims.

3.1.2 Phenotypic and genotypic of variation

The variability estimates such as phenotypic variance, genotypic variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h2), genetic advance (GA), genetic advance as a percent of mean (GAM) for fifteen characters are explained under the following heads (Table 3). For all the traits PCV was higher than matching GCV indicating that the environment had an impact. In the present investigation Genotypic coefficient of variation (GCV) ranged from 1.297 (Days to maturity) to 18.457 (Number of clusters per plant). Moderate GCV was recorded for Number of clusters per plant (18.457), Number of pods per plant (17.286), Seed yield per plant (g) (10.621), Plant height (cm) (10.027). Phenotypic coefficient of variation (PCV) ranged from 1.702 (Days to maturity) to 20.156 (Number of clusters per plant). High PCV was recorded Number of clusters per plant (20.156) Moderate PCV was recorded for Number of pods per plant (18.784), Seed yield per plant (g) (12.793), Plant height (cm) (12.17). In present investigation similar findings are reported by **Kumar *et al.* (2000) [4], Loganathan *et al.* (2001) [5], Sarkar *et al.* (2006) [6], Dadepeer *et al.* (2009) [7], and Neelawati *et al.* (2010) [8],** Provide genetic reasons to support your claims.

3.1.3 Heritability

The estimates of the Genotypic Coefficient of variation reflect the total amount of Genotypic variability, which is transmitted from parents to the progeny, is reflected by heritability which is the measure of genetic relationship between parent and progeny and had been widely used to assess the degree to which a character may be transmitted from parent to offspring.[9], gave the concept of broad sense of heritability. High heritability in the broad sense is not only enough to make sufficient improvement through selection unless accompanied by the amount of genetic advance. [10] suggested the genetic variation along with heritability estimates would give a better idea about the expected efficiency of selection thus a character possessing high GCV along the high heritability will be valuable in the selection program. The results of heritability for all the 13 characters are presented in (Table 3).

The estimates of heritability (%) in the broad sense for 13 characters studied, which range from 25.39 to 84.68%. High heritability (broad sense) was recorded for characters i.e., Number of pods per plant (84.68), Number of clusters per plant (83.84), Seed yield per plant (g) (68.91), Plant height (cm) (67.87), Biological yield per plant (g) (65.001), Seed Index (60.94), Days to 50%pod initiation (60.40), Number of seeds per pod (60.023), Moderate heritability (broad sense) was recorded for characters i.e., Days to maturity (58.019), Number of primary branches per plant (46.547), Pod length (cm) (45.077), Days to 50% flowering (34.683). Low heritability (broad sense) was recorded for characters i.e., Harvest Index (%) (25.39). In present investigation similar findings are reported by **Reddy *et al.* (2011) [11], Meshram *et al.* (2012) [12], Sowmini and Jayamani (2013) [13], Patel *et al.* (2014) [14].** Provide genetic reasons to support your claims.

3.1.4 Genetic advance

The estimation of genetic advance helps to understand the type of gene action involved in the expression of various varied from 0.161 (Harvest Index (%)) to 3.67 (Seed Index). Low genetic advance as % mean was recorded for Seed Index (3.67) followed by Number of pods per plant (3.56), Plant height (cm) (2.616), Number of clusters per plant (1.526), Days to maturity (1.514), Days to 50% pod initiation (1.172), Biological yield per plant (g) (1.005), Days to 50% flowering (0.83), Seed yield per plant (g) (0.763), Number of seeds per pod (0.378), Number of primary branches per plant (0.302), Pod length (cm) (0.211), and Harvest Index (%) (0.161) and no parameters have high and moderate genetic advance. In present investigation similar findings are reported by **Pradhan *et al.* (2005) [15], Singh and Singh (2006) [16], Pervin *et al.* (2007) [17], and Wani *et al.* (2007) [18].** Provide genetic reasons to support your claims.

3.1.5 Genetic advance as % of mean

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about genetic advance coupled with heritability is most useful. Genetic advance is the improvement in the mean of selected families over the base population **Lush (1949), Johnson and Robinson, (1955) [19].** Provide genetic reasons to support your claims.

Genetic advance as % of mean varied from 1.766 (Days to 50% flowering) to 34.816 (Number of clusters per plant). High genetic advance as % mean was recorded for Number of clusters per plant (34.816) and Number of pods per plant (32.769). Moderate genetic advance as % mean was recorded for Seed yield per plant (g) (18.163) and Plant height (cm) (17.017). In present investigation similar findings are reported by **Dadepeer *et al.* (2009), Konda *et al.* (2009) [20] and Netam *et al.* (2010) [21].** Provide genetic reasons to support your claims.

3.2 Correlation coefficient of different characters

The correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of the relationship between two or more variable components [22].

Correlation studies provide reliable information on nature and extent of relationship between different characters. Information on the association of traits of economic worth is of great value to plant breeders at a time. The association between two characters that can be directly observed measures the phenotypic correlation whereas genotypic correlation is the correlation of breeding values.

The genotypic and phenotypic correlation amongst the traits followed almost similar trends of association (Table 4), where the former being a little higher in most of the cases, indicated the existence of strong inherent association between the characters in the breeding material. Correlation coefficient was computed to assess the direction and magnitude of association existing between seed yield and other components and are furnished in table. Seed yield per plant exhibited positive and highly significant correlations with Number of pods per plant at both genotypic and phenotypic level and negative and significant correlation with Number of primary branches at Genotypic level and phenotypic level. In present investigation similar findings are reported by **Nimbalkar and Gujar (2000) [23], Bhagwati *et al.* (2001) [24], Khan *et al.* (2001) [25], and Kadam *et al.* (2008) [26].** Provide genetic reasons to support your claims.

3.3 Path coefficient analysis:

Knowledge of correlation between yield and its component characters is helpful in selection of superior plant types. When a greater number of characters are included in correlation study, the direct and indirect contribution are necessary. Path coefficient analysis is computed by the procedure described by [27] provides an effective means of partitioning the correlations coefficients into direct and indirect effects of component characters (Table 5 & fig 1).

So, from this aspect path analysis has emerged as a powerful and widely used technique to partition the observed correlation coefficient into direct and indirect effects of independent variables (yield) on the dependent (component) variables to provide clearer picture of characters association for formulating efficient selection strategy [28]. Path coefficient analysis is an efficient statistical technique specially designed to quantify the interrelationship of different components and their direct and indirect effects on seed yield [29].Path analysis revealed that Days to 50% flowering, Number of pods per plant, Number of clusters per plant showed a direct positive effect on seed yield at genotypic and phenotypic levels. In present investigation similar findings are reported by **Krishnan *et al.* (2002) Venkatesan *et al.* (2004) Sumarno *et al.* (2006) Jyothsna *et al.* (2016) and Hadimani (2019).** Provide genetic reasons to support your claims.

3.4 Principal Component Analysis

Principal component analysis is a method to recognize the relative importance and usefulness of different variables and genotypes in a data set. It transformed many correlated variables into few independent principal components explaining much of the variation in the data. In present investigation prncipal component analysis was carried out by method as given by [30] and the factors with eigen value more than one are considered. The eigen value from PCA were used to determine that how many factors to retain. The sum of the all eigen values is always equal to the number of variables. In our study out of thirteen only five of the principal components had eigen value greater than one and they cumulatively explained 80.67 per cent of the total variation present in original data set. The first principal component explained 22.81 per cent of the total variance. The second, third, fourth and fifth principal components explained 21.41, 15.64, 11.33, 9.49 per cent of the total variance, respectively (Table 6).

PC1 was contributed by most of the yield attributing traits, an intensive selection procedure can be designed to bring out rapid improvement of dependent traits (Table 7) i.e., seed yield per plant by selecting the lines of PC1. First principal component (PC1) contributed maximum towards variability (22.808%) was correlated with Seed Index(0.753) followed by, Plant height (cm)(0.668) and Number of seeds per pod(0.642). The second principal component (PC2) accounted (21.41%) of total variance and it reflected positive loading of Days to 50% pod initiation (0.864), Days to 50% flowering (0.844), and Pod length (cm) (0.632) whereas; the third principal component (PC3) accounted (15.64%) per cent of total variance and positive loading of Harvest Index (%) (0.610) followed by Seed Index (0.539). Fourth principal component (PC4) contributed 11.325% of variability reflected loadings of Days to maturity followed by seed yield per plant. The fifth principal component (PC5) contributed 9.489% variability of seed yield per plant, followed by days to 50% flowering. Characters with high variability are expected to provide high level of gene transfer during breeding programs **(Gana *et al.* 2013 [31]and Nachimuthu *et al.* 2014) [32].** In present investigation similar findings are reported by **Mohanlal *et al.* (2018) [33] and Reni *et al.* (2022) [34].** Provide genetic reasons to support your claims.

3.4.2 Distribution of 13 traits of Blackgram based on principal component PC1 and PC2

In figure 2: 13 traits of Blackgram are distributed on the bases of their relative performance with respect to principal factor one and two. All the traits showed significance relation to the variance, post of the traits showed positive loading and few showed negative loadings, depending on the distance from center of origin represent the variance of a particular trait. Trait enabled high positive loading for No. of pods per plant, days to 50% flowering, and days to 50% pod setting and high negative loading for Seed yield per plant and Days to Maturity. Provide genetic reasons to support your claims.

In figure 2: 23 Genotypes of Blackgram are distributed on the bases of their relative performance with respect to principal factor one and two. Genotypes PU-31, LBG-20, PLU-302, PU-09-37, TBG-104, KU-96-7, BGP-21-28, CO-6, VBN-6, KU-96-4, AKU-16-03 cluster towards positive side of PC1, so they were better in terms of grain yield. The genotypes IC-240-183, KU-48, PDV-103, SHEKHAR-2 ©, AZAD-1, IPU-95-13, PDV-2, TLU-328, PLU-708, PLU-103, ADT-3, LBG-645 were clusters towards negative side of PC2, so they were less effective on grain yield. Provide genetic reasons to support your claims.

Table 2: Analysis of variance for 13 characters in 23 blackgram genotypes

Sl. No.	Characters	Replication	Treatment	Error
	Degrees of freedom (df)	2	22	44
1	Days to 50% flowering	1.9280	2.287**	0.882
2	Days to 50% pod initiation	0.2750	1.958**	0.351
3	Plant height (cm)	1.0540	8.255**	1.125
4	Number of primary branches per plant	0.1150	0.191**	0.053
5	Number of clusters per plant	0.0770	2.09**	0.126
6	Number of pods per plant	0.7840	11.218**	0.638
7	Pod length (cm)	0.0580	0.098**	0.028
8	Number of seeds per pod	0.0040	0.205**	0.037
9	Days to maturity	1.3490	3.468**	0.674
10	Biological yield per plant (g)	0.0670	1.296**	0.197
11	Harvest Index (%)	0.0970	0.143*	0.071
12	Seed Index	6.6460	18.96**	3.337
13	Seed yield per plant (g)	0.0690	0.686**	0.09

Table 3: Genetic parameters for 13 biometrical traits of blackgram

S.No.	Character	GCV	PCV	Heritability (%) Broad Sense	Genetic Advance	GA as % mean
1	**Days to 50% flowering**	1.456	2.472	34.683	0.83	1.766
2	**Days to 50% pod initiation**	1.369	1.762	60.401	1.172	2.192
3	**Plant height (cm)**	10.027	12.171	67.872	2.616	17.017
4	**Number of primary branches per plant**	6.336	9.287	46.547	0.302	8.905
5	**Number of clusters per plant**	18.457	20.156	83.849	1.526	34.816
6	**Number of pods per plant**	17.286	18.784	84.683	3.56	32.769
7	**Pod length (cm)**	4.145	6.173	45.077	0.211	5.732
8	**Number of seeds per pod**	4.848	6.258	60.023	0.378	7.737
9	**Days to maturity**	1.297	1.702	58.019	1.514	2.034
10	**Biological yield per plant (g)**	4.761	5.905	65.001	1.005	7.908
11	**Harvest Index (%)**	3.018	5.989	25.39	0.161	3.132
12	**Seed Index (g)**	5.611	7.188	60.942	3.67	9.024
13	**Seed yield per plant (g)**	10.621	12.793	68.919	0.763	18.163

Table 4: **Genotypic and phenotypic correlation coefficient for yield contributing traits of blackgram**

Traits		Days to 50% flowering	Days to 50% pod setting	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	Biological yield (g)	Days to maturity	Seed Index	Harvest Index (%)	Seed yield per plant
Days to 50% flowering	G P	1.0000 1.0000	-0.311* -0.1644	-0.496** -0.326*	-0.2178 -0.0367	-0.404** -0.276*	-0.317* -0.243*	0.1591 -0.0709	-0.253* -0.2108	0.312* 0.278*	0.489** 0.7860	-0.2062 -0.1605	0.0463 -0.0014	0.1570 0.0639
Days to 50% pod setting	G P		1.0000 1.0000	-0.358* -0.1988	-0.523** -0.260*	0.590** 0.326*	0.340* 0.1971	0.428** 0.0716	0.721** 0.372*	0.302* 0.0016	-0.1838 -0.2149	0.393** 0.1267	-0.665** -0.385*	0.1221 0.0423
Plant height (cm)	G P			1.0000 1.0000	0.427** 0.356*	-0.0527 0.0212	0.2138 0.1846	0.0711 0.1767	-0.2067 0.1183	-0.1612 0.0700	0.1695 0.0715	0.1195 0.245*	0.278* 0.1911	**-0.282*** -0.0552
Number of primary branches	G P				1.0000 1.0000	-0.1674 -0.1449	-0.0993 -0.1047	0.0544 0.0460	0.1157 0.1135	-0.1938 -0.1182	-0.1340 -0.0840	0.2300 0.1715	0.1045 0.1564	**-0.364*** **-0.294***
Number of clusters per plant	G P					1.0000 1.0000	0.590** 0.535**	0.383* 0.2323	0.607** 0.441**	0.478** 0.402**	-0.334* -0.1843	0.271* 0.2234	-0.669** -0.570**	**0.290*** 0.2330
Number of pods per plant	G P						1.0000 1.0000	0.577** 0.1980	0.0590 0.0825	0.396** 0.363*	-0.299* -0.2166	0.0402 0.0893	-0.2042 -0.1774	**0.353*** **0.364***
Pod length (cm)	G P							1.0000 1.0000	0.445** 0.327*	0.648** 0.427**	0.0766 0.261*	0.1100 0.0286	-0.475** -0.1591	**-0.292*** -0.0328
Number of seeds per pod	G P								1.0000 1.0000	-0.0367 0.0094	-0.0045 -0.0341	-0.0558 0.0913	-0.928** -0.387*	**-0.527**** -0.1569
Biological yield (g)	G P									1.0000 1.0000	0.0920 0.0496	0.396** 0.304*	-0.334* -0.239*	-0.0608 0.0923
Days to maturity	G P										1.0000 1.0000	0.0749 0.0190	0.0079 0.0351	**-0.303*** -0.1621
Seed Index	G P											1.0000 1.0000	-0.246* -0.1514	-0.2197 -0.1449
Harvest Index (%)	G P												1.0000 1.0000	-0.0679 -0.0247

G: Genotypic , P: Phenotypic.

Table 5: Genotypic and Phenotypic path coefficient for yield contributing traits of blackgram

Traits		DTFF	DTFP	PH (cm)	NPB	NCPP	NPPP	PL (cm)	NSPP	BY (g)	DM	HI (%)	SI (g)	SYPP
DTFF	G P	**0.7850** **0.2766**	-0.3545 -0.0455	-0.5659 -0.0900	-0.2485 -0.0101	-0.4604 -0.0763	-0.3612 -0.0672	0.1814 -0.0196	-0.2882 -0.0583	0.3557 0.0769	0.5582 0.0218	-0.2352 -0.0444	0.0528 -0.0004	0.1570 0.0639
DTFP	G P	0.3779 0.0051	**-0.8150** **-0.0313**	0.4349 0.0062	0.6362 0.0081	-0.7172 -0.0102	-0.4128 -0.0062	-0.5205 -0.0022	-0.8766 -0.0116	-0.3668 -0.0001	0.2235 0.0067	-0.4784 -0.0040	0.8092 0.0120	0.1221 0.0423
PH (cm)	G P	-0.0930 -0.0319	-0.0670 -0.0195	**0.1875** **0.0981**	0.0801 0.0349	-0.0099 0.0021	0.0401 0.0181	0.0133 0.0173	-0.0388 0.0116	-0.0302 0.0069	0.0318 0.0070	0.0224 0.0241	0.0520 0.0187	-0.282* -0.0552
NPB	G P	0.2708 0.0096	0.6503 0.0681	-0.5312 -0.0934	**-1.2429** **-0.2622**	0.2080 0.0380	0.1235 0.0275	-0.0676 -0.0121	-0.1438 -0.0298	0.2409 0.0310	0.1666 0.0220	-0.2859 -0.0450	-0.1299 -0.0410	-0.364* -0.294*
NCPP	G P	-0.1844 -0.0996	0.2694 0.1178	-0.0241 0.0077	-0.0765 -0.0523	**0.4568** **0.3609**	0.2694 0.1930	0.1749 0.0838	0.2773 0.1592	0.2181 0.1452	-0.1524 -0.0665	0.1239 0.0806	-0.3057 -0.2058	0.290* 0.2330
NPPP	G P	-0.2673 -0.0723	0.2865 0.0586	0.1804 0.0549	-0.0838 -0.0312	0.4977 0.1591	**0.8440** **0.2976**	0.4871 0.0589	0.0498 0.0245	0.3344 0.1080	-0.2524 -0.0644	0.0340 0.0266	-0.1723 -0.0528	0.353* 0.364*
PL (cm)	G P	-0.0114 -0.0049	-0.03069 0.0050	-0.0051 0.0123	-0.0039 0.0032	-0.0273 0.0162	-0.0412 0.0138	**-0.0714** **0.0697**	-0.0318 0.0228	-0.0462 0.0297	-0.0055 0.0182	-0.0079 0.0020	0.0339 -0.0111	-0.292* -0.0328
NSPP	G P	-0.0394 0.0489	0.1124 -0.0863	-0.0322 -0.0275	0.0180 -0.0263	0.0946 -0.1023	0.0092 -0.0191	0.0694 -0.0758	**0.1559** **-0.2320**	-0.0057 -0.0022	-0.0007 0.0079	-0.0087 -0.0212	-0.1447 0.0898	-0.527** -0.1569
BY (g)	G P	-0.3886 -0.0705	-0.3758 -0.0004	0.2008 -0.0177	0.2415 0.0299	-0.5949 -0.1019	-0.4937 -0.0920	-0.8069 -0.1081	0.0458 -0.0024	**-1.2459** **-0.2534**	-0.1146 -0.0126	-0.4939 -0.0770	0.4164 0.0605	-0.0608 0.0923
DM	G P	-0.4082 -0.0082	0.1533 0.0224	-0.1414 -0.0075	0.1118 0.0088	0.2783 0.0192	0.2494 0.0226	-0.0639 -0.0272	0.0037 0.0036	-0.0767 -0.0052	**-0.8340** **-0.1043**	-0.0624 -0.0020	-0.0066 -0.0037	-0.303* -0.1621
HI %	G P	-0.2210 -0.0001	0.4217 -0.0378	0.1281 0.0188	0.2465 0.0154	0.2906 -0.0561	0.0431 -0.0174	0.1179 -0.0156	-0.0598 -0.0381	0.4249 -0.0235	0.0802 0.0035	**1.0718** **-0.0149**	-0.2637 0.0983	-0.2197 -0.0247
SI(g)	G P	-0.0189 0.0112	0.2723 -0.0088	-0.1136 -0.0088	-0.0428 -0.0120	0.2739 -0.0156	0.0836 -0.0062	0.1943 -0.0020	0.3799 -0.0064	0.1368 -0.0212	-0.0032 -0.0013	0.1007 **-0.0697**	**-0.4093** **0.0106**	-0.0679 -0.1449

DTFF: Days to fifty percent flowering, DTFP: Days to fifty percent pod setting, PH(cm): Plant Height(cm), NPB: Number of primary branches, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, PL: Pod length(cm), NSPP: Number of seeds per pod, BY: Biological yield(g), DM: Days to maturity, HI: Harvest index(%), SI: Seed index, SYPP: Seed yield per plant(g). G: Genotypic, P: Phenotypic.

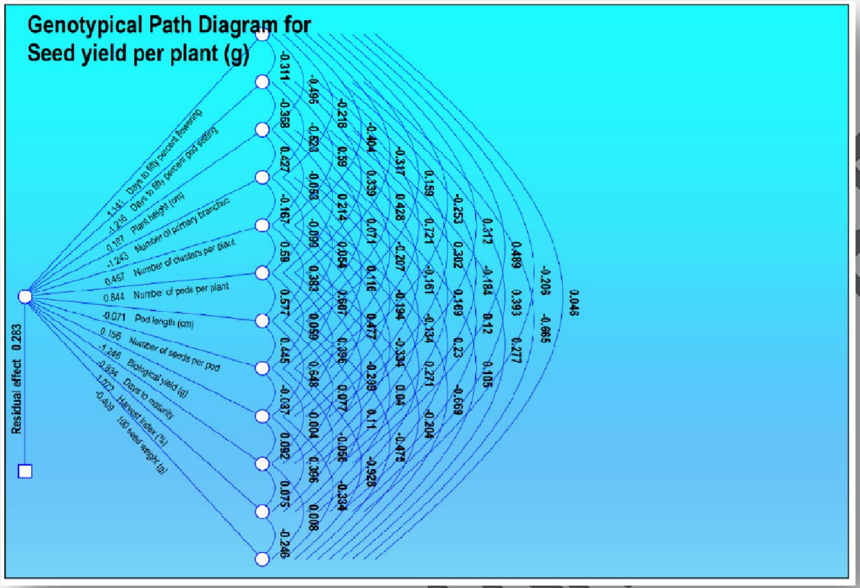


Fig.1a Genotypic path for yield contributing traits of blackgram

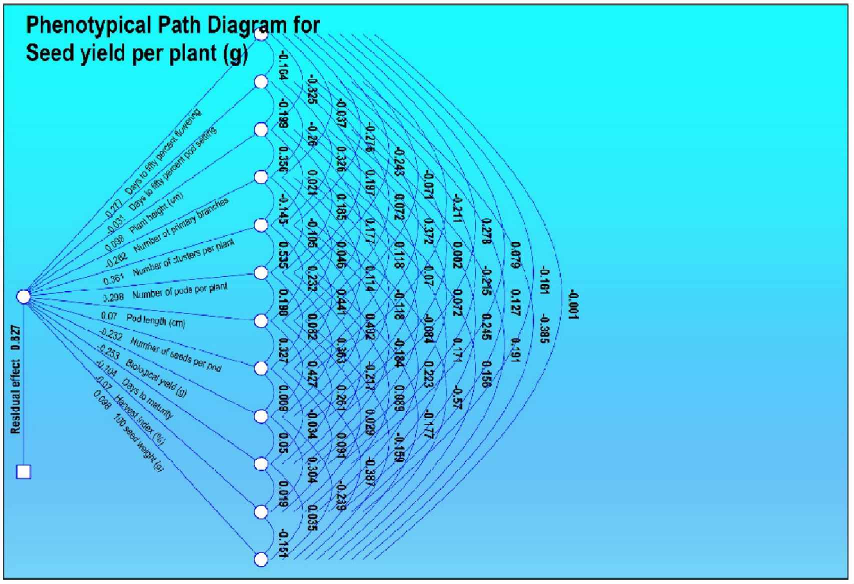


Fig.1b Phenotypic path for yield contributing traits of blackgram

Table 6: Total variance explain by different principal components in blackgram genotypes

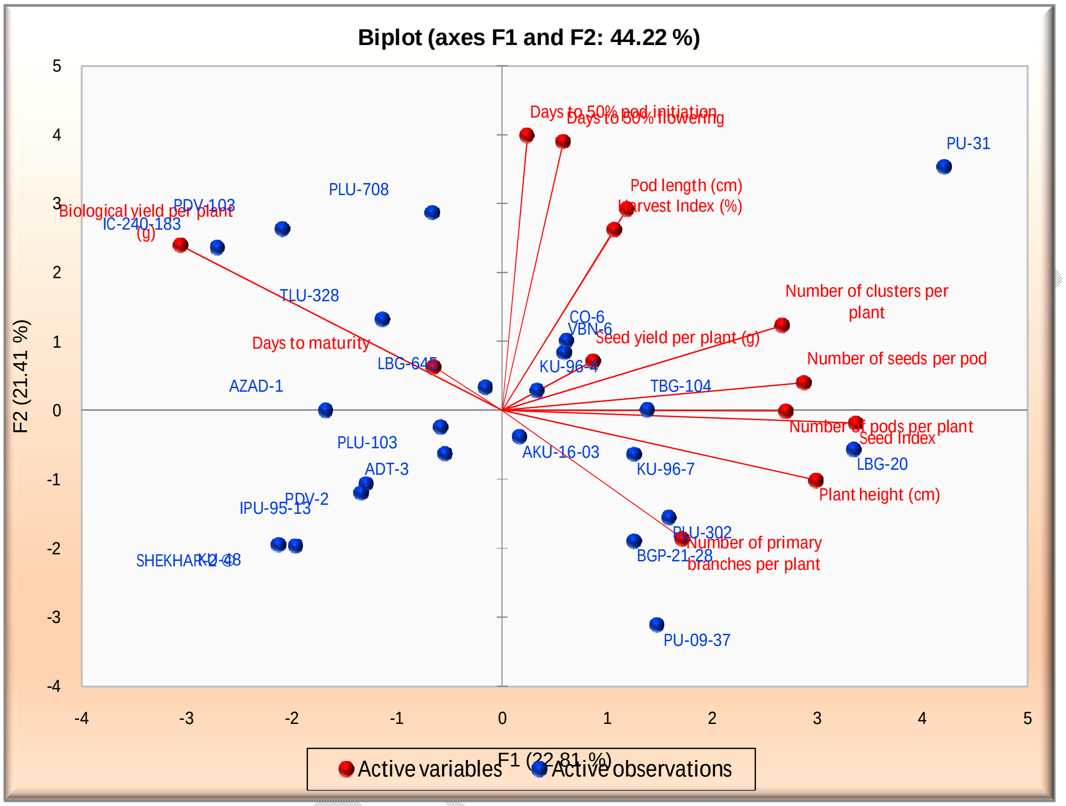
	Eigenvalue	Variability (%)	Cumulative %
PC1	2.965	22.808	22.808
PC2	2.783	21.410	44.218
PC3	2.033	15.642	59.860
PC4	1.472	11.325	71.185
PC5	1.234	9.489	80.674
PC6	0.805	6.191	86.865
PC7	0.596	4.588	91.453
PC8	0.513	3.945	95.398
PC9	0.263	2.025	97.423
PC10	0.201	1.544	98.968
PC11	0.092	0.708	99.676
PC12	0.041	0.319	99.995
PC13	0.001	0.005	100.000

Table 7: PCA Analysis of 13 traits of Blackgram genotypes during *Zaid*-2021

Sl.no.	Characteristics	PC1	PC2	PC3	PC4	PC5
1	Days to 50% flowering	0.1302	0.8442	0.2368	-0.258	0.1454
2	Days to 50% pod initiation	0.0535	0.8637	0.1839	-0.1015	-0.0472
3	Plant height (cm)	0.6682	-0.2188	0.3004	0.4407	0.0556
4	Number of primary branches per plant	0.3837	-0.4035	0.4215	0.2682	-0.1583
5	Number of clusters per plant	0.5957	0.2665	-0.4929	-0.2858	-0.0506
6	Number of pods per plant	0.6041	-0.0017	-0.4771	-0.2773	-0.4328
7	Pod length (cm)	0.2657	0.6322	-0.3578	0.4195	-0.2955
8	Number of seeds per pod	0.6421	0.0876	-0.4019	0.4108	0.0173
9	Days to maturity	-0.1445	0.1368	0.402	0.5082	-0.534

10	Biological yield per plant (g)	-0.683	0.5183	-0.1334	0.299	-0.0581
11	Harvest Index (%)	0.2392	0.5678	0.6099	-0.0371	0.0902
12	Seed index	0.7527	-0.0389	0.5389	-0.2626	0.1038
13	Seed yield per plant (g)	0.1938	0.1557	-0.2716	0.4561	0.7728

Fig 2: Distribution of 13 traits of Blackgram based on principal component PC1 and PC2



CONCLUSION

It is concluded from the present study that all the 23 genotypes of Blackgram showed significant differences among them. Genotypes LBG-645, IPU-95-13 and PDV-103 showed better performance for seed yield over the check (SHEKHAR-2). Number of clusters per plant, number of pods per plant exhibited high GCV, PCV and genetic parameters revealed that heritability and genetic advance as percent mean values are high for the number of clusters per plant and the number of pods per plant.Correlation coefficient analysis revealed that seed yield per plant exhibited a positive and significant association with the number of pods per plant at genotypic and phenotypic levels. Path coefficient analysis revealed that characters Days to 50% flowering, Number of pods per plant, and the number of clusters per plant have a positive direct effect on seed yield per plant at genotypic and phenotypic levels. It can also be concluded from the findings of principal component analysis that the highest PC values comprising three traits viz., Harvest Index, Plant height (cm), and Number of seeds per pod should be considered for genetic gain in blackgram genotypes. Genotypes PU-31, LBG-20, KU-96-7, and IPU-95-13 depicted a high PC score for characters Seed Index followed by Plant height (cm) and Number of seeds per pod. These characters can be given due consideration for further improvement and development of Blackgram .

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