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STUDIES ON THE COMPONENT APPROACH OF SELECTION IN BLACK GRAM [*Vigna mungo* (L.) HEPPER]

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ABSTRACT

The present investigation on variability, correlation, and path coefficient analysis for yield and yield attributing traits was conducted as a field experiment comprising 25 genotypes of black gram [*Vigna mungo* (L.) Hepper] during *Kharif*-2019. Among these characters Highest GCV and PCV and high estimates of heritability were recorded for the character number of pods per plant and number of pods per cluster (rg=0.579**, rp= 0.405**), number of seeds per pod (rg=0.369**, rp=0.410**), and biological yield (rg= 0.776**, rp= 0.613**) are highly significant and positively correlated with seed yield at both genotypic and phenotypic level. The highest positive direct effect on seed yield was recorded for plant height (0.8259) followed by harvest index (0.7132), number of pods per plant (0.6054), number of primary branches per plant (0.5908), days to maturity (0.5638), and biological yield (0.1975) at the genotypic level. While at the phenotypic level high positive direct effects were observed for harvest index (0.9518) followed by biological yield (0.2201), the number of clusters per plant (0.0583), days to maturity (0.0392), number pods per cluster (0.0317) and pod length (0.0215). Selections of these traits are expected to lead to positive results in the improvement of seed yield in the characters studied.

INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper] is an economically important short duration tropical pulse crop distinguished by comparatively more nutritious, appetizing, cheap source of superior quality and easily digestible protein, less flatulence than other legume crops (K.K.Panigrahi *et al.*,2014). It belongs to family Leguminosae and subfamily Papilionaceae having chromosome number 2n=2x=22 in its somatic cells with a small genome size of 0.56g/PC (574Mbp) (Gupta and Gopalakrishna, 2009). Elucidating the facts it is believed that the centre of origin of black gram is India. *Vigna radiate* var. sublobata is considered to be the probable progenitor of black gram (De Candolle, 1882, Vavilov, 1926 and Zukovskij,1962).

In India, black gram is grown over an area of 5.03 million hectares with an average production of 3.28 million tonnes (Ministry of Agriculture and Farmers Welfare, GOI, 2018). It is grown in different agro-ecological conditions and cropping systems with diverse cultural practices (Gupta *et al.*, 2001). besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dryland conditions (Parveen *et al.*, 2011). It is consumed in various forms Dehusked grains are used for the preparation of fermented foods such as idly, dosa, and non-fermented foods like cooked dhal, hopper, papad and waries (spicy hollow balls) (Batra and Millner,1974). Black gram occupies an important position due to its high seed protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins and the ability to restore the soil fertility through symbiotic nitrogen fixation.

Progress in any crop improvement program depends mainly on the degree of variability for the desired characters existing in the germplasm collection. Variability is the basic requirement for improving a particular trait on which greater emphasis should be given during selection (Singh *et al.*, 1981). Estimation of heritability along with genetic advance is more useful than heritability alone (Mesharam *et al.*, 2013 and Tulasi *et al.*,2016). Estimation of correlation, path coefficient analysis, heritability and genetic advance would be useful in developing appropriate breeding and selection strategies. Knowledge of variability, heritability, genetic advance and diversity of yield and yield component traits of black gram indicates the scope of improvement through selection (Deepalakshmi and Anandakumar, 2004). Path analysis identifies the yield components which directly and indirectly influence the yield (Rao, *et al.*, 2006). Therefore, genetic variability is the basic requirement for making progress in crop breeding (Appalaswamy and Reddy, 2004). Hence it is important to develop black gram cultivars with high seed yield coupled with stable performance across different environments through selection based on genetic parameters.

MATERIALS AND METHODS

The present investigation was carried out in Black gram [*Vigna mungo* (L.) Hepper] comprising of 25 blackgram genotypes. These genotypes were evaluated in Randomized Block Design with three replications during *kharif* 2019 at Field experimentation centre of the Department of Genetics and

Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P). Each plot consists of 3 rows consists of 10 plants with a spacing of 10 cm between the plants and 30cm between rows was maintained. Chemical fertilizers, at the rate of 20:40:20 NPK kg/ha were applied in the form of Urea, Di-ammonium phosphate (DAP) and Murate of potash (MOP) and other standard agronomical operation and plant protection measures were adapted to rise healthy and uniform crops.

The observations were recorded on a plot basis for traits like days to 50% flowering and days to maturity while data for plant height (cm), number of primary branches/ plant, number of clusters/plant, number of pods/plant, number of pods/cluster, number of seeds/pod, pod length (cm), 100 seed weight, biological yield/plant, harvest index and seed yield/plant were taken from five randomly selected plants from the middle of each row of each entry in each replication. After attaining physiological maturity, the plots were harvested manually. Mean values of different traits were subjected to Analysis of Variance (Fisher, 1936). The character association was estimated from variance and covariance components as per Al Jibouri, *et al*. (1958), GCV and PCV by Burton (1952), Heritability (h2)(Broad sense) by Burton and Devane (1953) and Genetic gain (genetic advance as percent of the mean) by Johnson *et al*.(1955). While the direct and indirect effects of components traits up on seed yield were measured by path analysis as described by Dewey and Lu, (1959).

RESULTS AND DISCUSSION

Analysis of variance revealed that significant differences were existed for the genotypes studied and it is represented in Table.1. The results revealed that the PCV was higher than the GCV for all traits under study which indicated that the environmental factors influencing the traits studied (Table 2). The present findings are in accordance with the findings of Panigrahi *et al*. (2014), Harish *et al*. (2018), Priya *et al*. (2018), Lenin *et al*. (2014). The estimated GCV and PCV helped in getting a clear understanding of the variability present among various genotypes. The high GCV was recorded for number of pods per plant (20.68 %) (Table 2) Vijay *et al*. (2015), Sathees *et al*. (2019), Hemalatha *et al*. (2107),Neelavathi and Govindarasu (2010) had also reported similar findings. Moderate GCV was observed for Biological yield (19.52 %), number of pods per cluster (19.51 %), number of clusters per plant (15.11 %), seed yield per plant (15.11 %), Harvest index (13.01%), number of primary branches per plant (11.15%), and number of seeds per pod (10.43 %). The present findings are in accordance with the findings of Harish *et al*. (2018), Lenin *et al*. (2014), and Vijay *et al*. (2015). The low GCV was recorded for hundred seed weight (8.58%), plant height (6.98%), pod length (6.25%), days to maturity (3.98%), and days to 50% flowering (3.28%). These results are in agreement with Panigrahi *et al*. (2014), Harish *et al*. (2018), Priya *et al*. (2018), Lenin *et al*. (2014).

The high PCV value was recorded for the number of pods per cluster (23.45), number of clusters per plant (22.62), number of pods per plant (21.64) (Table 2), biological yield (21.61). Patel *et al*. (2014), Nashra et al. (2018) and Hari *et al*. (2018) had also reported similar findings. Moderate PCV was observed for plant height (10.93%), hundred seed weight (11.49%), pod length (13.94%), number of primary branches per plant(17.01%),seed yield per plant (17.77%), number of seeds per pod (17.89%), harvest index (19.81%). These results are in accordance with results of Lenin *et al*. (2014), Hari *et al*. (2018), Harish *et al*. (2018) and Nashra *et al*. (2018).The PCV

Table1: Analysis of variance for 13 quantitative characters in 25 black gram genotypes.

Characters	Mean Sum of Squares		
	Replications (df=2)	Treatments (df=24)	Error (df=48)
Days to 50 % Flowering	11.25	10.26**	4.32
Days to maturity	2.28	33.66**	9.34
Plant Height	34.23	66.34**	21.58
Number of Branches per plant	0.05	0.63**	0.2
Number of Clusters per plant	5.86	6.34**	1.86
Number of Pods per plant	0.8	81.66**	2.5
Number of pods per cluster	0.13	1.05**	0.14
Number of seeds Per Pod	0.17	1.69**	0.67
Pod Length	0.09	0.65*	0.37
Hundred Seed Weight	0.03	0.35**	0.07
Biological Yield	7.52	29.39**	2.05
Harvest Index	4.89	80.26**	24.5
Seed Yield	0.42	1.91**	0.22

*,** Indicates Significant at 5% and 1% level of significance respectively.

Table : 2 Genetic Parameters for 13 quantitative characters of 25 black gram genotypes.

Character	Genotypic Coefficient of variation	Phenotypic Coefficient of variation	Heritability (Broad sense) %	Genetic advance	Genetic advance as % mean
Days to 50 % flowering	3.28	5.851	31.421	1.625	3.787
Days to maturity	3.982	5.84	46.491	4	5.593
Plant height	6.989	10.931	40.885	5.088	9.206
No. of Primary branches /Plant	11.158	17.011	43.028	0.52	15.078
No. of clusters per plant	15.115	22.627	44.623	1.683	20.8
No. of pods per plant	20.686	21.645	91.337	10.113	40.725
No. of pods per clusters	19.512	23.455	69.206	0.95	33.439
No. of seeds per pod	10.43	17.893	33.978	0.704	12.524
Pod length	6.256	13.943	20.133	0.283	5.783
100 Seed weight	8.583	11.492	55.784	0.467	13.206
Biological yield	19.525	21.613	81.609	5.618	36.335
Harvest index	13.014	19.815	43.137	5.833	17.608
Seed yield	15.111	17.771	72.304	1.319	26.469

Table 3: Genotypic and Phenotypic correlation coefficients among the eleven characters of black gram

Characters		Days to 50% flowering	Days to Maturity	Plant height	No. of primary branches/ plant	No. of clusters per plant	No. of pods per plant	No. of pods per clusters	No. of seeds per pod	Pod length	100seed weight	Biological yield	Harvest Index	Seed Yield
Days to 50% flowering	P	1	0.338**	-0.033NS	0.028NS	-0.049NS	0.026NS	0.027NS	0.222NS	0.140NS	0.094NS	0.035NS	-0.126NS	-0.058NS
	G	1	0.429**	-0.242*	-0.225*	-0.027NS	0.018NS	0.238*	0.965**	0.157NS	-0.135NS	0.163NS	-0.307**	0.049NS
Days to Maturity	P		1	-0.016NS	0.055NS	-0.039NS	-0.230*	-0.155NS	0.249*	0.172NS	0.197NS	0.158NS	-0.354**	-0.131NS
	G		1	-0.537**	-0.121NS	-0.119NS	-0.333**	0.007NS	0.753**	0.059NS	0.209NS	0.239*	-0.831**	-0.314**
Plant height	P			1	0.071NS	0.224NS	0.102NS	0.194NS	-0.131NS	0.036NS	-0.117NS	-0.025NS	0.119NS	0.094NS
	G			1	0.428**	0.477**	0.260*	0.476**	-0.340**	-0.434**	-0.174NS	-0.001NS	0.264*	0.207NS
No. of Primary branches /Plant	P				1	-0.037NS	0.139NS	0.135NS	-0.140NS	-0.266*	-0.164NS	-0.096NS	0.088NS	-0.038NS
	G				1	-0.008NS	0.211NS	0.420**	-0.512**	-0.718**	-0.270*	-0.143NS	0.051NS	-0.128NS
No. of clusters per plant	P					1	0.278*	0.217NS	-0.192NS	0.217NS	-0.022NS	0.125NS	0.107NS	0.332**
	G					1	0.426**	0.452**	-0.571**	0.337**	-0.078NS	0.226*	0.257*	0.552**
No. of pods per plant	P						1	0.427**	-0.195NS	-0.148NS	-0.230*	0.192NS	0.118NS	0.405**
	G						1	0.518**	-0.229*	-0.256*	-0.274*	0.241*	0.150NS	0.497**
No. of pods per clusters	P							1	-0.148NS	-0.117NS	-0.370**	0.063NS	0.240*	0.377**
	G							1	-0.420**	-0.361**	-0.541**	0.025NS	0.634**	0.579**
No. of seeds per pod	P								1	0.254*	0.012NS	0.178NS	-0.363**	0.410**
	G								1	0.088NS	0.212NS	0.262*	-0.565**	0.369**
Pod length	P									1	0.246*	0.088NS	-0.188NS	-0.056NS
	G									1	0.441**	0.111NS	0.078NS	0.187NS
100seed weight	P										1	0.131NS	-0.165NS	-0.072NS
	G										1	0.192NS	-0.361**	-0.085NS
Biological yield	P											1	-0.648**	0.613**
	G											1	-0.707**	0.776**
Harvest Index	P												1	0.177NS
	G												1	-0.102NS
Seed Yield	P													1
	G													1

*,** Indicates Significant at 5% and 1% level of significance respectively. P – Phenotypic correlation coefficient; G – Genotypic correlation coefficient

Table : 4 Direct and indirect effect of thirteen characters on seed yield in black gram at genotypic level.

Characters at genotypic level	Days to 50% flowering	Days to Maturity	Plant height	No. of pri mary bran ches/ plant	No. of clusters per plant	No. of pods per plant	No. of pods per clusters	No. of seeds per pod	Pod length	100seed weight	Biological yield	Harvest I ndex	Seed Yield
Days to 50% flowering	-0.7371	0.242	-0.1996	-0.1329	0.0233	0.0107	0.0421	0.4958	0.2494	0.0794	0.1949	-0.2191	0.049NS
Days to Maturity	-0.3164	0.5638	-0.4438	-0.0715	0.1035	-0.2016	0.0012	0.3868	0.0931	-0.1225	0.286	-0.5925	-0.314**
Plant height	0.1781	-0.3029	0.8259	0.2531	-0.4141	0.1573	0.084	-0.1744	-0.6896	0.1022	-0.0009	0.1885	0.207NS
No. of primary branches/plant	0.1658	-0.0682	0.3539	0.5908	0.0073	0.1275	0.0742	-0.2629	-1.1404	0.1588	-0.1711	0.0361	-0.128NS
No. of clusters per plant	0.0198	-0.0672	0.394	-0.005	-0.8681	0.2582	0.0799	-0.2931	0.5346	0.0459	0.2702	0.1831	0.552**
No. of pods per plant	-0.013	-0.1877	0.2146	0.1244	-0.3702	0.6054	0.0915	-0.1174	-0.4073	0.161	0.2885	0.1071	0.497**
No. of pods per clusters	-0.1755	0.0037	0.3928	0.2483	-0.3924	0.3137	0.1767	-0.2155	-0.573	0.3176	0.0304	0.4525	0.579**
No. of seeds per pod	-0.7116	0.4246	-0.2804	-0.3025	0.4954	-0.1384	-0.0741	0.5136	0.1404	-0.1245	0.3142	-0.4026	0.369**
Pod length	-0.1157	0.033	-0.3586	-0.4241	-0.2922	-0.1553	-0.0637	0.0454	0.5884	-0.2589	0.1331	0.0553	0.187NS
100seed weight	0.0997	0.1177	-0.1438	-0.1597	0.0678	-0.166	-0.0955	0.1089	0.7005	-0.5872	0.2304	-0.2574	-0.085NS
Biological yield	-0.12	0.1347	-0.0006	-0.0844	-0.1959	0.1459	0.0045	0.1347	0.1766	-0.113	0.1975	-0.5043	0.776**
Harvest Index	0.2264	-0.4684	0.2183	0.0299	-0.2229	0.0909	0.1121	-0.2899	0.1231	0.2119	-0.8467	0.7132	-0.102NS

Residual are 0.06663;NS- Non- Significant;*,** Indicates Significant at 5% and 1% level of significance respectively

Table 5: Direct and indirect effect of thirteen characters on seed yield in black gram at phenotypic level.

Characters at Phenotypic level	Days to 50% flo wering	Days to Maturity	Plant height (cm)	No. of primary branches / plant	No. of clusters per plant	No. of pods per plant	No. of pods per clusters	No. of seeds per pod	Pod length (cm)	100seed weight (g),	Biological yield (g)	Harvest Index (%)	Seed Yield
Days to 50% flowering	0.0172	0.0133	0.0007	-0.0006	-0.0029	0.0006	0.0009	-0.0068	0.003	-0.0072	0.0429	-0.1195	-0.058NS
Days to Maturity	0.0058	0.0392	0.0003	-0.0012	-0.0023	-0.0051	-0.0049	-0.0077	0.0037	-0.015	0.1934	-0.3371	-0.131NS
Plant height (cm)	-0.0006	-0.0006	-0.021	-0.0016	0.013	0.0023	0.0062	0.004	0.0008	0.0089	-0.0309	0.1133	0.094NS
No. of primary branches/plant	0.0005	0.0022	-0.0015	-0.0224	-0.0022	0.0031	0.0043	0.0043	-0.0057	0.0125	-0.1171	0.0839	-0.038NS
No. of clusters per plant	-0.0009	-0.0015	-0.0047	0.0008	0.0583	0.0062	0.0069	0.0059	0.0047	0.0017	0.1523	0.1023	0.332**
No. of pods per plant	0.0005	-0.009	-0.0021	-0.0031	0.0162	0.0222	0.0135	0.006	-0.0032	0.0175	0.2346	0.1119	0.405**
No. of pods per clusters	0.0005	-0.0061	-0.0041	-0.003	0.0127	0.0095	0.0317	0.0046	-0.0025	0.0282	0.0769	0.2289	0.377**
No. of seeds per pod	0.0038	0.0098	0.0028	0.0031	-0.0112	-0.0043	-0.0047	-0.0308	0.0055	-0.0009	0.2172	-0.3456	0.410**
Pod length (cm)	0.0024	0.0068	-0.0008	0.006	0.0126	-0.0033	-0.0037	-0.0078	0.0215	-0.0188	0.1077	-0.1787	-0.056NS
100seed weight (g),	0.0016	0.0077	0.0024	0.0037	-0.0013	-0.0051	-0.0117	-0.0004	0.0053	-0.0762	0.1594	-0.1574	-0.072NS
Biological yield (g)	0.0006	0.0062	0.0005	0.0022	0.0073	0.0043	0.002	-0.0055	0.0019	-0.01	0.2201	-0.617	0.613**
Harvest Index (%)	-0.0022	-0.0139	-0.0025	-0.002	0.0063	0.0026	0.0076	0.0112	-0.004	0.0126	-0.7909	0.9518	0.177NS

Residual are 0.04218;NS- Non significant;*,** Indicates Significant at 5% and 1% level of significance respectively was low for the rest of the characters like Days to maturity (5.84%) and days to 50 % flowering (5.85%) the results are in agreement with Nitesh *et al*. (2019), Awnindra *et al*. (2014), Shilpa *et al*. (2020) and Nashra *et al*. (2018).

An estimate of heritability is a good index for predicting the transmission of characters from parents to their offspring (Falconer, 1981). The estimates of heritability (%) in the broad sense for 13 characters studied (Table 2), which ranged from 20.133 to 91.337%. High heritability (broad sense) (>60%) was recorded for character number of pods per plant (91.337%), number of pods per clusters (69.206%), Biological yield (g) (81.206%) and Seed yield per plant (g) (72.304%). Moderate heritability (broad sense) (30-60%) was recorded for characters *i.e.* days to 50% flowering (31.421%), days to maturity (46.491%), plant height (cm) (40.885%), number of primary branches per plant (43.028%). number of clusters per plant (44.623%), number of seeds per pod (33.978%),100-seed weight (55.784%) and harvest index (43.137%). Low heritability (broad sense) (<30%) was recorded for pod length (cm) (20.133%) only. These findings are in accordance with Rajasekhar *et al*. (2017), Gowsalya *et al*. (2016) and Harish *et al*. (2018).

Genetic advance predicts the genetic gain under selection. Genetic advance as a percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because its estimated value is derived by the involvement of heritability, phenotypic standard deviation and intensity of selection. Genetic advance as % of mean varied from 3.787 to 40.725 (Table 2). High genetic advance as % mean (>20%) was recorded for the number of clusters per plant (20.8%), Number of pods per plant (40.725%), Number of pods per clusters (33.439%), Biological yield (g) (36.335%), Seed yield per plant (g) (26.469%). Moderate genetic advance as % mean (10-20%) was recorded for Number of primary branches/plant (15.078%), Number of seeds per pod (12.524%) and 100seed weight (g), (13.206%) and Harvest Index (%) (17.608). Low genetic advance as % mean (<10%) was recorded for days to 50% flowering (3.787%), days to maturity (5.593%), plant height (cm) (9.206%), and pod length (cm) (5.783%). Similar findings were reported by Vijay *et al*. (2015), Nashra *et al*. (2018), Gowsalya *et al*. (2016) and Harish *et al*. (2018). Number of pods per plant , number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, biological yield (g), harvest index (%) and seed yield per plant(g) showed high heritability coupled with high genetic advance as percent of mean pointing towards these results are in agreement with Shilpa *et al*. (2020) and Hari *et al*. (2018).

The genotypic and phenotypic correlation coefficients were computed among 13 characters (Table 3). This indicated an inherent association between various traits. In the present investigation, seed yield per plant was found a negative and significant correlation with days to maturity (-0.314**) at the genotypic level. It also had a negative and significant correlation with days to 50 % flowering at the phenotypic level also. Seed yield per plant exhibited positive and significant correlation with the number of clusters per plant (0.552**), number of pods per plant (0.497**),number of pods per cluster (0.579**), seeds per pod (0.369**) and biological yield per plant (0.776**) at both genotypic and phenotypic levels. While with rest of the characters seed yield has a non-significant association. Similar results were also obtained by Patel *et al*. (2014), Rajasekhar *et al*. (2017), Tufran khan *et al*. (2020), Manish and Hemlata (2017) and Bharti *et al*. (2013)

Path coefficient analysis is a statistical technique to split the observed coefficient into direct and indirect effects of independent variables on the dependent variable. In the present

study path coefficient analysis was carried out using genotypic (Table 4) and phenotypic correlation (Table 5) matrix of 13 characters. Path analysis revealed that In the present investigation, the highest positive direct effect on grain yield was recorded for plant height followed by harvest index, the number of pods per plant, number of primary branches per plant, days to maturity, biological yield and 100-seed weight at genotypic level (Table 4). While at phenotypic level (Table 5) high positive direct effects were observed for harvest index followed biological yield, number of clusters per plant, days to maturity, pods per cluster, pod length and 100-seed weight. The negative direct effect of number of clusters per plant was high followed by days to 50% flowering and 100 seed weight at genotypic level. While at phenotypic level high negative direct effects were observed for 100seed weight, Number of seeds per pods and number of primary branches per plant. These are in accordance with findings of Gopinath *et al*. (2018), Shilpa *et al*. (2018), Isha praveen *et al*. (2011), Bharti *et al*. (2013) Nitish *et al*. (2019) and Sathya *et al*. (2018). Thus, the yield was mainly affected by the direct and indirect effects through days to maturity, the number of clusters per plant, number of pods per cluster, 100-seed weight, biological yield per plant and harvest index.

CONCLUSION

From the present investigation, some of the inferences were derived like isolation of superior genotypes with good quality is possible amongst the genotypes studied. Based on correlation studies, five-component characters viz., Biological yield, number of pods per cluster, number of clusters per plant, number of pods per plant and seeds per pod proved to be the major yield attributing traits in that order. Path analysis revealed that harvest index, days to maturity and biological yield were the major characters having a positive direct effect on seed yield per plant at genotypic and phenotypic levels. Further selection for grain yield based on biological yield, number of pods per cluster, number of pods per plant and seeds per pod exhibited maximum gain in the desired direction. It is expected therefore, these characters should be given priority during selection for yield improvement in black gram.

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