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Correlation and path analysis in m_4 generation of Blackgram [*Vigna mungo* (L.) Hepper]

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Abstract
The present investigation was carried out in a set of 72 M_4 mutants of blackgram. The progenies employed in the present investigation were derived from parents PU 1 and CO 6 with three doses of physical mutagen (gamma rays) *viz*., 200 Gy, 400 Gy and 600 Gy. The experiment was conducted at the Agronomy farm, S.K.N. College of Agriculture, Jobner during *kharif*, 2021. Mutants were evaluated in augmented randomized block design with four blocks during *kharif*, 2021. The significant positive correlation with seed yield per plant was found in pods per plant, branches per plant, seeds per pod, pods per cluster, plant height, pod length, clusters per plant and days to 50% flowering. While it was positive and non-significant with days to maturity and protein content. Path analysis revealed that branches per plant, pods per plant, seeds per pod and plant height were effective for the selection of high yielding mutants as they exhibited high positive direct effect along with significant positive correlation with seed yield per plant. It was suggested that the selection of higher yielding blackgram genotypes may be helpful on the basis of performance and Germplasm may be used for mutation programme.

Keywords: Blackgram, physical mutagen, gamma rays, correlation and path analysis

Introduction
Blackgram [*Vigna mungo* (L.) Hepper] is a self-pollinated diploid grain legume which belongs to the family Fabaceae and sub- family Papilionaceae with chromosome number 2n=22 (Arumuganathan and Earle, 1991; Sarvani *et al.*, 2020) [3, 13]. Indian subcontinent is the centre of origin of blackgram (Zukovskiji, 1962) [17]. It is popularly known as blackgram, urdbean and *urd* or mash. Blackgram is a rich source of protein (25-28%), carbohydrates (62-65%), fiber (3.5-4.5%), ash (4.5-5.5%), oil (0.5- 1.5%), amino acids mainly lysine, vitamins like thiamine, niacin, riboflavin and much needed iron and phosphorus (Sohel *et al.*, 2016) [16]. The dried seeds are used to make dal, soups, curries and added to various spiced or fried dishes (Sarvani *et al.*, 2020) [13].

Blackgram can be grown throughout the year and adjust well into many cropping systems. It is mostly cultivated as a fallow crop after rice cultivation in India. Both local and international requirements for blackgram are exalted. This crop also plays a vital role in harbouring soil fertility by ameliorating soil physical properties and fixing atmospheric nitrogen. Being a drought resistant crop, suitable for dry land farming and principally used as an inter-crop with other crops (Gomathi *et al.*, 2020a) [6].

India is the largest producer of blackgram with 70 per cent of the world's production. It is the fourth most important pulse crop in India covering an area of about 41 lakh ha, but producing only 22.90 lakh tonnes and thus productivity comes to only 538 kg/ha during 2020-21 (Anonymous, 2021) [1]. The average of last five-year area, production and productivity of blackgram crop in India is 48 lakh ha, 27.5 lakh tonnes and 567 kg/ha, respectively. More than 90 per cent of blackgram production comes from nine states *viz*., Madhya Pradesh, Andhra Pradesh Uttar Pradesh, Maharashtra, Tamil Nadu, Rajasthan, Jharkhand, Gujarat and Karnataka (Anonymous, 2021) [1]. In Rajasthan, blackgram crop accounts 4.25 lakh ha area, 1.56 lakh tonnes of production with a productivity of 366 kg/ha during 2021-22. The average of last five-year area, production and productivity of blackgram crop in Rajasthan is 5.99 lakh ha, 2.97 lakh tonnes and 476 kg/ha, respectively. It is mainly grown in Bundi, Tonk, Sawai Madhopur, Bhilwara, Baran, Kota, Ajmer and Jhalawar districts of Rajasthan (Anonymous, 2022) [2].

The inter-relationship between seed yield and its important components is effectively predicted by correlation and path coefficient analysis. These techniques are used in the crop improvement programmes to exploit the yield potential for enhancing the productivity of the blackgram and to develop high yielding improved varieties. Correlation coefficient estimates degree of association of different component characters of yield among themselves and with the yield. When there is a positive correlation between major yield components, breeding strategies would be very effective but, on the reverse, selection becomes very difficult.

Materials and Methods

The experiment was conducted at Agronomy Farm, S.K.N. College of Agriculture, Jobner during *kharif*, 2021. The experimental material consisted of 72 mutant (M_3) lines of blackgram variety Pratap Urd 1 and CO 6 obtained from the Department of Plant Breeding and Genetics, Sri Karan Narendra College of Agriculture, Jobner. The experimental material consisting of 72 M_3 lines and check variety *viz.*, PU1, CO6, MU 2, TPU 4, KU 96-3 were evaluated in Augmented randomized block design sown on 19th July during *kharif*, 2021. Each genotype was sown in a plot of 4 meter length and width 0.60 meter accommodating two rows spaced at 30 cm apart. The plant to plant distance was maintained as 10 cm. All the agronomical practices were followed to raise a good and healthy crop.

Correlation and path analysis were analyzed as proposed by Johnson *et al*. (1955b) [7] and Dewey and Lu, (1958) [5], respectively.

Results and Discussion

Correlation Coefficient Analysis

The correlation between all possible combinations among the characters was estimated at genotypic and phenotypic levels and is presented in tables 1 and 2, respectively. The results of present research showed that pods per plant, branches per plant, seeds per pod, pods per cluster, plant height, pod length, clusters per plant and days to 50% flowering were observed positive and significant with seed yield per plant, while it was positive and non-significant with days to maturity and protein content. Both the genotypic and phenotypic correlations were in the similar direction, although the levels of genotypic correlation coefficients were superior in extent than the corresponding phenotypic correlation coefficient. This low degree of phenotypic correlation may be due to effect of the environment on the phenotype of the plants. The similar results are also demonstrated earlier by Punia *et al*. (2014) [11], Asari *et al*. (2019) [4], Sathees *et al*. (2019) [14] and Partap *et al*. (2019) [10].

Path Coefficient Analysis

The grain yield is reliant on numerous yield related traits. Minor alteration in any one yield character will eventually disquiet the complex. Therefore traits has to be study for its action namely direct effect of yield related attributes on grain yield and also the indirect effects through other yield related traits on grain yield. Hence characters associations were separated into direct and indirect effects and given in (Table 3 & 4).

The path analysis revealed that branches per plant, pods per plant, seeds per pod and plant height were effective for the selection of high yielding mutants as they exhibited high positive direct effect along with significant positive correlation with seed yield per plant. Similar results were earlier reported by Ranjeet *et al.* (2018) [12], Partap *et al.* (2019) [10], Senthamizhselvi *et al.* (2019) [15] and Khan *et al.* (2020) [8] and Mishra and Lavanya (2021) [9].

Table 1: Correlation coefficients between different characters in M_4 generation of blackgram at genotypic level

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	1.000	0.011	-0.024	0.402**	0.234*	-0.008	0.372**	0.253*	0.176	0.149	0.299*	0.357**
Days to maturity		1.000	0.024	0.123	0.179	0.090	0.224	0.382**	0.113	0.090	0.167	0.137
Plant height (cm)			1.000	0.326**	0.484**	0.416**	0.384**	0.229	0.062	0.476**	-0.098	0.432**
Branches per plant				1.000	0.392**	0.455**	0.931**	0.419**	0.421**	0.312**	0.051	0.951**
Clusters per plant					1.000	0.236*	0.402**	0.299*	0.147	0.337**	0.041	0.388**
Pods per cluster						1.000	0.458**	0.074	0.248*	-0.064	-0.071	0.462**
Pods per plant							1.000	0.492**	0.468**	0.369**	0.102	0.953**
Pod length (cm)								1.000	0.207	0.216	0.184	0.410**
Seeds per pod									1.000	0.119	0.004	0.514**
100-seed weight (g)										1.000	-0.042	0.379**
Protein content (%)											1.000	0.042

* significant at P = 0.05 and ** significant at P = 0.01

Table 2: Correlation coefficients between different characters in M_4 generation of blackgram at phenotypic level

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	1.000	-0.079	-0.312**	0.131	0.072	-0.203	0.077	0.047	0.113	0.058	0.184	0.106
Days to maturity		1.000	0.005	0.034	0.113	0.048	0.091	0.295*	0.079	0.102	0.112	0.070
Plant height (cm)			1.000	0.340**	0.443**	0.240*	0.385**	0.158	-0.019	0.467**	-0.105	0.401**
Branches per plant				1.000	0.344**	0.414**	0.937**	0.304**	0.371**	0.352**	-0.014	0.954**
Clusters per plant					1.000	0.163	0.311**	0.210	0.120	0.386**	0.039	0.358**
Pods per cluster						1.000	0.392**	-0.114	0.207	-0.119	-0.072	0.386**
Pods per plant							1.000	0.296*	0.420**	0.403**	-0.010	0.971**
Pod length (cm)								1.000	0.156	0.277*	0.131	0.324**

Seeds per pod									1.000	0.131	0.004	0.473**
100-seed weight (g)										1.000	0.057	0.414**
Protein content (%)											1.000	0.035

* significant at P = 0.05 and ** significant at P = 0.01

Table 3: Path coefficient between different characters in M_4 generation of blackgram at genotypic level

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Protein content (%)	Correlation with seed yield per plant (g)
Days to 50% flowering	-0.00244	-0.00007	-0.00338	0.20754	-0.01067	0.00034	0.16004	-0.01382	0.02027	0.0005	-0.00108	0.357**
Days to maturity	-0.00003	-0.00602	0.00338	0.06356	-0.00815	-0.00382	0.09611	-0.02087	0.01304	0.0003	-0.0006	0.137
Plant height (cm)	0.00006	-0.00014	0.14176	0.16837	-0.02207	-0.0176	0.16505	-0.01253	0.00713	0.0016	0.00035	0.432**
Branches per plant	-0.00098	-0.00074	0.04621	0.5165	-0.01788	-0.01924	0.40017	-0.02288	0.04852	0.00105	-0.00018	0.951**
Clusters per plant	-0.00057	-0.00108	0.06854	0.20226	-0.04565	-0.00999	0.1729	-0.01631	0.01697	0.00113	-0.00015	0.388**
Pods per cluster	0.00002	-0.00054	0.05896	0.23487	-0.01078	-0.04232	0.19678	-0.00403	0.02856	-0.00021	0.00026	0.462**
Pods per plant	-0.00091	-0.00135	0.05443	0.48083	-0.01836	-0.01937	0.42985	-0.02687	0.05397	0.00124	-0.00037	0.953**
Pod length (cm)	-0.00062	-0.0023	0.03253	0.21643	-0.01364	-0.00312	0.2115	-0.05461	0.0239	0.00073	-0.00067	0.410**
Seeds per pod	-0.00043	-0.00068	0.00877	0.21753	-0.00672	-0.01049	0.20137	-0.01133	0.11521	0.0004	-0.00002	0.514**
100-seed weight (g)	-0.00036	-0.00054	0.06754	0.16092	-0.0154	0.00269	0.15854	-0.0118	0.01371	0.00336	0.00015	0.379**
Protein content (%)	-0.00073	-0.001	-0.01387	0.02622	-0.00188	0.003	0.04405	-0.01005	0.00049	-0.00014	-0.00362	0.042

Residual effect = 0.03918, **significant at P = 0.01

Table 4: Path coefficient between different characters in M_4 generation of blackgram at phenotypic level

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Seeds per pod	100-seed weight (g)	Protein content (%)	Correlation with seed yield per plant (g)
Days to 50% flowering	0.0078	0.0008	-0.0207	0.0505	0.0009	0.0035	0.0417	0.0005	0.0118	0.0003	0.0089	0.106
Days to maturity	-0.0006	-0.0100	0.0003	0.0131	0.0015	-0.0008	0.0490	0.0032	0.0082	0.0005	0.0054	0.070
Plant height (cm)	-0.0024	-0.0001	0.0662	0.1316	0.0057	-0.0041	0.2071	0.0017	-0.0019	0.0022	-0.0051	0.401**
Branches per plant	0.0010	-0.0003	0.0225	0.3866	0.0044	-0.0071	0.5036	0.0033	0.0388	0.0017	-0.0007	0.954**
Clusters per plant	0.0006	-0.0011	0.0294	0.1331	0.0128	-0.0028	0.1674	0.0023	0.0125	0.0018	0.0019	0.358**
Pods per cluster	-0.0016	-0.0005	0.0159	0.1599	0.0021	-0.0172	0.2107	-0.0012	0.0216	-0.0006	-0.0035	0.386**
Pods per plant	0.0006	-0.0009	0.0255	0.3621	0.0040	-0.0067	0.5376	0.0032	0.0439	0.0019	-0.0005	0.971**
Pod length (cm)	0.0004	-0.0030	0.0104	0.1174	0.0027	0.0020	0.1590	0.0108	0.0163	0.0013	0.0063	0.324**
Seeds per pod	0.0009	-0.0008	-0.0012	0.1436	0.0015	-0.0036	0.2258	0.0017	0.1044	0.0006	0.0002	0.473**
100-seed weight (g)	0.0005	-0.0010	0.0309	0.1360	0.0050	0.0020	0.2167	0.0030	0.0137	0.0048	0.0027	0.414**
Protein content (%)	0.0014	-0.0011	-0.0070	-0.0053	0.0005	0.0012	-0.0056	0.0014	0.0004	0.0003	0.0482	0.035

Residual effect = 0.02833, **significant at P = 0.01

Conclusion

From the inference of current investigation it can be concluded that the correlation and path analysis showed that most of the traits such as branches per plant, pods per plant, seeds per pod and pods per cluster were positively significant with seed yield per plant indicating that selection based on these characters may result in high seed yield. All these above traits correlate with seed yield significantly and positively at both genotypic as well as phenotypic level. Whereas path analysis also suggests that these traits had the positive and direct effect on the grain yield.

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