Correlation and Path Coefficient Studies in Blackgram

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ABSTRACT

The present investigation was undertaken with 40 blackgram germplasm to study the character associations and path effects for yield, yield components and quality characters. The results on character associations revealed positive and significant association of seed yield per plant with plant height, number of clusters per plant, number of pods per plant and hundred seed weight indicating the scope for improvement of yield through selection of these traits. In contrast, negative and significant correlation of seed yield per plant was noticed with the yield component traits, pod length, number of seeds per pod and seed protein content, both at phenotypic and genotypic levels, indicating the need for balanced selection, for simultaneous improvement of these traits. Further, number of clusters per plant, number of pods per plant and pod length had high and positive direct effects on seed yield per plant, indicating the importance of these traits in effective selection criteria for improvement of seed yield per plant and development of high yielding blackgram genotypes.

Blackgram (*Vigna mungo* (L.) Hepper) is the third important pulse crop grown in all seasons viz., *kharif*, *rabi* and *summer* in India. It contains 24% protein, 60% carbohydrates, 1.3% fat and is the richest source of phosphoric acid (5-6% richer than other) among all the pulses . India is the largest producer as well as consumer of blackgram in the world. In India blackgram occupies an area of 56.02 lakh hectares producing 30.60 lakh tons with a productivity of 546 kg/ha (www.indiagristat.com, 2018-19). In Andhra Pradesh, it occupies an area of 3.18 lakh ha, with a production and productivity of 3.10 lakh tons and 977 kg/ha, respectively (www.indiagristat.com, 2018-19).The crop productivity is very low in blackgram (Kiran and Lal, 2021). Hence, there is a strong need to improve the crop productivity to meet increasing demand. However, seed yield is a complex trait governed by several component characters. In this context, correlation studies give an idea about the contribution of different characters towards seed yield and reveal the type, nature and magnitude of association between yield components with seed yield and among themselves, aiding in effective selection. Further, path analysis identifies the yield components which directly and indirectly influence the seed yield. The present investigation was undertaken in this direction with the objective of assessing the correlation coefficients and path coefficients in order to identify and formulate effective selection criteria for evolving of high yielding genotypes.

MATERIAL AND METHODS

The experimental material consisted of 40 blackgram genotypes obtained from Agricultural Research Station, Ghantasala; Regional Agricultural

Research Station, Lam Farm, Guntur; and Regional Agricultural Research Station, Tirupati, Andhra Pradesh State in addition to collections from G. B. Pant University of Agricultural Sciences and Technology, Pantnagar and National Pulses Research Centre, Vamban. All the 40 blackgram genotypes were sown at Agricultural College Farm, Bapatla during *Rabi* 2020-21 in Randomized Complete Block Design in three replications. Each genotype was sown in 6 rows of 4 meters length with a spacing of 30 cm × 10 cm. All the recommended package of practices were followed to raise a good crop. Observations were recorded for days to 50 per cent flowering, days to maturity, plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, seed protein content and seed yield per plant. Data for quantitative traits were recorded from five randomly selected plants and the mean was taken for analysis. The traits, days to 50 % flowering and days to maturity were recorded on plot basis. For protein content, the nitrogen content in each sample was estimated by Microkjeldahl method and seed protein content of each sample was estimated as per the procedure described by Sadasivam and Manickam (1992). Standard statistical procedures were used for the analysis of correlation coefficient values (r) at genotypic and phenotypic levels using the procedures detailed by Johnson *et al.* (1955) and described by Singh and Choudhary (1985). Path coefficient analysis was utilized to partition the phenotypic and genotypic correlation coefficients into direct and indirect effects of the yield contributing traits on seed yield. The analysis was carried out as per the procedures suggested by Wright (1921) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

Correlation coefficient is a statistical measure used to find out the degree and direction of relationship between two or more variables. The results on correlation analysis between seed yield, yield components and seed protein content obtained in the present study are presented in Table 1. A perusal of these results revealed phenotypic and genotypic correlations to be of similar direction and significance. Further, positive and significant association of seed yield per plant was hoted with yield component traits, *viz.*, plant height (r_p=0.6852**, r_g= 0.7174**), number of clusters per plant (r_p=0.8108**, r_g= 0.8426**), number of pods per plant (r_p=0.6594**, r_g= 0.6761**) and hundred seed weight (r_p=0.284**, r_g= 0.3062**) both at phenotypic and genotypic levels, respectively indicating the scope for improvement of seed yield through selection of these traits. These results are in agreement with the reports of Sridhar *et al.* (2020) for number of clusters per plant, plant height and hundred seed weight and Teja and Lal (2021) for number of pods per plant. In contrast, negative and significant correlation of seed yield per plant was noticed with the yield component traits, pod length (r_p= -0.3419**, r_g= -0.3798**), number of seeds per pod (r_p= -0.3727**, r_g= -0.4164**) and seed protein content (r_p=-0.4029**, r_g= -0.4222**) both at phenotypic and genotypic levels. These findings are in agreement with the reports of Ranjeet *et al.* (2018) for pod length, and Tank and Sharma (2019) for seed protein content. The occurrence of negative association between the traits could be due to competition for a common causes such as nutrient supply, indicating the need for balanced selection simultaneous improvement of these traits.

Significant positive correlations were also noticed for days to 50 % flowering with days to maturity (Hadimani *et al.*, 2019), hundred seed weight (Rajasekhar *et al.*, 2017) and plant height (Teja and Lal 2021); days to maturity with plant height (Reddy *et al.,* 2020) and hundred seed weight (Kyaw *et al.*,

2017); plant height with number of clusters per plant (Sushmitaraj *et al.*, 2018), seed yield per plant (Sridhar *et al.*, 2020), number of pods per plant (Mesfin, 2018) and hundred seed weight (Ragul *et al.*, 2018); number of clusters per plant with number of pods per plant (Teja and Lal 2021), hundred seed weight (Ragul *et al.*, 2018) and number of seeds per pod with hundred seed weight (Rajasekhar *et al.*, 2017). These results revealed a scope for simultaneous improvement of these traits. In contrast, significant negative correlations were also noticed for days to 50 % flowering with pod length days to maturity with pod length and number of seeds per pod plant height with pod length (Reddy *et al.,* 2020), number of seeds per pod (Reddy *et al.,* 2020) and seed protein content; number of clusters per plant with pod length (Teja and Lal 2021), number of seeds per pod and seed protein content; number of pods per plant with pod length (Reddy *et al.,* 2020) and seed protein content; pod length with seed yield per plant (Teja and Lal 2021); number of seeds per pod with seed protein content (Lad *et al.,* 2017) and seed yield per plant (Hadimani *et al.,* 2019); and seed protein content with seed yield per plant (Tank and Sharma 2019), similar to the reports of earlier workers. These results revealed a need for balanced selection, for simultaneous improvement of these traits.

Days to 50 per cent flowering recorded non-significant association with number of pods per plant, seed protein content and seed yield per plant both at phenotypic and genotypic levels for number of pods per plant; Lad *et al.* (2011) for seed protein content; Tank and Sharma *et al.* (2019) for seed yield per plant. Further, days to maturity recorded non-significant association with number of clusters per plant, number of pods per plant, seed yield per plant and seed protein content at phenotypic and genotypic levels, respectively. Similar results were reported by Teja and Lal (2021) for number of clusters per plant;

Reddy *et al.* (2020) for number of pods per plant; Ranjeet *et al.* (2018) for seed yield per plant; and Lad *et al.* (2011) for seed protein content. In addition, non-significant associations were also observed between number of pods per plant with hundred seed weight; pod length with hundred seed weight and seed protein content; and hundred seed weight with seed protein content.

The path coefficient analysis of yield components on seed yield per plant are presented in Table 2 and Fig. 1 and 2. A perusal of these results revealed a residual effect of 0.51(Phenotypic) and 0.446 (Genotypic) indicating that the characters included in the present investigation accounted for only 49 per cent phenotypic and 55 per cent genotypic variability observed for seed yield per plant High and positive direct effects were observed for number of clusters per plant (Yadav and Gangwar, 2020), number of pods per plant (Kiran and Lal 2021), hundred seed weight (Baig *et al.*, 2017) and plant height (Partap *et al.,* 2020) on seed yield per plant in the present study, similar to the results of earlier workers. These traits also recorded high positive and significant correlation with seed yield per plant indicating the effectiveness of direct selection for these traits in improvement of seed yield per plant. However, moderate to negligible or negative direct effects were noticed for pod length (Ranjeet *et al.*, 2018), days to 50% per cent flowering (Kiran and Lal 2021), days to maturity (Partap *et al.,* 2020), number of seeds per pod (Jyothsna *et al.*, 2016) and seed protein content (Lad *et al.,* 2011) indicating the role of indirect effects as the cause of correlation.

Considering the nature and magnitude of character associations and their direct and indirect effects, it is inferred that, plant height, number of clusters per plant, number of pods per plant and hundred seed weight are useful in formaing a selection criteria for effecting improvement of seed yield per

Table 1. Phenotypic and genotypic correlations for seed yield per plant and yield components and quality character in blackgram

Character	r	DFF	DM	PH	NCPP	NPPP	PL	NSPP	HSW	SPC	SYPP
DFF	r_p		0.8100**	0.3254**	0.1736	0.0824	-0.2186*	-0.1603	0.4011**	0.0815	0.0817
	r_g		0.8988**	0.3407**	0.1827*	0.0833	-0.2266 *	-0.1711	0.4319**	0.0841	0.0879
DM	r_p			0.2798**	0.147	0.1092	-0.2303*	-0.2119*	0.2296*	0.0646	0.0871
	r_g			0.3153**	0.1549	0.1124	-0.2623**	-0.2588**	0.2381**	0.0783	0.0834
PH	r_p				0.7427 **	0.5857**	-0.2118*	-0.1867	0.4522**	-0.450**	0.6852**
	r_g				0.7815**	0.6097**	-0.2348**	-0.2256*	0.4991**	-0.4723**	0.7174**
NCPP	r_p					0.6672**	-0.3858**	-0.3417**	0.4280**	-0.3396**	0.8108**
	r_g					0.6829**	-0.4096**	-0.3778**	0.456**	-0.359**	0.8426**
NPPP	r_p						-0.5266**	-0.1746	0.1253	-0.4453**	0.6594**
	r_g						-0.5567**	-0.1943*	0.1314	-0.4633**	0.6761**
PL	r_p							0.6110**	0.1294	-0.0299	-0.3419**
	r_g							0.6792**	0.1475	-0.029	-0.3798**
NSPP	r_p								0.2407**	-0.2007*	-0.3727**
	r_g								0.2680**	-0.2212*	-0.4164**
HSW	r_p									-0.0998	0.284**
	r_g									-0.1106	0.3062**
SPC	r_p										-0.4029**
	r_g										-0.4222**

*, ** Significant at 5% and 1% levels, respectively; r_p = Phenotypic correlation and r_g = Genotypic correlations

DFF-Days to fifty percent flowering, **DM**-Days to maturity, **PH**-Plant height, **NCPP**-Number of clusters per plant, **NPPP**-Number of pods per plant, **PL**-Pod length, **NSPP**-Number of seeds per pod, **HSW**-Hundred seed weight, **SPC**-Seed protein content, **SYPP**-Seed yield per plant

Table 2. Path analysis of yield components and quality characters on seed yield per plant in blackgram

Character		DFF	DM	PH	NCPP	NPPP	PL	NSPP	HSW	SPC	SYPP
DFF	P	-0.092	-0.075	-0.03	-0.016	-0.008	0.02	0.015	-0.037	-0.008	0.082
	G	-0.058	-0.052	-0.02	-0.011	-0.005	0.013	0.01	-0.025	-0.005	0.088
DM	P	-0.009	-0.011	-0.003	-0.002	-0.001	0.002	0.002	-0.002	-0.001	0.087
	G	-0.056	-0.063	-0.02	-0.01	-0.007	0.017	0.016	-0.015	-0.005	0.083
PH	P	0.037	0.032	0.114	0.084	0.067	-0.024	-0.021	0.051	-0.051	0.685**
	G	0.002	0.001	0.004	0.003	0.003	-0.001	-0.001	0.002	-0.002	0.717**
NCPP	P	0.075	0.063	0.319	0.43	0.287	-0.166	-0.147	0.184	-0.146	0.811**
	G	0.065	0.055	0.278	0.356	0.243	-0.146	-0.135	0.162	-0.128	0.843**
NPPP	P	0.022	0.029	0.154	0.175	0.263	-0.138	-0.046	0.033	-0.117	0.659**
	G	0.03	0.041	0.22	0.247	0.361	-0.201	-0.07	0.048	-0.167	0.676**
PL	P	-0.03	-0.031	-0.029	-0.052	-0.071	0.135	0.083	0.018	-0.004	-0.342**
	G	-0.055	-0.064	-0.057	-0.099	-0.135	0.242	0.165	0.036	-0.007	-0.380**
NSPP	P	0.049	0.065	0.058	0.105	0.054	-0.188	-0.308	-0.074	0.062	-0.373**
	G	0.086	0.13	0.113	0.189	0.097	-0.341	-0.501	-0.134	0.111	-0.416**
HSW	P	0.04	0.023	0.045	0.042	0.012	0.013	0.024	0.099	-0.01	0.284**
	G	0.091	0.05	0.105	0.096	0.028	0.031	0.057	0.211	-0.023	0.306**
SPC	P	-0.011	-0.008	0.058	0.044	0.057	0.004	0.026	0.013	-0.129	-0.403**
	G	-0.017	-0.015	0.092	0.07	0.091	0.006	0.043	0.022	-0.196	-0.422**

Residual effect = 0.51 (**P**= Phenotypic) and 0.446 (**G**= Genotypic); *, ***Significant at 5% and 1% levels, respectively; Diagonal bold values indicate direct effects

DFF-Days to fifty percent flowering, **DM-**Days to maturity, **PH-**Plant height, **NCPP-**Number of clusters per plant, **NPPP-**Number of pods per plant, **PL-**Pod length, **NSPP-**Number of seeds per pod, **HSW-**Hundred seed weight, **SPC-**Seed protein content, **SYPP-**Seed yield per plant
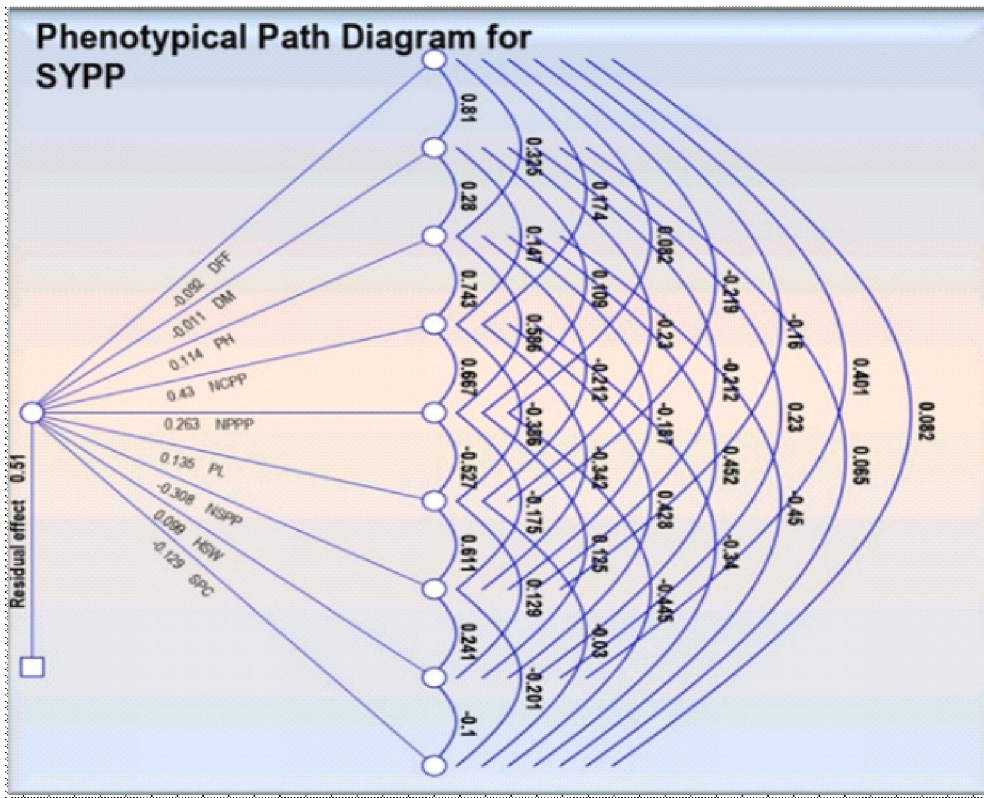
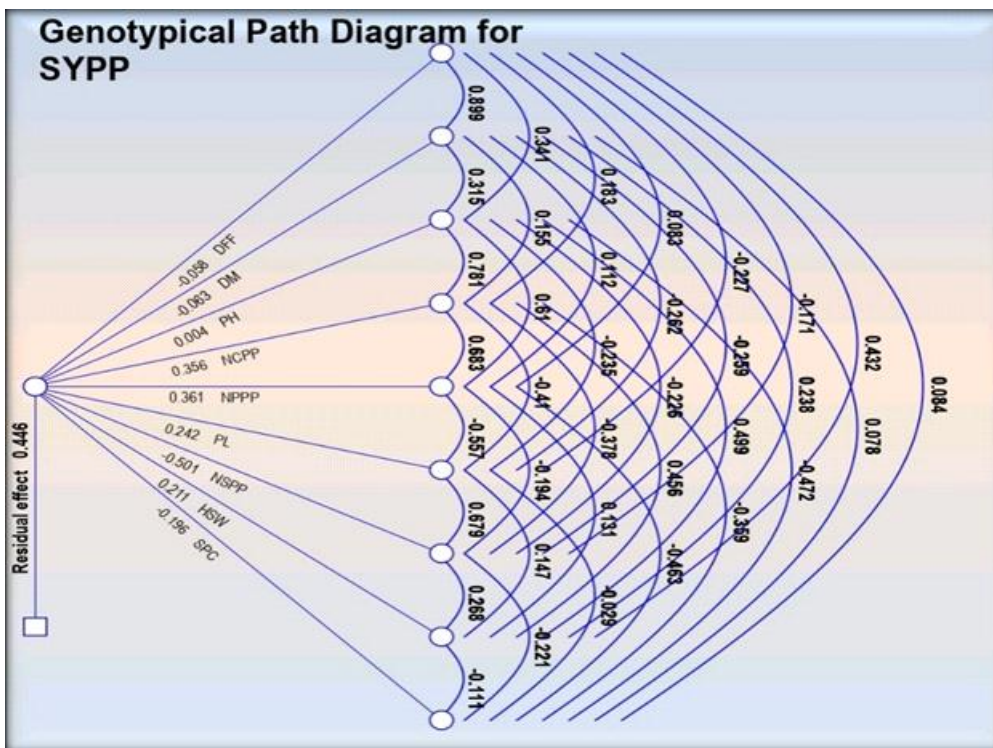**Fig 1. Phenotypic path diagram for seed yield per plant in blackgram**

Fig 2. Genotypic path diagram for seed yield per plant in blackgram

DFF-Days to fifty percent flowering**, DM-**Days to maturity**, PH-**Plant height**, NCPP-**Number of clusters per plant**, NPPP-**Number of pods per plant**, PL-**Pod length**, NSPP-**Number of seeds per pod**, HSW-**Hundred seed weight**, SPC-**Seed protein content**, SYPP-**Seed yield per plant

plant in blackgram and useful for the development of high yielding genotypes of blackgram.

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