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PATH COEFFICIENT ANALYSIS IN BLACKGRAM*

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ABSTRACT

Variability, heritability and genetic advance were estimated for sixteen characters in twenty blackgram (Urd) types. phenotypic and genotypic coefficient of variation for dry leaf weight was high followed by seed yield and leaf area. Genetic advance was high for seed yield followed by dry leaf weight. Seed yield per plant showed significant positive correlation with all the characters except number of primary branches, specific leaf weight and protein per cent. path coefficient analysis revealed plant height and primary leaf area had higher positive direct effect on seed yield and 100 seed weight recorded highest negative direct effect on seed yield.

INTRODUCTION

Yield improvement of any crop can be achieved by developing superior varieties by altering the genetic make up of the existing varieties. For this, information on genetic variability existing in the material chosen will facilitate the improvement knowledge on association of grain yield with yield components will help the breeder to formulate the selection criteria for improving the yield of blackgram. With this objective, the present investigation was undertaken to determine the correlation and direct and indirect association among the yield

attributes through path coefficient analysis.

MATERIALS AND METHODS

Twenty genotypes of blackgram were raised in a randomized block design with three replications during summer, 1984 at Millet Breeding Station, Agricultural College and Research Institute, Coimbatore. Each genotype was sown in a row of 3 m long spaced at 45 cm apart. Plant to plant distance was maintained at 30 cm. Observations were recorded on five randomly selected plants for sixteen characters (Table - 1) and were subjected to analysis of variance and covariance as suggested by Panse

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and Sukhatme (1961). Mean performance of the twenty genotypes were presented in Table -2. Path coefficient analysis was conducted according to the method of Dewey and Lu (1959).

RESULTS AND DISCUSSION

Estimation of genotypic (GCV) and Phenotypic (PCV) coefficient of variation is necessary for comparing the extent of variability of different populations. In this study high GCV and PCV were obtained for dry leaf weight, seed yield,

leaf area and primary branches (Table-3). Veerasamy et.al. (1973). Singh et.al. (1975), Muthiah (1976) and Patel and Shah (1982) reported similar results. High heritability estimates were recorded for peduncle length, petiole length and plant height. Seed yield, dry leaf weight and leaf area recorded highest estimates of genetic advance. These results are in corroboration with the findings of Veeraswamy et. al. (1973), Singh et.al. (1975), and Soundarapandian et.al. (1975)

Table - I

	Character	Abbreviation in	
		Text	Tables
1.	Primary leaf ares		PLA
2.	Leaf area at 50 per cent flowering	Leaf area	LAF
3.	Plant height	-	
4.	Number of primary branches	Primary branches	PBS
5.	Petiole length	-	PTL
6.	Peduncle length	-	PDL
7.	Dry leaf weight at 50 % flowering	Dry leaf weight	DLW
8.	Total dry matter production at 50% flowering	Total DMP	DMP
9.	Specific leaf weight	-	SLW
10.	Leaf Area Index	LAI	LAI
11.	Length of the pod	pod length	POL
12.	Number of seeds per pod	Seeds per pod	NSP
13.	Number of pods per plant	Pods per plant	NPP
14.	100 seed weight	-	HSW
15.	Protien per cent	-	PRP
16.	Seed yield	-	SYD

Table : 2 Mean performance of the genotypes of blackgram

Sl. No.	Genotype	PLA	LAF	PLH	PBS	PTL	PDL	DLM	DMP	SLM	LAI	POL	NPP	NSP	HSW	PRP	SYD
1.	CO 5	14.24	1058.54	28.51	3.33	10.31	11.91	3.06	9.80	0.0034	352.85	4.81	20.00	6.33	5.45	23.43	23.43
2.	TMV.1	12.09	606.44	18.91	2.33	7.92	8.80	1.93	4.71	0.0035	202.15	4.76	17.00	6.67	4.77	22.50	5.20
3.	T 9	8.23	334.10	14.65	2.67	7.55	7.37	4.70	8.81	0.0030	111.26	4.23	14.33	6.00	3.92	23.67	3.40
4.	M 12/3	8.48	1101.27	30.89	3.33	10.68	9.06	3.98	7.59	0.0036	367.09	4.78	22.00	6.33	4.90	23.47	7.55
5.	CLM	8.12	542.04	19.80	2.00	3.46	4.83	2.13	4.96	0.0039	180.68	4.45	8.33	6.33	4.68	25.00	1.69
6.	SLM	5.83	781.54	28.20	6.00	6.06	8.48	2.93	6.18	0.0038	260.51	3.04	18.67	4.67	3.33	26.70	1.42
7.	H-10	18.07	104.95	36.73	3.00	11.75	11.49	4.30	9.95	0.0046	337.32	4.95	22.33	5.67	5.38	23.73	5.73
8.	CCO 2/23	11.65	712.80	18.27	2.00	7.63	8.12	2.42	7.09	0.0034	319.74	4.27	22.67	6.33	4.33	20.13	4.49
9.	Ettawa Black	13.44	1124.08	31.37	3.67	10.85	11.78	3.81	10.10	0.0035	374.70	4.73	19.00	6.67	4.83	21.60	3.63
10.	Lam BG 295	14.63	1087.77	30.85	3.67	10.13	11.90	3.60	9.12	0.0035	362.62	5.07	15.67	6.67	4.90	25.37	4.12
11.	Bhuvanagiri	11.16	1368.71	33.87	2.67	10.96	12.44	4.82	10.38	0.0035	476.24	5.10	15.67	7.67	5.80	19.70	3.53
12.	UG 135	11.84	361.54	14.11	1.33	5.91	7.10	1.43	4.36	0.0041	120.51	4.21	10.33	5.33	4.73	22.00	2.80
13.	K 78	14.12	858.03	21.73	4.00	9.39	8.90	2.65	5.49	0.0030	286.01	4.37	15.67	6.00	4.72	24.03	3.29

14.	Agra Black	14.28	1309.87	37.17	4.33	11.16	10.32	4.89	10.20	0.0036	436.62	5.11	25.33	7.00	5.65	23.23	6.12
15.	UG 153	11.57	479.67	16.52	2.00	8.00	7.24	0.81	4.56	0.0022	159.82	3.98	11.33	5.33	4.08	22.63	2.12
16.	VZM 189/63	14.86	962.97	31.78	3.00	10.75	9.85	4.03	9.25	0.0042	320.99	4.89	12.33	6.33	5.82	21.40	4.81
17.	VZM 189/8	14.28	870.25	24.47	2.67	9.33	11.08	3.37	8.57	0.0038	290.08	5.12	11.67	6.67	5.32	26.03	4.00
18.	PLS 364/43	14.07	832.76	30.01	3.00	10.48	10.78	3.85	5.11	0.0044	277.59	4.93	16.00	6.33	5.47	23.30	2.46
19.	Trichy	14.27	1241.85	29.91	3.33	11.70	11.85	7.13	8.13	0.0041	413.95	4.88	21.33	6.67	5.22	21.47	4.44
20.	Anaipurathan	14.18	831.17	22.91	3.33	8.08	10.01	2.92	6.22	0.0037	275.94	4.68	16.00	6.00	5.23	23.87	4.21
	Mean	12.47	828.52	26.03	3.08	9.11	9.67	3.47	7.53	0.0036	296.33	4.62	16.78	6.25	4.93	23.16	3.93

Table : 3 Parameters of variability and heritability in Blackgram.

Sl. No.	Character	Range	Mean	Phenotypic Variance	Genotypic Variance	PCV Per cent	GCV Per cent	PCV-GCV	Heritability %	Genetic advance as Percentage of mean.
1.	PLA	5.83 - 21.08	20.47	20.41	10.56	26.06	22.25	3.81	72.92	23.85
2.	LAF	334.10 - 1368.70	873.64	120146.00	75328.80	39.67	32.51	8.15	62.70	51.25
3.	PLH	14.11 - 37.17	25.35	62.96	50.06	30.28	27.00	3.27	79.51	51.27
4.	PBS	1.33 - 6.00	3.05	1.46	0.81	39.62	29.66	9.96	55.48	45.28
5.	PTL	3.46 - 11.75	9.10	5.56	4.61	25.91	23.59	2.32	82.91	44.26
6.	PDL	4.83 - 12.44	9.68	4.92	4.19	22.90	21.15	1.75	85.16	40.20
7.	DLW	0.81 - 7.13	3.64	6.30	2.61	68.91	44.38	24.52	41.43	58.85
8.	DMP	4.36 - 10.38	7.52	7.50	3.24	36.39	23.90	12.48	43.20	32.41
9.	SLM	0.0022 - 0.0046	0.0036	0.00	0.00	18.48	12.19	6.29	43.60	16.58
10.	LAI	111.26 - 476.24	295.32	13443.30	8190.25	39.26	30.64	8.61	60.92	49.27
11.	POL	3.04 - 5.12	4.61	0.29	0.23	11.73	10.45	1.27	79.31	19.09
12.	NPP	8.33 - 25.33	16.78	24.82	19.55	29.68	26.35	3.33	78.77	48.18
13.	NSP	4.67 - 7.67	6.25	0.66	0.31	13.07	8.95	4.11	46.97	12.58
14.	HSW	3.33 - 5.82	4.92	0.50	0.38	14.35	12.53	1.82	76.00	22.50
15.	PRP	19.70 - 26.70	23.16	3.83	3.03	8.45	7.51	0.93	79.11	13.77
16.	SYD	1.42 - 7.55	3.93	2.93	1.96	43.56	35.61	7.95	66.89	60.01

Table 4: Phenotypic (P) and Genotypic (G) correlation coefficients among the sixteen characters of Blackgram.

Characters	LAF	PLH	PBS	PTL	PDL	DLW	DMP	SLM	LAI	POL	NPP	NSP	HSW	PRP	SYD
PLA	P 0.35**	0.39**	0.01	0.59**	0.56**	0.24	0.29*	0.22	0.33**	0.59**	0.17	0.31*	0.65**	-0.09	0.26*
	G 0.46**	0.44**	-0.07	0.69**	0.65**	0.23	0.41**	0.40**	0.46**	0.73**	0.23	0.27*	0.73**	-0.24	0.42**
LAF	P 0.75**	0.32	0.32	0.66**	0.68**	0.47**	0.68**	0.18	0.98**	0.50**	0.51**	0.45**	0.46**	-0.15	0.46**
	G 0.99**	0.56**	0.56**	0.88**	0.91**	0.74**	0.74**	0.35**	0.98**	0.64**	0.65**	0.76**	0.76**	-0.22	0.51**
PLH	P 0.47**	0.47**	0.47**	0.70**	0.71**	0.41**	0.57**	0.35**	0.71**	0.47**	0.46**	0.29*	0.54**	0.01	0.33**
	G 0.56**	0.56**	0.56**	0.79**	0.77**	0.61**	0.83**	0.60**	0.95**	0.54**	0.57**	0.50**	0.64**	-0.03	0.52**
PBS	P 0.16	0.32*	0.32*	0.16	0.32*	0.17	0.24	0.07	0.29*	-0.16	0.38**	-0.04	-0.08	0.35**	-0.02
	G 0.29*	0.39**	0.39**	0.29*	0.37**	0.34**	0.34**	0.07	0.51**	-0.28	0.47**	-0.25*	-0.17	0.52**	-0.06
PTL	P 0.82**	0.44**	0.44**	0.82**	0.82**	0.44**	0.49**	0.13	0.64**	0.58**	0.50**	0.38**	0.59**	-0.24	0.48**
	G 0.88**	0.74**	0.74**	0.88**	0.88**	0.74**	0.85**	0.26*	0.86**	0.71**	0.61**	0.59**	0.68**	-0.35**	0.67**
PDL	P 0.40**	0.40**	0.40**	0.40**	0.40**	0.40**	0.54**	0.19	0.66**	0.57**	0.45**	0.38**	0.56**	-0.12	0.28*
	G 0.68**	0.68**	0.68**	0.68**	0.68**	0.68**	0.87**	0.34**	0.88**	0.64**	0.48**	0.62**	0.63**	-0.19	0.39**
DLW	P 0.49**	0.28*	0.28*	0.49**	0.49**	0.28*	0.49**	0.28*	0.46**	0.34**	0.30	0.30*	0.27*	-0.16	0.26*
	G 0.58**	0.41**	0.41**	0.58**	0.58**	0.41**	0.58**	0.19	0.71**	0.44**	0.60**	0.54**	0.45**	-0.26*	0.37**
DMP	P 0.19	0.68**	0.68**	0.19	0.68**	0.43**	0.19	0.19	0.68**	0.43**	0.33**	0.38**	0.32	-0.15	0.42**
	G 0.12	0.73**	0.73**	0.12	0.73**	0.61**	0.12	0.12	0.73**	0.61**	0.59**	0.67**	0.61**	-0.18	0.47**
SLM	P 0.16	0.23	0.23	0.16	0.23	0.09	0.09	0.09	0.16	0.23	0.09	-0.01	0.30*	-0.01	0.18
	G 0.34**	0.39**	0.39**	0.34**	0.39**	0.19	0.19	0.19	0.34**	0.39**	0.19	0.12	0.62**	0.08	0.20
LAI	P 0.48**	0.56**	0.56**	0.48**	0.56**	0.44**	0.44**	0.56**	0.48**	0.48**	0.56**	0.44**	0.42**	-0.21	0.47**
	G 0.61**	0.72**	0.72**	0.61**	0.72**	0.61**	0.61**	0.72**	0.61**	0.61**	0.72**	0.79**	0.73**	-0.29*	0.53**
POL	P 0.16	0.69**	0.69**	0.16	0.69**	0.16	0.16	0.16	0.16	0.69**	0.16	0.69**	0.77**	-0.20	0.48**
	G 0.18	0.92**	0.92**	0.18	0.92**	0.18	0.18	0.18	0.18	0.92**	0.18	0.92**	0.96**	-0.28*	0.63**
NPP	P 0.16	0.12	0.12	0.16	0.12	0.12	0.12	0.16	0.16	0.12	0.16	0.16	0.12	-0.15	0.60**
	G 0.21	0.14	0.14	0.21	0.14	0.20	0.20	0.21	0.21	0.14	0.21	0.21	0.14	-0.20	0.61**
NSP	P 0.59**	-0.26*	-0.26*	0.59**	-0.26*	-0.26*	-0.26*	-0.26*	0.59**	-0.26*	-0.26*	-0.26*	0.59**	-0.26*	0.32*
	G 0.75**	-0.54**	-0.54**	0.75**	-0.54**	-0.54**	-0.54**	-0.54**	0.75**	-0.54**	-0.54**	-0.54**	0.75**	-0.54**	0.50**
HSW	P -0.19	-0.41**	-0.41**	-0.19	-0.41**	-0.41**	-0.41**	-0.41**	-0.19	-0.41**	-0.41**	-0.41**	-0.19	-0.41**	0.34**
	G -0.20	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.20	-0.23	0.52**
PRP	P -0.20	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.20	-0.23	0.52**
	G -0.20	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.23	-0.20	-0.23	-0.23	-0.23	-0.20	-0.23	0.52**

In general, genotypic correlation coefficient were higher than phenotypic correlation coefficient which is in agreement with the reports of Patel and Shah (1982). Seed yield per plant (Table - 4) showed significant and positive correlations (both phenotypic and genotypic) with all the characters except primary branches, specific leaf weight and protein per cent. Similar results were expressed by Premsagar and Lal (1979) and Sambasiva Rao et.al. (1983). A knowledge among the yield components will provide more reliable estimation in identifying very useful combination. The inter-correlation estimated for the yield components showed leaf area, primary leaf area, petiole length, peduncle length, total DMP, LAI and pod length were significantly and positively associated with each other.

Path Coefficient analysis revealed that plant height exerted maximum direct effect on seed yield followed by primary leaf area, 100 seed weight and maximum negative direct effect on seed yield followed by peduncle length.

The residual effect observed in path analysis was 0.46 indicating that some of the important components contributing to the seed yield have not been involved in this analysis.

Petiole length, total DMP, LAI, pod length, seed per pod and 100 seed weight have shown high magnitude of positive correlation with seed yield and intercorrelation among themselves, selection can perhaps be based on these characters for effecting improvement in seed yield.

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