

Original Research Article

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Parent Progeny Regression and Correlation Analysis in Segregating Population of Black Gram (*Vigna mungo* (L.) Hepper)

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ABSTRACT

In the present investigation, nine crosses of black gram (*Vigna mungo* L.) were evaluated in F₂ and F₃ generations for the effective selection for yield and yield components. The segregating generation of the crosses included were PU 06-20 x VBN 4, IPU 2006-01 x ADT3, IPU 2006-01 x VBN 4, IPU 2006-01 x TNY LOCAL, IPU 02-33 x VBN 4, IPU 02-33 x VBN 4, IPU 02-33 x TNY LOCAL, WBG 26 x VBN 3, MASH 114 x VBN 3 and MASH 114 x TNY LOCAL. One way of ascertaining the influence of environment on different characters is parent-progeny regression. In the present study all characters exhibited non-significant both positive and negative direction. This indicated that there is no relationship between F₂ values and its progeny mean.

Keywords

Black gram,
Correlation
and Regression.

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Introduction

Black gram is also called as urd bean and black lentil. It is an important multipurpose grain legume extensively cultivated in arid, semi-arid and subtropics. Black gram is photo insensitive in nature and can be cultivated throughout the year. Black gram fits well in different cropping system as it is relatively drought tolerant. It is also grown as catch crop, mulch crop inter crop, mixed crop and green crop. Jayamani *et al.*, (2012) reported that about 70 percent of the total pulse production area is in the central and southern parts of the country and this contributes about more than 77 per cent of the total production. To evolve new black gram varieties, recombination breeding has been recognized as successful method by plant breeders. This

involves a systemic pedigree selection initiated in the F₂ which exhibits a wide range of variation. Selection made on F₂ based on grain yield is insufficient, since the single plant yield is the result of cumulative effect of both genotype and environment. Selection is effective only if the performance of F₃ lines is more dependable than that of F₂ performance. Hence it is necessary to evaluate that how far the F₂ values have bearing on F₃ mean and whether such parameter relied upon selection. Its real genetic potentiality can be ascertained by only the progeny performance of the individual selection, since the mean of progeny is more reliable estimate than, individual values of selected parents. One way of ascertaining the influence of environment

on different characters is parent-progeny regression (Lush, 1940).

Materials and Methods

The material for the present study was generated at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute (TNAU) Killikulam. Nine high yielding cross combinations were selected from the F_1 generation of the previous study based single plant yield along with the VBN 4 variety as the check.

The experiment was laid out in homogenous block following randomized block design (RBD) with three replications. The spacing between the rows was 30 cm and spacing between the individual plants was 10 cm. Recommended agronomic practices were followed to raise the crop.

Observations on 8 quantitative characters were recorded. The correlation and regression coefficient values were estimated by using the statistical methods suggested by Lush (1940).

Results and Discussion

In the present study all characters exhibited non-significant both positive and negative direction (Table 1). This indicated that there is no relationship between F_2 values and its progeny mean. MC Ginnis and Shebeski (1968) also obtained non - significant correlation between F_2 and F_3 reported that on this basis alone, there was no advantage in selecting F_2 plants for high yield.

The absence of relationship between F_2 and F_3 indicates that the interference of non-additive components is very considerable, and hence the scheme of selection should be postponed to later generations. The selected trait, single plant yield exhibits non-significant positive

correlation observed in pods per cluster, number of pods per plant, number of seeds per pod and 100 seed weight such positive correlation and regression between F_2 and F_3 indicates that it is possible to exercise selection effectively in a wide population (Singh and Alie, 2009).

The trait plant height exhibited non-significant positive values for all the crosses where as WBG 26 x VBN 3 showed non- significant negative values for single plant yield, seeds per pod, pods per plant and pod length.

The unselected characters or traits non-significant and positive correlation values were recorded for plant height and clusters per plant in all the crosses. The trait plant height exhibited non-significant positive values for all the crosses where as WBG 26 x VBN 3 showed non- significant negative values for single plant yield, seeds per pod, pods per plant and pod length (Table 1).

IPU 2006- 01 x VBN 4 and IPU 2006-01 x TNY LOCAL showed non-significant negative values for the trait seeds per pod and pods per cluster (Table 1). The reason for such negative inter relationship was that the genotypes which were heterozygous and heterogeneous in F_2 fails to transfer their genetic potentiality completely (Ramesh, 1990).

This might be also due to the higher accumulation of heterozygous genes in F_2 , which is generated further in F_3 . In these crosses phenotypic selection of segregants should not be restored to in F_2 generation or otherwise, selection is to postponed to succeeding generations. Instead selection based on yield components done and not by yield directly (Manuel *et al.*, 1997).

Table.1 Parent progeny regression and correlation

Characters		PU 06-20 x VBN 4	IPU 2006- 01 x ADT 3	IPU 2006- 01 x VBN 4	IPU 2006- 01 x TNY LOCAL	IPU 02-33 x VBN 4	IPU 02-33 x TNY LOCAL	WBG 26 x VBN 3	MASH 114x VBN 3	MASH 114 x TNY LOCAL
PH	r	0.103	0.313	0.809	0.464	0.554	0.709	0.752	0.886	0.463
	b	0.040	0.405	0.955	0.647	0.727	0.939	0.802	0.968	0.444
CPP	r	0.457	0.776	0.905	0.467	0.547	0.494	0.226	0.422	0.575
	b	0.121	0.378	0.519	0.214	0.341	0.580	0.054	0.615	0.209
PPC	r	0.515	0.446	-0.172	-0.443	-0.372	0.417	0.407	0.602	-0.358
	b	0.898	0.987	-0.971	-0.860	-0.859	0.806	0.853	0.869	-0.952
PL	r	0.509	0.920	0.509	0.916	0.114	-0.148	-0.047	0.209	0.885
	b	0.904	0.843	0.825	0.846	0.857	-0.756	-0.839	0.956	0.786
PPP	r	0.467	-0.059	0.504	0.961	0.935	0.096	-0.345	-0.102	0.995
	b	0.862	-0.869	0.408	0.789	0.836	0.925	-0.965	-0.856	0.800
SPP	r	0.112	0.508	-0.121	-0.574	0.308	0.511	-0.345	-0.325	-0.528
	b	0.107	0.336	-0.865	-0.995	0.300	0.752	-0.774	-0.921	-0.886
HSW	r	0.553	0.409	0.256	0.256	-0.207	0.299	0.156	0.259	0.289
	b	0.956	0.968	0.785	0.859	-0.864	0.789	0.964	0.635	0.864
SPY	r	-0.084	0.703	0.955	0.659	-0.546	0.685	-0.089	0.702	0.802
	b	-0.089	0.435	0.352	0.985	-0.869	0.796	-0.974	0.578	0.616

There are several reasons by Meredith and Bridge (1973) to explain why the F₂ performance may not closely related to that of F₃ progeny mean. The environment of an individual plant differs greatly from the progeny rows. The second factor is that the genotype x environment interactions from one year to the next at a single selection may be large. Dominance gene action in an F₂ population may not be useful in the later generations *i.e.*, large non – additive gene effects.

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