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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN GREEN GRAM

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ABSTRACT

Genetic association among 27 genotypes of green gram was carried out for 7 characters. The seed yield, number of pods, number of clusters and number of seeds per pod showed high genetypic coefficient of variation. High heritability estimates were observed for plant height, days to 50 per cent flowering and number of clusters. Plant height showed highest genetic advance followed by days to flowering. The correlation study revealed that the high positive correlation values obtained for number of pods, number of clusters and number of seeds per pod and significant inter correlations existing themselves revealed that these characters may be considered for improvement of yield.

KEY WORDS : Green gram, Variability, Character Asssociation, GCV, PCV, Heritability.

Green gram *Vigna radiata*(L.) Wilczek) is one of the important legume crops grown in India. A through knowledge of existing genetic variation and extent of association between various yield contributing characters is essential for developing high yielding genotypes in green gram. The observed variability is a combined measure of genetic and environmental causes. It is only the genetic variability that is heritable from generation to generation. However, a measure of heritability alone does not give an idea about the expected gain in the next generation but it has to be considered in conjuction with genetic advance. Correlation and path analysis will establish the extent of association between yield and yield components and bring out relative importance of their direct and indirect effects and thus give a clear understanding of their association with yield. The present investigation is an attempt in this direction.

MATERIALS AND METHODS

Twenty seven genotypes were raised at the National pulses Research Centre, Vamban, pudukkottai district, Tamil Nadau in a randomised block design with three replications during *kharif* adopting a spacing of 30 x 10 cm. observations were recorded on five randomly selected plants from each plot on days to 50 per cent flowering, plant height, number of clusters per plant, pod length, number of pods per plant, number of seeds per pod, 100 seed weight and grain yield per plant. Coefficients of variations were worked out (Burton, 1952). Heritability in broad sense was workedout according to Lush (1940) Genetic advance and correlation coefficient (Johnson *et al* (1955) and Path analysis (Deway and Lu, 1959) were estimated.

RESULTS AND DISCUSSION

Mean, range, phenotypic-and genotypic coefficients of variation, (PCV and GCV),

Table 1. Mean, variability, heritability and genetic advance of yield and yield contributing characters in green gram.

Characters	Mean	GCV	PCV	Heritability	Genetic advance	Genetic advance as % of mean
Days to 50% flowering	33.60	9.28	9.70	91.48	6.15	18.30
Plant height	52.07	18.98	19.51	94.64	19.82	38.07
No. of Clusters/plant	4.67	21.41	22.40	91.35	1.97	42.19
No. of Pods/Plant	19.12	22.30	24.33	84.01	5.61	42.14
Pod Length	6.80	4.81	7.71	38.89	0.42	6.18
No. of seeds/Pod	10.29	5.06	7.97	40.27	0.68	6.62
100 grain weight	3.45	8.85	9.96	78.93	0.54	16.20
Grain yield	4.87	26.91	28.63	88.32	2.54	52.14

GCV : Genotypic co-efficient of variation; PCV : Phenotypic co-efficient of variation.

Table 2. Genotype correlation coefficients of yield components in green gram

Characters	Days to 50% flowering	Plant height	No. of Clusters/ plant	Pod Length	No. of Pods/Plant	No. of seeds/Pod	100 grain weight	Grain yield/plant
Days to 50% flowering	1.000	0.7829**	-0.3755**	0.2118	0.3343*	-0.1585	-0.1238	-0.3316
Plant height		1.000	-0.4071**	-0.1402	-0.3742**	-0.2020	-0.3132*	-0.3691**
No. of Clusters/plant			1.000	0.2322	0.9508**	0.5719**	-0.0616	0.8290**
Pod Length				1.000	0.2380	0.6989**	0.4558**	0.4066**
No. of Pods/Plant					1.000	0.5459**	0.0810	0.9305**
No. of seeds/Pod						1.000	0.1380	0.6356**
100 grain weight							1.000	0.3642**
Grain yield/plant								1.000

** : Significant at 1% level. * : Significant at 5% level.

heritability and genetic advance are presented in Table 1.

The genotypes showed significant differences in respect of all the characters studied. The seed yield, number of pods per plant and number of clusters per plant showed high GCV indicating that these characters are highly amenable for selection. Pod length, and number of seeds showed minimum variability as evidenced from the low values of GCV. similar results were reported by paramasivam and Rajaskaran (1980) and Natarajan *et al.* (1988). Heritability estimates give the best picture of the extent of advance to be expected by selection. High heritability estimates were observed for plant height, days to 50 per cent flowering, number of clusters and seed yield as reported earlier by Boomikumaran (1980) and Natarajan *et al.* (1988) The genetic gain that can be expected by selection for a character is given by the estimates of genetic advance. Genetic advance expressed as per cent of mean was the highest for seed yield followed by number of clusters and number of pods per plant.

The correlation analysis (Table 2) revealed that grain yield was significantly and positively correlated with number of pods, number of clusters per plant, number of seeds per pod, pod length and 100 grain weight. This indicate that selection based on these characters may result in improved yield. Similar results were reported by Boomikumaran and Rathinam (1981), Singh and Sharma (1981) and Natarajan *et al* (1988). plant height and days to 50 per cent flowering showed significant, low negative correlation with yield. The inter correlation estimated for the yield components showed that plant height, number of clusters, pod length, number of pods per plant were significantly and positively correlated among themselves. It indicates that simultaneous improvement of these characters can be effected by selection.

The high positive correlation values obtained for number of pods, number of clusters per plant and number of seeds per pod and the significant inter correlations existing among themselves revealved that these charcters may be considered for improvement of yield.

Table 3. Direct and Indirect effects of yield components on yield in green gram

Characters	Days to 50% flowering	Plant height	No. of Clusters/ plant	Pod Length	No. of Pods/Plant	No. of seeds/Pod	100 grain weight	Genotypic correlation co-efficent
Days to 50% flowering	-0.1687	0.1465	0.0959	0.0260	-0.3499	-0.0416	-0.0397	-0.3316
Plant height	-0.1321	0.1871	0.1039	0.0172	-0.3917	-0.0530	-0.1006	-0.3691**
No. of Clusters/plant	-0.0633	-0.0762	-0.2553	0.0285	0.9953	0.1501	-0.0198	0.8290**
Pod Length	0.0357	-0.0262	0.0593	-0.1226	0.2492	0.1835	0.1463	0.4066**
No. of Pods/Plant	0.0564	-0.0700	-0.2428	-0.0292	0.0468	0.1433	0.02060	0.9305**
No. of seeds/Pod	0.0267	-0.0378	-0.1460	-0.0857	0.5714	0.2625	0.0443	0.6356**
100 grain weight	0.209	-0.0586	0.0157	0.0559	0.0848	0.0362	0.3211	0.3642**

Residual Value : 0.1297; Underlined figures denotes direct effects.

Path analysis (Table 3) revealed that number of ds recorded the highest positive direct effect on d yield followed by number of clusters per plant. indirect effect of other characters *viz;* plant ght and number of seeds per pod through mber of clusters per plant were also much reciable indicating that these characters played important role in determining yield. In contrast these results, Boomiumaran and Rathinam 81) reported negative direct effects for pods per nt and seeds per pod on seed yield. It is resting to note that number of pods and number clusters showed high magnitude of positive notypuc correlations with seed yied.

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COMPONENT ANALYSIS OF SOME METRIC TRAITS IN BARLEY

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ABSTRACT

The performance of the eight genetically diverse varieties of barley and their 28 F_1s was evaluated to assess their genetic architecture for the yield and yield contributing traits in a set of diallel crosses. The component analysis indicated the presence of additive ($\hat{D}$) and dominance ($\hat{H}_1$ and $\hat{H}_2$) genetic variances for plant height length of main spike and grain yield/plant. $\hat{D}$ component was higher than $\hat{H}_1$ for plant height, number of grains/main spike and biological yield per plant. For remaining characters $\hat{H}_1$ was higher than $\hat{D}$ component, indicating the preponderance of dominance genetic variance. Over dominance was observed for days to reproductive phase, number of productive tillers/plants, length of main spike and grain yield/plant. Highly significant values of $\hat{F}$ were observed only for plant height indicating the predominance of dominant alleles. While highly significant values of $\hat{h}_2$ were recorded for all the traits except days to reproductive phase revealing the predominance of dominant alleles.

KEY WORDS : Component, Analysis, Metric Traits, Barley

Barley is a major cereal crop which can resist ought and does better than other crops under low tility level and in late sown conditions. The ncept of drought resistance in barley has been oved to be boon both for breeders as well as mers. In order to meet this goal, information in e pattern of inheritance of quantitative characters essential for the breeder to efficiently plan the eeding procedure. In the present study, an attempt as made to analyse the genetic basis of heritance of yield and some of the important yield ributes through diallel analysis.

MATERIAL AND METHODS

A diallel set of crosses (excluding reciprocals) involving eight diverse varieties/strains of barley, *viz.*, Jyoti, Azad, K-226, K- 329, P-147, P-267, Karan 92 and RD-883 were used in this investigation. All the 28F_1 and eight parents were planted in a randomised block design with three replications during *rabi* 1985-86. The recommended spacings and agronomic practices were followed to raise a good crop. Ten plants were selected at random from each plot and observations