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Correlation and Genetic Variability Studies Yield Components and Thrip Resistance in Cowpea (*Vigna unguiculata* L.)

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Abstract

The genotypic and phenotypic correlations of yield with different components were estimated from 28 genotypes of grain cowpea. The genotypic and phenotypic correlations agreed closely with each other. Yield contributing characters viz., number of pods per plant had positive and highly significant association with plant height (0.481), number of pods per plant (r = 0.640), pod length (r = 0.621) and 100 - seed weight (r = 0.690). Thrips resistance was positively correlated with pod length (0.329). Therefore, number of pods per plant and pod length were important components for improving yield in cowpea.

Key Words : *cowpea, correlation, thrip resistance, yield contributing traits*

Introduction

Cowpea (*Vigna unguiculata* L. Walp) is one of the important food legumes in the hot-dry tropics and sub-tropics and especially, in the sub-Saharan Africa[19]. Cowpea feeds millions of people in the developing world with an annual worldwide production estimated around 4.5 million metric tons with an area of 12 to 14 million ha[8]. In the context of yield enhancement, in order to have a good choice of character for selection of desirable genotypes under planned breeding programme, knowledge of the nature and magnitude of variation existing in available plant breeding materials, the association of component characters with yield and their exact contribution through direct and indirect effects are very important. Genotypic and different components of variance, heritability and genetic advance have been calculated for different yield characters in cowpea by several workers[20 & 16] which revealed that selection was effective for a population with broad genetic variability and character with high heritability. Correlation analysis is a handy technique which provides information that selection for one character results in progress for other positively correlated characters. The importance of correlation studies in selection programmes is appreciable when highly heritable characters are associated with the important character like yield. Correlation coefficients, although, very useful in quantifying the size and direction of trait associations can be misleading if the high correlation between two traits is a consequence of the indirect effect of other traits[4]. Several workers have estimated the correlation between different yield attributing characters and their direct and indirect effects on yield in cowpea[21 & 14]. The objective of the present investigation was to estimate the genetic variability, association of different characters and their direct and indirect effect on grain yield with a view to identify the accessions with best potentiality for upgrading grain yield and its component characters.

Materials and Methods

Twenty eight cowpea genotypes were selected for the present investigation. Randomized block design with three replications was used. The material was grown during summer season at Seed Production Centre, G.B. Pant University of Agriculture & Technology, Pantnagar. The plot consisted of four rows each of 4 m length. The plants were planted at a spacing of 45 cm between the rows and 10 cm plant to plant, respectively. The recommended package of practices was followed for cultivation. The observations were recorded on 8 morphological characters *viz.*, days to 50 per cent flowering, days to maturity, thrips score, plant height (cm), number of pods per plant, pod length (cm), number of seeds per pod and seed yield (gm/plot). The correlation co-efficient [2] were analysed. Data for all the variables measured were subjected to Analysis of Variance (ANOVA), to estimate the level of variability among the cowpea accessions, using Genstat Discovery Edition 3 software. The phenotypic variation for each trait was partitioned into genetic and non-genetic factors and estimated using equation[11]: Vp=MSg/r; Vg=(MSg-MSe)/r; Ve=Mse, where Vp, Vg and Ve are phenotypic variance, genotypic variance and environmental variance, respectively; MSg, MSe and r are mean squares of accessions, mean squares error and number of replications respectively. To compare the variations among traits, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were computed according to the method suggested earlier[3, 5]:

$PCV = (\sqrt{Vp}/X)\ 100$

$GCV = (\sqrt{Vg}/X)\ 100$

$ECV = (\sqrt{Ve}/X)\ 100$

Where X is the grand mean for each of the studied traits. Broad sense heritability (h^2B) was calculated[3, 6] as the ratio of the genotypic variance (Vg) to the phenotypic variance (Vp). The correlation coefficients (r) were computed among all the measured traits using SPSS for Windows Version 16 (SPSS, Inc., Chicago, IL).

Results and Discussion

Analysis of variance revealed significant differences among all the geneotypes studied. The mean values of the characters observed are shown in Table 1.

Table 1: Mean values of the 8 characters studied in 28 genotypes

S.No	Entries	Days to 50% flowering	Days to maturity	thrip score	Plant height	Pods/plant	Pod length	Seed/pod	Yield (g/plot)
1	GCP-348	55	71	3	34.66	11.5	14.66	10	0.124
2	GCP-349	57	83	3	33.66	14	16	12	0.294
3	GCP-350	55	68	3	33	12.33	16.66	11	0.314
4	GCP-351	53	67	3	31	15	14.33	9	0.316
5	GCP-352	54	69	4	38	10.66	16.66	16	0.556
6	GCP-353	55	78	2	41.33	18	16	8	0.314
7	GCP-354	57	82	2	37	15.33	14.66	11	0.706
8	GCP-355	57	73	3	37.66	15.66	17	8	0.126
9	GCP-356	54	72	3	21.66	8.66	14.66	7	0.44
10	GCP-357	55	71	2	33.66	13.66	19.33	9	0.422
11	GCP-358	55	69	1	35.33	12.66	19.66	14	0.884
12	GCP-359	53	72	2	42.66	15	15.33	9	0.602
13	GCP-360	56	81	3	33.33	7.66	16.33	8	0.258
14	GCP-361	54	70	4	37.66	15	16.33	16	0.142
15	GCP-362	57	87	3	35.66	7.33	16	10	0.066
16	GCP-363	55	71	4	31.33	8.33	19.66	10	0.032
17	GCP-364	71	85	3.5	43.33	12	20.33	9	0.066

18	GCP-365	55	83	3.5	33.33	7.66	13.33	6	0.042
19	GCP-366	55	81	5	33.33	7.66	35	9	0.086
20	GCP-367	56	82	3.5	33.33	14	37.33	12	0.1
21	GCP-368	56	73	3.5	32	13.33	17	10	0.064
22	GCP-369	57	69	4	33.33	9	37	11	0.082
23	GCP-370	55	72	4	34	10.66	25.33	9	0.196
24	GCP-371	55	69	2	30.66	9.66	21	17	0.216
25	GCP-376	55	73	3.5	44.66	25.66	16.33	8	0.304
26	GCP-378	54	80	3	32.66	10.33	17.66	15	0.228
27	PL-3	55	71	2	44	15.33	16.66	16	0.186
28	PL-4	56	83	4	36.66	6.66	14	3	0.032

Table 2: Best entries selected for each character studied

Days to 50% flowering	Days to maturity	thrip score	Plant height	Pods/plant	Pod length	Seed/pod	Yield (g/plot)
GCP-351	GCP-350	GCP-358	GCP-376	GCP-376	GCP-367	GCP-371	GCP-358
GCP-359	GCP-351	GCP-353	GCP-364	GCP-355	GCP-370	GCP-352	GCP-354
	GCP-358	GCP-354	GCP-359	GCP-354	GCP-364	GCP-361	GCP-359
	GCP-369	GCP-357	GCP-353		GCP-363		
	GCP-371	GCP-359			GCP-358		

The thrip score was least in GCP-358, GCP-353, GCP-354, GCP-357 and GCP-359. The plant height was maximum in GCP-376, GCP-364, GCP-359, GCP-353. GCP-376 also recorded highest no. of pods per plant followed by GCP-355 and GCP-354 However the pod length was maximum in GCP-367 and GCP-370. Thus the best resistant lines selected on the basis of the characters studied comes out to be GCP-358, GCP-354 and GCP-359. These lines also reported less thrip damage and thus could be considered as resistant lines for thrips.

Table 3 : Analysis of variance for different characters under study

Source of Variation	df	Mean Sum of Square for different observation							
		days to 50% flowering	days to maturity	thrip score	plant height	pods/plant	pod length	seed/pod	yield (g/plot)
Replication	2	1.664	3.660	.967	9.657	1.801	1.195	2.083	2.033
Treatment	27	34.947**	114.873**	1.618**	86.072**	36.746**	135.849**	20.036**	0.132**
Error	54	1.160	.987	.167	11.315	.64720	.638	.552	2.998

Table 4 Estimates of variance components and heritability of 28 cowpea accessions

	h^2	ga	gcv	pcv	ecv
Days to 50% flowering	90.687	6.578	6.018	6.319	1.928
Days to maturity	97.463	12.530	8.15	8.256	1.314
thrip score	74.23	1.234	23.649	27.449	13.934
Plant height	68.77	8.527	14.307	17.253	9.641
pods/plant	94.895	6.961	28.829	29.594	6.685
Pod length	98.604	13.732	35.883	36.136	4.269
Seed/pod	92.16	5.039	23.919	24.915	6.976
Yield (g/plot)	93.519	0.414	78.08	80.74	20.554

Genetic variability

The analysis of variance showed that the mean squares for the accessions were highly significant for all traits measured. The phenotypic variance was partitioned into heritable (genotypic variance) and non heritable (environmental variance) components. Generally, the phenotypic variance was higher than the genotypic variance in all the traits studied. The magnitude of the genotypic variance for all the yield traits were however higher than the environmental variance (Table 4). The phenotypic coefficient of variation (PVC) and Genotypic Coefficient of Variation (GCV) were highest for yield (g/plot) (80.740 and 78.079 respectively), followed by pod length (36.136 and 35.882 respectively), pods/plant (29.594 and 28.829 respectively), thrip score (27.448 and 23.649 respectively), seed/pod (24.915 and 23.918 respectively) and plant height (17.252 and 14.307 respectively). Low PCVs and GCVs were recorded for days to 50 % flowering (6.319 and 6.017 respectively) and days to maturity (8.255 and 8.150 respectively). The Environmental Coefficient of Variation (ECV) was generally low for all traits assessed and ranged from 1.98 to 20.554. Broad sense heritability estimates was high (Table 4) for pod length (98.604%), days to maturity (97.463), number of pods per plant (94.89%), yield per plot (93.51%) and seeds per pod (92.16%).

Table 5 Correlation coefficients of the different character studied of 28 cowpea genotypes

	days to 50% flowering	days to maturity	thrip score	plant height	pods/plant	pod length	seed/pod	yield (g/plot)
days to 50% flowering	1							
days to maturity	0.444**	1						
thrip score	0.041	0.119	1					
plant height	0.196^{NS}	0.166	-0.037	1				
pods/plant	-0.040	-0.255*	-0.237*	0.481**	1			
pod length	0.095	0.027	0.329**	-0.098	-0.183	1		
seed/pod	-0.206	-0.287**	-0.159	0.045	0.026	0.029	1	
yield (g/plot)	-0.192	-0.262*	-0.413**	0.091	0.305**	-0.289**	0.149	1

Correlation

Simple correlation coefficients calculated among the characters are presented in Table 5. Significantly positive correlations were found between Days to 50% flowering and days to maturity (r = 0.444**) thrip score and pod length (0.329**), plant height and pods/plant (0.481**), pods/plant and yield (0.305**), Conversely, grain yield was negatively correlated with days to 50% flowering (r= - 0.192).

The highly significant difference in mean squares implied that there is discernable evidence of inherent genetic variability among the cowpea genotypes with respect to days to 50% flowering, days to maturity, thrips score, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and grain yield. The result of the variance components in this study showed that the phenotypic variance was higher than the genotypic variance in all the traits studied. The magnitude of the genotypic variance for all the yield components were however higher than the environmental variance. This result is in accord with the report of several authors [7,16, 20 & 24] in cowpea. The low environmental influence observed compared to genetic factors suggests that the traits may be under genetic control rather than the environment, hence improvement can be achieved through selection [17 & 22]. The minimum magnitudinal differences in GCV and PCV coupled with low ECV for all the traits studied implied that the traits are mostly governed by genetic factors with little role of environment in the phenotypic expression of these characters. Thus, selection of these traits on the basis of the phenotypic value may be effective. It is reported that polygenic variation may be phenotypic, genotypic or environmental and the relative values of these three types of coefficients give an idea about the magnitude of the variability[15]. Broad sense heritability refers to the ratio of heritable variance to total variance. In a narrow sense, heritability is defined as the ratio of additive genetic variance to total variance. Broad sense heritability estimates in this study were generally high for all the traits studied. The heritability values obtained in this study are within the values reported from several published studies in cowpea [1,7,9,14, 16,20 &24]. Heritability estimates along with genetic advance are more useful in predicting the resultant effect for the selection of the best individuals from a population[20]. High broad sense heritability values indicated the predominance of additive gene action in the expression of these traits and can be improved through individual plant selection[13,18 &22]. The significantly positive relationships between grain yield and number of pods per plant and pod length agrees with an earlier study on cowpea a positive correlation of 0.88 for pods per plant, and 0.66 for seeds per pod with grain yield [12]. The positive association between grain yield and yield attribute is also in accord with an earlier study on character association in cowpea [21]. The author implicated pods per plant and seeds per pod as the major yield determining traits. The vegetative phase of the plant has been found useful in allowing for the development of optimum canopy necessary for high yield [10]. The linear relationship between days to flowering and these yield traits is therefore not out of place; since increase in days to flowering allows for proper development of the vegetative part leading to production of more number of pods per plant and other yield traits. Within in the range of materials used in this study, there exist substantial genetic variability and heritability in the character studied to warrant selection in the cowpea accessions for improvement. The level of genetic variability observed for different traits would be useful for breeding varieties of cowpea for high yield. The high genetic variance components and heritability estimates coupled with significantly positive correlations of plant height, number of pods per plant, and 100-seed weight on grain yield, these traits were identified in this study and could be listed in selection criteria for good parental lines in a cowpea.

Conclusion

The identification of lines with resistance factors among landraces is a new development that will go a long way in alleviating the plight of the local farmers. Further evaluation is needed to be carried out on the selected landraces over time and space. There is need for further breeding work in order to improve their agronomic characters as well as resistance genes by transferring the useful genes in them from other elite genotypes under this changing climate regime.

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