Annals of Plant and Soil Research 19(2):168 - 174 (2017)

Character associations between seed yield and its components traits in cowpea (*Vigna unguiculata* L.)

POONAM SAHARAN, MUKESH VYAS, P.P. SHARMA AND D.R. MEGHAWAL

Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur-313 001, (Raj.)India

Received: January, 2017; Revised accepted: April, 2017

ABSTRACT

Sixty diverse genotypes including three checks viz.,RC-101, RC-19 and RCV-7 of cowpea, collected from Rajasthan Agriculture Research Institute, Durgapura were evaluated during Kharif season of 2015 at the Research Farm Rajasthan College of Agriculture, Udaipur for correlation and path coefficient analysis. Seed yield/ plant was positively and significantly correlated at both genotypic as well as phenotypic level with number of flowers/plant, number of pods/plant, number of primary branches/ plant, pod length, number of seeds/pod, test weight, biological yield /plant and harvest index. Highest positive indirect effect on seed yield was exhibited by number of pods/plant. However, as revealed that the traits like number of flowers/plant, number of primary branches/plant, biological yield/plant, harvest index, number of seeds/ pod and pod length can be selected for further crop improvement in cowpea.

Keywords: Correlation, path coefficient analysis, cowpea genotypes

INTRODUCTION

Among all legumes, cowpea (*Vigna unguiculata* (Linnaeus.) is one the important legume crop (Kaushik *et al.,* 2015) which belongs to family Leguminoseae with a diploid chromosome number of 2n=2x=22. It is grown as mainly as vegetable, for seed and to a lesser extent as a fodder crops. Cowpea contains 24 % protein, 60 % carbohydrate and 2% fat besides being good sources of vitamins and phosphorus. Cowpea is grown in India particularly for dry seed as pulse in the northern drier tracts while some forms of cowpea are also grown as fodder crops in the semi-arid western regions and in the humid tropic regions. Major objective of crop breeding programmes is to achieve higher yield. Yield is regarded as an end product of a set of plant process which is related to each other. It is also a complex character with low heritability and therefore, direct selection for yield to improve it is often not so successful. Therefore, it is advantageous to find out the closely related and highly contributing component traits of yield, so that suitable selection strategies can be devised to improve yield. The knowledge of character association *i.e.* genotypic and phenotypic correlation between yield and its component characters is essential for yield improvement through selection programme (Fraser and Eaton, 1983). Association analysis provides measures of relationship among the traits and serves to assess the opportunity of mutual improvement of two desirable traits by common selection programme (Kumar and Ojha, 2004). The path analysis helps in partitioning the correlation coefficients of yield components with seed yield into direct and in direct effects to ensure the actual contribution of an attributes as well as its influence through other traits.

MATERIALS AND METHODS

The sixty diverse genotypes including three checks *viz.,*RC-101, RC-19 and RCV-7 of cowpea were collected from Rajasthan Agriculture Research Institute, Durgapura and the collection maintained at Rajasthan College of Agriculture, Udaipur. The experimental material consisting of sixty genotypes of cowpea were sown in randomized block design in three replications. Two rows of each genotype were sown in a plot of 4 m length. The row to row and plant to plant distances were kept at 30 cm and 10 cm, respectively. All the recommended packages of practices were followed to raise a healthy crop. The observations on 14 morphological traits were recorded on a random sample of 5 competitive plants selected for each genotype in each replication except days to 50% flowering and days to pod maturity which were recorded on plot basis. Mean value of 5 plants were used for statistical analysis. The main value of five plant of each genotypes selected at random were used for statistical analysis. The following 14 morphological characters studied were days to 50% flowering, days to maturity, number of branches / plant, number of flowers/ plant, number of seeds/ pod, number of clusters/ plant, harvest index, biological yield/ plant, seed protein content, pod length, plant height, test weight, number of pods/ plant and seed yield/ plant. The correlation co-efficient (Al-Jibouri *et al.*,1958) and path co-efficient analysis (Dewey and Lu, 1959)were analysed.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for different characters was presented in Table 1. The treatment i.e. mean sum of squares due to genotypes showed highly significant differences for all 14 characters under study at 1% level of significant. This indicates that there is ample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environ- mental influence affecting the phenotypes. Correlation co-efficient at genotypic and phenotypic levels between paired characters, computed in all possible combinations are presented in Table 2. In general, genotypic correlations were greater than the phenotypic correlations, indicating the preponderance of genetic variance in expression of different characters. However, genotypic and phenotypic correlation agreed closely with each other. Positive and significant association of green pod yield/plant was observed with number of pods/plant and pod length. The present observations were in accordance with the findings of Sreekumar *et al.* (1996), Singh and Verma (1999) and Pal *et al.* (2004). However, days to 50% flowering and days to first pod picking exhibited a significant negative correlation with green pod yield/ plants indicating early flowering which would help to minimize the crop duration and ultimately crop could be adjusted profitably in crop rotation. The results are in accordance with those of Singh *et al.* (1982). For selection of a suitable plant type, information regarding nature and extent of association of various morphological characters with the character of economic importance would be helpful in developing a suitable plant type. For the improvement of complex characters like seed yield for which direct selection is not very effective, while selection for associated characters would be effective.

Table 1: Mean squares for various characters in cowpea

S.No.	Characters	Mean sum of squares		
		Replication (d.f.= 2)	Treatments (d.f.= 59)	Error (d.f.= 118)
1	Days to 50% Flowering	0.539	7.286**	1.674
2	Flowers/ Plant	8.492	45.533**	3.558
3	Days to Maturity	0.906	3.688**	1.578
4	Plant Height cm	7.761	4090.239**	11.029
5	Primary Branches/ Plant	1.082	27.191**	0.895
6	Pods/ Plant	3.947	38.943**	3.976
7	Clusters/ Plant	0.112	4.348**	0.418
8	Pod Length	1.986	15.921**	1.161
9	Seeds/ Pod	0.049	18.442**	0.473
10	Test Weight	0.004	9.299**	0.189
11	Biological Yield/ Plant	17.150	7673.127**	13.359
12	Harvest Index	4.416	358.165**	3.602
13	Seed Protein Content	0.009	1.939**	0.004
14	Seed Yield/ Plant	8.506	965.050**	4.342

*** Significance at 1% level of significance*

In the present investigation, correlation coefficients were estimated among 14 characters to find out association of seed yield per plant with its components at genotypic (r_g) as well as phenotypic (r_p) levels. The result revealed that, genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlations for all the characters studied indicating negligible effect of

Table 2: Genotypic (r_g) and phenotypic (r_p) correlation coefficients among 14 characters in 60 genotypes of cowpea

Character		Days to 50% flowering	Flowers/ plant	Days to maturity	Plant height cm	Primary branches/ plant	Pods/ plant	Clusters/ plant	Pod length	Seeds/ pod	Test weight	Biological yield/ plant	Harvest index	Seed protein content	Seed yield/ plant
Days to 50% flowering	G	**1.000**	-0.194**	0.768**	-0.048	-0.190*	-0.190*	-0.020	-0.231**	0.207**	-0.318**	-0.129	0.096	0.031	-0.147*
	P	**1.000**	-0.146*	0.643**	-0.040	-0.110	-0.111	0.019	-0.138	0.147	-0.223**	-0.092	0.057	0.024	-0.111
Flowers/ plant	G		**1.000**	-0.166*	-0.046	0.101	0.879**	0.088	-0.081	0.087	0.211**	0.139	0.232**	0.009	0.437**
	P		**1.000**	-0.086	-0.045	0.089	0.837**	0.095	-0.095	0.070	0.192**	0.124	0.199**	0.013	0.385**
Days to maturity	G			**1.000**	-0.106	-0.318**	-0.072	0.192**	-0.335**	-0.066	-0.412**	-0.348**	0.192**	-0.064	-0.233**
	P			**1.000**	-0.062	-0.148*	0.005	0.062	-0.126	-0.031	-0.247**	-0.195**	0.092	-0.030	-0.147*
Plant height cm	G				**1.000**	0.018	-0.033	0.118	0.073	0.179*	0.183*	0.251**	-0.132	-0.231**	0.029
	P				**1.000**	0.019	-0.028	0.103	0.062	0.173*	0.178*	0.250**	-0.130	-0.229**	0.028
Primary branches/ Plant	G					**1.000**	0.112	0.114	0.082	-0.018	0.066	0.203**	0.053	0.207**	0.332**
	P					**1.000**	0.114	0.094	0.065	-0.027	0.060	0.197**	0.049	0.194**	0.310*
Pods/ plant	G						**1.000**	-0.053	-0.122	0.035	0.075	0.090	0.204**	-0.057	0.341**
	P						**1.000**	-0.004	-0.109	0.042	0.081	0.077	0.165*	-0.048	0.287**
Clusters/ plant	G							**1.000**	-0.039	0.061	-0.134	-0.128	-0.016	-0.204**	-0.107
	P							**1.000**	-0.044	0.063	-0.099	-0.111	-0.019	-0.179*	-0.099
Pod length	G								**1.000**	0.371**	0.216**	0.091	0.026	-0.028	0.185*
	P								**1.000**	0.315**	0.180*	0.075	0.023	-0.025	0.159*
Seeds/ pod	G									**1.000**	0.314**	0.035	0.194**	-0.198**	0.255*
	P									**1.000**	0.300*	0.034	0.182*	-0.191**	0.243*
Test weight	G										**1.000**	0.187*	0.164*	0.016	0.395**
	P										**1.000**	0.179*	0.154*	0.015	0.380**
Biological yield/ plant	G											**1.000**	-0.518**	-0.026	0.301**
	P											**1.000**	-0.513**	-0.026	0.298*
Hrvest index	G												**1.000**	-0.103	0.616**
	P												**1.000**	-0.101	0.616**
Seed protein content	G													**1.000**	-0.046
	P													**1.000**	-0.046
Seed yield/ plant	G														**1.000**
	P														**1.000**

**and ** significant at 5% and 1% G- Genotypic, P- Phenotypic* environment. These findings were in accordance with Huque *et al.*(2012) and Sharma *et al.*(2015). Seed yield per plant was positively and significantly correlated at both genotypic as well as phenotypic level with number of flowers per plant, number of pods per plant, number of primary branches per plant, pod length, number of seeds per pod, test weight, biological yield per plant and harvest index. These findings are in accordance with Eswarana *et al.* (2009), Nehru *et al.*(2009), Huque *et al.*(2012), Manggoel *et al.* (2012) and Sharma *et al.* (2015). Likewise, it was negatively and significantly correlated at genotypic level with days to 50% flowering and at both level with days to maturity.These findings are in accordance with Manggoel *et al.* (2009).

Significant positive correlations of days to 50% flowering at both genotypic and phenotypic level with days to maturity and at genotypic level with seeds per pod. Likewise, flowers/plant exhibited significant positive correlation at both genotypic and phenotypic level with pods/ plant, test weight, harvest indexand seed yield/ plant. Similar results were also reported by Manggoel *et al.* (2012). Days to maturity exhibited significant positive correlation at genotypic level with number of cluster/plant and harvest index. These findings are in accordance with Sharma *et al.* (2015). Further plant height exhibited significant positive correlation at both genotypic and phenotypic level with number of seeds/ pod, test weight and biological yield. Number of primary branches/ plant exhibited significant positive correlation at both genotypic and phenotypic level with biological yield, seed protein and seed yield. These findings are in accordance with Nehru *et al.* (2009). Similarly, Pods/ plant exhibited significant positive correlation at both genotypic and phenotypic level with harvest index and seed yield. These findings are in accordance with Sharma *et al.* (2015). Pod length exhibited significant positive correlation at both genotypic and phenotypic level with seeds/pod, test weight and seed yield. These are in accordance with Manggoel *et al.* (2012) and Huque *et al.* (2012). However, number of seeds/pod exhibited significant positive correlation at both genotypic and phenotypic level with test weight, harvest index and seed yield/plant. Whereas, test weight exhibited significant positive correlation at both genotypic and phenotypic level with biological yield, harvest index and seed yield. These results are in accordance with Manggoel *et al.* (2012). Biological yield/plant exhibited significant positive correlation with seed yield/ plant at both genotypic and phenotypic level. The present findings are in accordance with Eswarana *et al.*(2007). Harvest index exhibited significant positive correlation with seed yield/ plant at both genotypic and phenotypic level. These findings are in accordance with those of Parmer *et al.* (2003), Eswarana *et al.* (2007), Nehru *et al.* (2009) and Sharma *et al.* (2015).

There also existed some negative correlation between different characters like days to 50 % flowering exhibited significant negative correlation at genotypic level with pod length, primary branches/plant, pods/plant. These results are in accordance with those of Manggoel *et al.*(2012). It also existed negative correlation at both genotypic and phenotypic level with flowers/plant and test weight. Likewise, flowers/plant exhibited significant negative correlation with days to maturity at genotypic level. Days to maturity exhibited significant negative correlation at both genotypic and phenotypic level with primary branches/plant, test weight, biological yield and seed yield/plant. It also exhibited significant negative correlation with pod length at genotypic level only. Likewise, plant height exhibited significant negative correlation with seed protein content at both genotypic and phenotypic level. Further, Cluster/plant exhibited significant negative correlation with seed protein content at both genotypic and phenotypic level. Seeds/pod exhibited significant negative correlation with seed protein content at both genotypic and phenotypic level and finally, biological yield/plant exhibited significant negative correlation with harvest index at both genotypic and phenotypic level. Present experimental findings revealed that number of flowers/plant, number of pods/plant, number of primary branches/ plant, pod length, number of seeds/pod, test weight, biological yield/ plant and harvest index are important contributing traits for seed yield/ plant because they showed significant positive correlation with seed yield. Hence, these traits can be used for selection of high seed yield.

Path Coefficient Analysis

Correlation studies alone cannot provide a clear cut picture of cause and effect of

Table 3: Genotypic path coefficient analysis effect of different characters on grain yield in cowpea genotypes

Character	Days to 50% flowering	Flowers/ plant	Days to maturity	Plant height cm	Primary branches/ plant	Pods/ plant	Clusters/ plant	Pod length	Seeds/ pod	Test weight	Biological yield/ plant	Harvest index	Seed protein content	Seed yield/ plant	Partial R²
Days to 50% flowering	-0.1116	0.0217	-0.0857	0.0054	0.0212	0.0212	0.0022	0.0258	-0.0231	0.0355	0.0143	-0.0107	-0.0035	-0.1470	0.0164
Flowers/ plant	-0.0189	0.0973	-0.0162	-0.0044	0.0099	0.0855	0.0085	-0.0079	0.0085	0.0205	0.0136	0.0226	0.0009	0.4378	0.0426
Days to maturity	-0.0150	0.0032	-0.0195	0.0021	0.0062	0.0014	-0.0037	0.0065	0.0013	0.0080	0.0068	-0.0037	0.0013	-0.2332	0.0045
Plant height cm	0.0019	0.0018	0.0042	-0.0394	-0.0007	0.0013	-0.0046	-0.0029	-0.0070	-0.0072	-0.0099	0.0052	0.0091	0.0285	-0.0011
Primary branches/ plant	-0.0131	0.0070	-0.0219	0.0013	0.0689	0.0077	0.0079	0.0057	-0.0012	0.0045	0.0140	0.0037	0.0143	0.3318	0.0229
Pods/ plant	0.0090	-0.0418	0.0034	0.0016	-0.0053	-0.0475	0.0025	0.0058	-0.0017	-0.0036	-0.0043	-0.0097	0.0027	0.3412	-0.0162
Clusters/ plant	-0.0002	0.0008	0.0018	0.0011	0.0010	-0.0005	0.0092	-0.0004	0.0006	-0.0012	-0.0012	-0.0001	-0.0019	-0.1073	-0.0010
Pod length	-0.0086	-0.0030	-0.0125	0.0027	0.0031	-0.0045	-0.0014	0.0372	0.0138	0.0080	0.0034	0.0010	-0.0010	0.1853	0.0069
Seeds/ pod	0.0110	0.0046	-0.0035	0.0095	-0.0009	0.0019	0.0033	0.0197	0.0531	0.0167	0.0019	0.0103	-0.0105	0.2547	0.0135
Test weight	0.0006	-0.0004	0.0007	-0.0003	-0.0001	-0.0001	0.0002	-0.0004	-0.0006	-0.0018	-0.0003	-0.0003	0.0000	0.3945	-0.0007
Biological yield/ plant	-0.1016	0.1102	-0.2746	0.1984	0.1603	0.0714	-0.1009	0.0717	0.0280	0.1481	0.7901	-0.4093	-0.0206	0.3011	0.2380
Hrvest index	0.0972	0.2357	0.1949	-0.1336	0.0542	0.2073	-0.0164	0.0264	0.1966	0.1659	-0.5254	1.0144	-0.1047	0.6162	0.6250
Seed protein content	0.0021	0.0006	-0.0044	-0.0158	0.0141	-0.0039	-0.0140	-0.0019	-0.0135	0.0011	-0.0018	-0.0071	0.0683	-0.0458	-0.0031

R SQUARE = 0.9476 RESIDUAL EFFECT = 0.2288 relationship between yield attributes and their extent of association. Path analysis devised by Wright (1921) provides measure of direct and indirect effects of traits on yield, splitting the correlation coefficients into direct and indirect effects. Seed yield/plant exhibited positive and significant correlation with number of flowers/ plant was mainly due to its low direct effect, number of pods/ plant due to its low indirect effect, number of primary branches/ plant due to its low direct effect, pod length due to its low direct effect, number of seeds/ pod due to its direct effect, test weight due to its very low indirect effect, biological yield/plant due to its high direct effect and harvest index due to its very high direct effect. These findings are in accordance with Renukadevi and Subbslskhmi (2006) Eswarana *et al.*(2007) and Manggoel *et al.*(2012). The value of residual effect of undefined factors was 22 % indicating that the character studied contributed 78% of higher yield production. Highest positive direct effect on seed yield was exhibited by harvest index. Highest positive indirect effect on seed yield was exhibited by number of pods/plant. However, as revealed that the traits like number of flowers/plant, number of primary branches/plant, biological yield/plant, harvest index, number of seeds/pod and pod length can be selected for further crop improvement in cowpea.

The present study illustrated the phenotypic and genotypic correlations showing positive correlation of seed yield with important agro-morphological characters. Hence, improving one or more of these traits could result in high seed yield for cowpea traits like number of flowers/plant, number of primary branches/plant, biological yield/plant, harvest index, number of seeds/ pod, pod length and test weight.

REFERENCE

Al-Jibouri, H. A., Miller, P. A. and Robinson, H.F. (1958) Genotypic and environmental variances in upland cotton cross of inter specific origin. *Agronomy Journal,* **50**(10): 633-635.

Dewey, D.R. and Lu, K.H. (1959) A correlation and path co-efficientanalysis of components of crested wheat grass seed production. *Agronomy Journal,* **51**(9): 511-518.

Eswaran, R. S., Kumar, T. and Venkatesan, M. (2007) Genetic variability and association of component characters for earliness in cowpea [*Vignaunguiculata* (L.)Walp.] *Legume Research*, **30**(1): 17-23.

Fraser, J. and Eaton, G.W. (1983) Application of yield component analysis to crop research. *Field Crop Abstracts*, **36**: 787-797.

Kaushik, A. K., Yadav, S. K. and Srivastava, P. (2015) Comparative efficacy of some insecticides for Thrips control in Cowpea (*Vigna unguiculata* L.). *Annals Plant Protection Science,* **23**(2): 294-297

Manggoel, W., Uguru, M.I., Ndam, O.N. and Dasbak, M.A. (2012) Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vignaunguiculata* (L.)Walp] accessions.*Journal of Plant Breeding and Crop Science*; **4**(5): 80-86.

Nehru S.D., Suvarna and Manjunath A. (2009) Genetic variability and character association studies in cowpea in early and late *kharif* seasons. *Legume Research*, **32**(4): 290-292.

Pal, A.K., Singh, B., Maurya, A.N. and Kumar, S. (2004) Correlation and path analysis in cowpea [*Vignaunguiculata* (L.)Walp].*South Indian Journal of Horticulture,* **52**(1-6):82-88.

Parmer, L.D, R.M., Tikka, S.B.S., Henry, A.., Kumar, D.and Singh, N.B. (2003) Association analysis forgrain yield and contributing characters incowpea. Proceedings of the NationalSymposium on Arid Legumes, for foodnutrition security and promotion of trade, Hisar, India.

Philip, M.C.A. (2004) Genetic analysis of legume pod borer(*Marucavitrata* Fab.) resistance and yield incowpea (*Vigna unguiculata* (L.)Walp.) Ph.D thesis, Kerala Agricultural College, Thirussur, p.171

Renukadevi, P. and Subbslskhmi, B. (2006) Correlation andpath coefficient analysis in chickpea. *Legume research,* **29**: 201 – 204.

Sharma, S.P., Sharma, P.P., Nehra, S.R. and Khatik, C.L. (2015) Variability and character association in cowpea using *Bradyrhizobium* strain. International Journal of plant sciences; 10:43-48.

Singh, M.K. and Verma, J.S. (1999)Variability and associationanalysis for yield and yield components in cowpeagermplasm.*Indian journal Plant Genetics,* **12**(1): 20-21.

Singh, R., Joshi, B.S. and Singh, S. (1982) Correlation studies incowpea [*Vigna unguiculata* (L.) Walp.]. Trop. *Grain Legume Bull*, **26**(3-5): 6.

Sreekumar, L., Inasi, K.A., Antony, A. and Nair, R.R. (1996) Geneticvariability, heritability and correlation studies in vegetablecowpea (*Vigna unguiculata* var. Sesquipedalis). *South Indian Journal Horticulture,* **44**(1-2): 15-18.

Wright, S. (1921) Correlation and causation. *Journal of Agricultural Research,* **20**:257-287.