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Correlation coefficient analysis for various quantitative traits in cowpea [*Vigna unguiculata* (L.) Walp] Genotypes under different environments (E₁, E₂, E₃ and pooled basis)

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Abstract

A field experiment was conducted during *kharif* season 2015 and *kharif* 2016 to determine correlation coefficient among 30 genotypes for twelve quantitative characters and one qualitative character i.e. protein content taken into consideration. The result revealed that seed yield per plant exhibited significant positive correlation at both genotypic and phenotypic level with biological yield, harvest index and 100-grain weight in (E₁, E₂, E₃ and over pooled basis) and also with pods per plant and number of cluster per plant in atleast two environment (E₁, E₂ and on pooled basis) and plant height in E₂ only. However, seed yield per plant exhibited positive correlation with plant height and pod length both in atleast two environments (E₁, E₃) at both genotypically and phenotypically. Seed yield also revealed with seed protein content non-significant and negative correlation at both genotypic and phenotypic level in environments (E₁, E₂, E₃ and also on pooled basis). Thus, the present study suggests that selecting high yielding Cowpea genotypes for further breeding program.

Keywords: Cowpea, Seed yield, correlation coefficient.

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp] is one of the most important food legumes which serve as vital source of protein in the diet of the people of developing countries. It is widely grown in the third world for its cheap source of dietary protein (Ibrahim *et al.*, 2010) [7]. Cowpea, also popularly called 'beans' is mostly grown in dry areas in mixtures. It is thought that the origin of the cultivated species of cowpea is Africa (Gibbon and Pain, 1988) [6]. Cowpea, a grain legume, very high in protein content (20 – 25%), has been an important crop grown in the tropical and sub-tropical regions of the world; where it serves as a source of protein for both urban and rural populations. It is primarily grown in drier regions of the world where it is one of the most drought-resistant food legumes (Dadson *et al.*, 2005) [5]. Generally, cowpea is one of the most important food leguminous crop plant of great socio-economic, cultural, nutritional importance and a valuable component of the traditional cropping systems in the semi-arid tropics. The choice of cowpea specific genotypes adaptable to this kind of unfavorable environmental condition should be determined by a careful breeding program. Correlation analysis is an easy to use 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 (Bizeti *et al.*, 2004) [4].

Material and Method

Thirty genotypes including three check (RC-101, RC-19 and RCV-7) were evaluated under three environments were created by raising cowpea genotypes in two successive years. In *kharif*, 2015 crop was raised and considered as Environment-1(E₁), while in *kharif*, remaining two crops were planted at two different dates of sowing and considered as Environment-2(E₂) and Environment-3(E₃). Each crop was sown in randomized block design with three replications keeping two rows of each genotype in a plot of 4m length in each replication with the spacing of 30×10 cm. Recommended and uniform agronomical practices was adopted for all the three environments. Five plants in each plot were tagged from the net plot of each treatment in each replication for three environments for recording the observations.

The observation *viz.*, Plant height (cm), Number of branches per plant, Number of pods per plant, Number of clusters per plant, Pod length (cm), Number of seeds per pod, 100-grain weight (g), Seed yield per plant (g), Biological yield per plant (g), Harvest index (%) and Seed protein content (%), whereas, Days to 50% flowering and Days to 75% maturity were recorded on plot basis.

Analysis of variance was estimated according to the procedure. Genotypic and phenotypic coefficients were estimated according to

$$VG = MSG - MSE/r \dots \dots \dots \text{eqn. 1}$$

$$VP = VG + MSE \dots \dots \dots \text{eqn. 2}$$

Where, MSG, MSE and r, are: mean square genotypes, mean square error and number of replicates respectively. The phenotypic coefficient of variation (PCV %) and Genotypic coefficient of variation (GCV %) were estimated by method as:

$$PCV = \sqrt{VP} \times 100 / \bar{X} \dots \dots \dots \text{eqn. 3}$$

$$GCV = \sqrt{VG} \times 100 / \bar{X} \dots \dots \dots \text{eqn. 4}$$

Where, VP, VG and \bar{X} are phenotypic variance, genotypic variance and grand mean respectively for traits under consideration, and were classified as follows:

0 – 10% = low; 10 – 20% = moderate; 20% = high.

Genotypic and phenotypic correlations were estimated according to [31]. $VXY (G) = COV XY (G) / \sqrt{VX (G)} \times \sqrt{VY (G)}$ eqn. 7 $VXY (P) = COV XY (P) / \sqrt{VX (P)} \times \sqrt{VY (P)}$ eqn. 8

Where $COVXY (G)$ is genotypic covariance between x and y; $COV XY (P)$ is phenotypic covariance between x and y; $VX (G)$ and $VX (P)$ are genotypic and phenotypic variances of character x; $VY (G)$ and $VY (P)$ are genotypic and phenotypic variances of character y.

Test of significance of correlation was tested by the following statistics: $t = r\sqrt{n - 2} / \sqrt{1 - r^2}$ eqn. 9

Where, r and n are correlation coefficients and number of observations respectively. The 't' table was entered with (n – 2) degree of freedom.

Result and Discussion

A perusal of Table 1 to 3 revealed that seed yield per plant exhibited significant positive correlation at both genotypic and phenotypic level with biological yield ($rg=0.738^{**}$ & $rp=0.705^{**}$), ($rg=0.878^{**}$ & $rp=0.817^{**}$), ($rg=0.740^{**}$ & $rp=0.646^{**}$), ($rg=0.877^{**}$ & $rp=0.730^{**}$), harvest index ($rg=0.223^{*}$ & $rp=0.244^{*}$), ($rg=0.39^{**}$ & $rp=0.393^{**}$), ($rg=0.361^{**}$ & $rp=0.261^{*}$), ($rg=0.323^{**}$ & $rp=0.241^{*}$) and 100-grain weight ($rg=0.354^{**}$ & $rp=0.340^{**}$), ($rg=0.260^{*}$ & $rp=0.256^{*}$) ($rg=0.433^{**}$ & $rp=0.416^{**}$), ($rg=0.359^{**}$ & $rp=0.331^{**}$) in E_1 , E_2 , E_3 and on pooled basis, respectively.

Seed yield showed significant correlation in positive direction at both genotypically and phenotypically with number of pods per plant ($rg=0.505^{**}$ & $rp=0.442^{**}$), ($rg=0.372^{**}$ & $rp=0.313^{**}$), ($rg=0.412^{**}$ & $rp=0.284^{**}$) and number of cluster per plant ($rg=0.466^{**}$ & $rp=0.361^{**}$), ($rg=0.339^{**}$ & $rp=0.269^{*}$), ($rg=0.327^{**}$ & $rp=0.263^{*}$) in at least two environment (E_1 , E_2) and also on pooled basis and plant height ($rg=0.268^{*}$ & $rp=0.266^{*}$) in E_2 only.

Seed yield exhibited significant genotypic association with days to 75% maturity ($rg=0.207^{*}$) and ($rg=0.511^{**}$) in E_3 and pooled basis, respectively, whereas, days to 50% flowering ($rg=0.511^{**}$) over pooled basis. Sharma *et al* (2016) [17] observed that seed yield per plant showed significant positive correlation with days to 50% flowering, number of cluster per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100-grain weight and

plant height. These finding also supported by Bhardwaj *et al.* (2014) [3], Kamai *et al.* (2014) [8] for harvest index and Bhradu and Navale (2011) [2].

However, seed yield per plant exhibited significant genotypic negative correlation with number of branches per plant ($rg= -0.215^{*}$), ($rg= -0.210^{*}$) and ($rg= -0.215^{*}$) in E_1 , E_2 and on pooled basis, respectively. Whereas in E_3 it showed significant negative association at both level ($rg= -0.230^{*}$ & $rp= -0.216^{*}$). The present findings are in accordance with the findings of Padi *et al.* (2003) [13] and Kaveris *et al.* (2007).

However, seed yield per plant exhibited positive correlation at both genotypically and phenotypically with plant height and pod length both in atleast two environments (E_1 , E_3) and also on pooled basis and seeds per pod in E_1 only. Whereas, genotypic negative correlation and positive phenotypic correlation for number of seeds per pod in E_3 only and pod length showed positive genotypic association in E_2 only.

Days to 50% flowering exhibited negative correlation in E_2 only at both level genotypic and phenotypic. Similar result also supported by Manggoel *et al* (2012) [11] and Saini *et al* (2007) [14].

Seed yield per plant showed significant genotypic positive correlation with Days to 75% maturity ($rg=0.207^{*}$) and ($rg=0.224^{*}$) in E_3 and on pooled basis and also exhibited correlation in negative direction at genotypic level in E_2 only. Kumari *et al* (2010) [10] it was observe that seed yield was positively and significantly correlated with days to maturity at genotypic level. In contradictory to this, similar finding as per Aliyu and Makinde (2016) [1] that seed yield per plant exhibited negative correlation with days to maturity. Seed yield revealed that seed protein content exhibited non-significant and negative correlation at both genotypic and phenotypic level in E_1 , E_2 , E_3 and pooled basis. Similar result as per Sharma *et al.* (2016) [17]. Seed protein content exhibited negative correlation with days to 75% maturity ($rg= -0.462^{**}$ & $rp= -0.251^{*}$), ($rg= -0.549^{**}$ & $rp= -0.382^{**}$) ($rg= -0.573^{**}$ & $rp= -0.276^{**}$) and 100-grain weight ($rg= -0.276^{**}$ & $rp= -0.280^{**}$), ($rg= -0.337^{**}$ & $rp= -0.318^{**}$), ($rg= -0.262^{*}$ & $rp= -0.242^{*}$) in atleast two environments (E_2 , E_3) and also on pooled basis and plant height ($rg= -0.313^{**}$, $rp= -0.301^{**}$) in E_2 only. Seed protein content showed significant negative correlation at both genotypically and phenotypically with days to 50% flowering ($rg= -0.549^{**}$ & $rp= -0.303^{**}$) in E_3 and ($rg= -1.427^{**}$) at only genotypic level over pooled basis. Sharma *et al* (2016) [17] they revealed that seed protein content showed significant negative correlation with days to maturity.

Seed protein content also expressed significant positive correlation at both genotypic and phenotypic level with pod length ($rg=0.235^{*}$ & $rp=0.221^{*}$) in E_2 and ($rg=0.223^{*}$) at only genotypic level in E_1 . However, exhibited significant genotypic association with harvest index ($rg=0.244^{*}$) in E_3 only.

Further, perusal of Table 4.4 to 4.7 showed that 100-grain weight exhibited significant positive correlation with biological yield per plant ($rg=0.558^{**}$ & $rp=0.540^{**}$), ($rg=0.400^{**}$ & $rp=0.368^{**}$), ($rg=0.244^{*}$ & $rp=0.246^{*}$), ($rg=0.484^{**}$ & $rp=0.384^{**}$) in all the environments and also on pooled basis.

100-grain weight showed significant correlation in negative direction at both genotypically and phenotypically with plant height ($rg= -0.227^{*}$ & $rp= -0.219^{*}$), ($rg= -0.359^{**}$ & $rp= -0.355^{**}$), ($rg= -0.284^{**}$ & $rp= -0.234^{*}$) in at least two environments (E_2 , E_3) and also on pooled basis. Selvakumar and Ushakumari (2013) [15] also revealed 100-grain weight

had significant positive correlation with plant height.

100-grain weight showed significant correlation in positive direction at both genotypically and phenotypically with pod length ($rg=0.575^{**}$ & $rp=0.524^{**}$), ($rg=0.679^{**}$ & $rp=0.536^{**}$), ($rg=0.580^{**}$ & $rp=0.419^{**}$) in E_1 , E_3 and on pooled basis and days to 75% maturity ($rg=0.334^{**}$ & $rp=0.309^{**}$), ($rg=0.442^{**}$ & $rp=0.214^*$), ($rg=0.448^{**}$, $rp=0.215^*$) in E_1 , E_2 and on pooled basis respectively, whereas pod length ($rg=0.263^*$) in E_2 and days to 75% maturity ($rg=0.227^*$) in E_3 both are genotypic positive correlation, also reported by Sharma *et al.* (2016)^[17] revealed that 100-grain weight exhibit significant positive correlation with number of branches per plant and Selvakumar and Ushakumari (2013)^[15] for pod length and days to maturity.

100-grain weight showed significant positive association with number of branches per plant ($rg=0.275^{**}$ & $rp=0.271^{**}$), ($rg=0.243^*$ & $rp=0.244^*$) at both genotypically and phenotypically in E_1 , E_2 and also on pooled basis ($rg=0.230^*$) at only genotypic level. Sharma *et al.* (2016)^[17] revealed that 100-grain weight exhibit significant positive correlation with number of branches per plant at both genotypic and phenotypic level.

100-grain weight exhibited significant positive correlation with days to 50% flowering ($rg=0.245^*$), ($rg=0.288^{**}$), ($rg=0.977^{**}$) at only genotypic level respective in E_2 , E_3 and pooled basis, however, exhibited significant negative correlation with harvest index ($rg=-0.287^{**}$ & $rp=-0.270^{**}$) at both genotypically and phenotypically in E_1 and ($rg=-0.228^*$) genotypically negative correlation over pooled basis. Similar finding as per Sharma *et al.* (2016)^[17] and Selvakumar and Ushakumari (2013)^[15].

Table 4.4 to 4.7 perusal that harvest index revealed significant and genotypic correlation in positive direction with days to 50% flowering ($rg=0.391^{**}$), ($rg=-0.601^{**}$) in E_1 and on pooled basis, respectively and significant negative genotypic correlation with days to 50% flowering ($rp=-0.239^*$) at phenotypic level in E_1 and also revealed significant positive correlation with number of clusters per plant ($rg=0.224^*$) at genotypically in E_2 only.

Harvest index exhibited significant correlation in positive direction at both genotypic and phenotypic level with number of pods per plant ($rg=0.372^{**}$ & $rp=0.321^*$) in E_2 only and showed significant negative association ($rg=-0.219^*$) in E_3 only.

Harvest index showed significant negative correlation at both genotypically and phenotypically in E_1 with number of branches per plant ($rg=-0.302^{**}$ & $rp=-0.266^*$), biological yield per plant ($rg=-0.485^{**}$ & $rp=-0.448^{**}$) and days to 75% maturity ($rg=-0.549^{**}$ & $rp=-0.482^{**}$) and also showed significant negative genotypic correlation with number of branches per plant ($rg=-0.291^{**}$) on pooled basis, number of seeds per pod ($rg=-0.219^*$) in E_3 and days to 75% maturity ($rg=-0.210^*$) and ($rg=-0.242^*$) in E_2 and E_3 , respectively. Sharma *et al.* (2016)^[17] revealed that harvest index exhibit significant negative correlation with days to maturity and biological yield at both genotypic and phenotypic level.

Biological yield per plant exhibited significant positive correlation at both genotypic and phenotypic level with days to 75% maturity ($rg=0.502^{**}$ & $rp=0.450^{**}$), ($rg=0.494^{**}$ & $rp=0.295^{**}$), ($rg=0.447^{**}$ & $rp=0.257^*$), number of clusters per plant ($rg=0.411^{**}$ & $rp=0.326^{**}$), ($rg=0.372^{**}$ & $rp=0.231^*$) ($rg=0.334^{**}$ & $rp=0.257^*$) ($rg=0.381^{**}$ & $rp=0.271^{**}$) in E_1 , E_2 , E_3 and over pooled basis except days to 75% maturity in E_2 , respectively.

Biological yield per plant exhibited significant association in

positive direction at both genotypically and phenotypically with days to 50% flowering ($rg=0.375^{**}$ & $rp=0.235^*$), pod length ($rg=0.248^*$ & $rp=0.231^*$) both in E_1 and number of pods per plant ($rg=0.439^{**}$ & $rp=0.380^{**}$), ($rg=0.348^{**}$ & $rp=0.241^*$) respective in E_1 and pooled basis. Whereas, significantly positive genotypic correlation with days to 50% flowering ($rg=0.722^{**}$) on pooled basis and pod length ($rg=0.219^*$), ($rg=0.251^*$) respective in E_3 and on pooled basis similar result also reported by Sharma *et al.* (2016)^[17] and Manggoel *et al.* (2012)^[11].

Number of seeds per pod showed significant positive correlation at both genotypic and phenotypic level with pod length ($rg=0.363^{**}$ & $rp=0.360^{**}$), ($rg=0.339^{**}$ & $rp=0.247^*$), ($rg=0.303^{**}$ & $rp=0.241^*$), plant height ($rg=0.394^{**}$ & $rp=0.316^{**}$), ($rg=0.259^*$ & $rp=0.215^*$), ($rg=0.296^{**}$ & $rp=0.230^*$) except pod length in E_2 and plant height in E_1 , whereas, number of branches per plant ($rg=0.213^*$ & $rp=0.213^*$) in E_2 only.

Number of seeds per pod revealed significant correlation in negative direction with days to 75% maturity ($rg=-0.517^{**}$), ($rg=-0.235^*$) in E_2 and pooled basis, respectively and days to 50% flowering ($rg=-0.314$), ($rg=-0.484^{**}$), ($rg=-0.631^{**}$) respective in E_1 , E_2 and over pooled basis and significant positive genotypic correlation with days to 50% flowering ($rg=0.292^{**}$) and number of clusters per plant ($rg=0.235^*$) both in E_3 , also reported by Sharma *et al.* (2016)^[17], Diriba Shanko *et al.* (2014)^[16] and Selvakumar and Ushakumari (2013)^[15] revealed number of seeds per pod showed significant positive correlation with days to 50% flowering, plant height and pod length.

Pod length showed significant negative correlation at both genotypic and phenotypic level with plant height ($rg=-0.314^{**}$ & $rp=-0.287^{**}$), ($rg=-0.530^{**}$ & $rp=-0.407^{**}$), ($rg=-0.419^{**}$ & $rp=-0.258^*$) in E_1 , E_3 and pooled basis and number of pods per plant ($rg=-0.396^{**}$ & $rp=-0.280^{**}$) in E_3 only.

Pod length also showed significant positive and genotypic correlation with days to 50% flowering ($rg=0.412^{**}$) and days to 75% maturity ($rg=0.303^{**}$) in E_2 and E_3 , respectively and significant negative genotypic correlation with days to 50% flowering ($rg=-0.280^{**}$) in E_1 only. Sharma *et al.* (2016)^[17] they revealed that pod length exhibit significant negative correlation with days to 50% flowering, days to maturity at both genotypic and phenotypic level. Similar studies was done by Diriba Shanko *et al.* (2014)^[16] and Selvakumar and Ushakumari (2013)^[15].

Table 4.4 to 4.7 further revealed number of pods per plant exhibited significant positive correlation with number of clusters per plant ($rg=0.869^{**}$ & $rp=0.638^{**}$), ($rg=0.523^{**}$ & $rp=0.344^{**}$), ($rg=0.402^{**}$ & $rp=0.311^{**}$) and ($rg=0.759^{**}$ & $rp=0.438^{**}$) plant height ($rg=0.328^{**}$ & $rp=0.257^*$) ($rg=0.368^{**}$ & $rp=0.318^{**}$) ($rg=0.328^{**}$ & $rp=0.214^*$) at both genotypic and phenotypic level in E_1 , E_2 , E_3 and pooled basis except plant height in E_1 , respectively, while number of branches per plant exhibited significant negative correlation ($rg=-0.471^{**}$ & $rp=-0.385^{**}$), ($rg=-0.410^{**}$ & $rp=-0.304^{**}$) ($rg=-0.419^{**}$ & $rp=-0.247^*$) in at least two environments (E_1 , E_2) and pooled basis, respectively. Diriba Shanko *et al.* (2014)^[16] resulting that number of pods per plant showed significant positive correlation with plant height, number of primary branches per plant and days to 50% flowering at both genotypic and phenotypic level.

However, number of pods per plant revealed significantly and genotypic positive correlation with days to 50% flowering ($rg=0.232^*$) in E_1 , whereas significant negative correlation

with days to 50% flowering ($rg = -0.441^{**}$) and days to 75% maturity ($rg = -0.319^{**}$) both at only genotypic level in E_2 , similar result was also reported by Meena *et al* (2015) [12] significant negative correlation with days to 50% flowering as well as days to maturity, Diriba Shanko *et al.* (2014) [16] and Kumari *et al* (2010) [10].

Number of clusters per plant exhibited significant negative correlation with number of branches per plant ($rg = -0.602^{**}$ & $rp = -0.401^{**}$), ($rg = -0.408^{**}$ & $rp = -0.312^{**}$), ($rg = -0.488^{**}$ & $rp = -0.373^{**}$) at both genotypic and phenotypic level, respective in E_1 , E_3 and over pooled basis, whereas significant negative phenotypic correlation ($rp = -0.412^{**}$) and significant positive genotypic correlation ($rg = 0.471^{**}$) in E_1 similar finding was also reported by Sharma *et al.* (2016) [17] that number of clusters per plant exhibit significant negative correlation with number of branches per plant at both genotypic and phenotypic level,

Number of clusters per plant exhibited significant positive correlation at both genotypically and phenotypically in E_2 with plant height ($rg = 0.276^{**}$ & $rp = 0.228^*$) and significant positive genotypic correlation and significant negative genotypic correlation both with days to 50% flowering ($rg = 0.232^*$) in E_1 and ($rg = -0.493^{**}$) in E_2 , respectively. Selvakumar and Ushakumari (2013) [15] they revealed cluster per plant revealed significant negative correlation with plant height at genotypic level.

Number of branches per plant showed significant association in positive direction with days to 75% maturity ($rg = 0.290^{**}$ & $rp = 0.274^{**}$) at both genotypic and phenotypic level in E_1 and days to 50% flowering ($rg = 0.335^{**}$) also showed significant positive genotypic correlation over pooled basis. Sharma *et al.* (2016) [17] revealed that number of primary branches per plant exhibited significant positive correlation with day to maturity at only genotypic level, similar studies also done by Meena *et al* (2015) [12], Selvakumar and Ushakumari (2013) [15] revealed number of branches per plant showed significant positive correlation with days to 50% flowering at only genotypic level and Kumari *et al* (2010) [10].

Plant height exhibited significant negative correlation at both genotypic and phenotypic level with days to 50% flowering ($rg = -0.713^{**}$ & $rp = -0.314^{**}$) in E_2 and days to 75% maturity ($rg = -0.556^{**}$ & $rp = -0.242^*$), ($rg = -0.354^{**}$ & $rp = -0.262^*$) in atleast two environment (E_2 and E_3), respectively and also for days to 75% maturity ($rg = -0.343^{**}$) at only genotypic level over pooled basis.

However, plant height showed significant and genotypic positive correlation with days to 50% flowering ($rg = 0.264^*$) and days to 75% maturity ($rg = 0.219^*$) both in E_1 , similar result was obtained by Selvakumar and Ushakumari (2013) [15] revealed plant height exhibited significant negative correlation with days to 50% flowering.

Further days to 75% maturity showed significant positive correlation at both genotypically and phenotypically with days to 50% flowering ($rg = 0.786^{**}$ & $rp = 0.514^{**}$) and ($rg = 1.174^{**}$ & $rp = 0.288^{**}$) in E_1 and on pooled basis, respectively and significant positive and genotypic correlation with days to 50% flowering ($rg = 0.560^{**}$) in E_3 . Whereas days to 75% maturity showed significant genotypic association in negative direction with days to 50% flowering ($rg = -0.213^*$) in E_2 . Meena *et al* (2015) [12] found days to maturity showed significant negative correlation with days to 50% flowering at both genotypic and phenotypic level, similar finding as per Diriba shanko *et al* (2014) [16] and Selvaumar and Ushakumari (2013) [15].

The trait days to 75% maturity had negative and non-

significant correlation with seed yield per plant in E_2 . Similar results are also obtained by Sharma *et al.* (2016) [17] and Kamai *et al.* (2014) [8].

From the present investigation, it was obvious that biological yield, 100-grain weight, harvest index, number of pods per plant and number of clusters per plant were the main attributes affecting the grain yield and simultaneous selection for all these traits would be an ideal criterion.

Table 1: Genotypic and Phenotypic correlation coefficient between seed yield per plant and other characters in cowpea in E1

Character	D/F	Days to 50% Flowering	Days to 75% Maturity	Plant Height (cm)	Branches/ Plant	Cluster/ Plant	Pods/ Plant	Pod Length (cm)	Seed/ Pod	Biological Yield/ Plant (g)	Harvest Index (%)	100-grain Weight (g)	Seed Protein Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	1.000	0.786**	0.264*	0.006	0.232*	0.232*	-0.280**	-0.314**	0.375**	0.391**	0.144	-0.134	0.140
	P	1.000	0.514**	0.192	0.007	0.156	0.102	-0.197	-0.132	0.235**	-0.239*	0.104	-0.097	0.143
Days to 75% Maturity	G		1.000	0.219*	0.290**	-0.034	-0.060	-0.157	-0.177	0.502**	-0.549**	0.334**	-0.141	0.167
	P		1.000	0.201	0.274**	0.014	-0.052	-0.133	-0.171	0.450**	-0.482**	0.309**	-0.133	0.142
Plant Height (cm)	G			1.000	0.032	0.074	0.148	-0.314**	0.201	0.176	-0.063	-0.168	0.010	0.193
	P			1.000	0.030	0.065	0.131	-0.287**	0.191	0.173	-0.060	-0.168	0.010	0.188
Branches/ Plant	G				1.000	0.471**	-0.471**	0.179	0.068	-0.046	-0.302**	0.275**	0.022	-0.215*
	P				1.000	-0.412**	-0.385**	0.149	0.062	-0.036	-0.266*	0.271**	0.022	-0.198
Cluster/ Plant	G					1.000	0.869**	-0.080	0.036	0.411**	0.020	-0.098	-0.155	0.466**
	P					1.000	0.638**	-0.044	0.016	0.326**	-0.037	-0.082	-0.131	0.361**
Pods/ Plant	G						1.000	-0.056	-0.063	0.439**	0.043	-0.157	0.056	0.505**
	P						1.000	-0.067	-0.064	0.380**	0.021	-0.136	0.048	0.442**
Pod Length (cm)	G							1.000	0.363**	0.248*	-0.095	0.575**	0.223*	0.191
	P							1.000	0.360**	0.231*	-0.093	0.524**	0.204	0.169
Seed/ Pod	G								1.000	-0.010	0.040	0.052	0.002	0.011
	P								1.000	-0.013	0.029	0.046	0.002	0.024
Biological Yield/ Plant (g)	G									1.000	-0.485**	0.558**	-0.063	0.738**
	P									1.000	-0.448**	0.540**	-0.064	0.705**
Harvest Index (%)	G										1.000	-0.287**	-0.080	0.223**
	P										1.000	-0.270**	-0.073	0.244**
100-grain Weight (g)	G											1.000	-0.106	0.354**
	P											1.000	-0.106	0.340**
Seed Protein Content (%)	G												1.000	-0.146
	P												1.000	-0.143

*and ** significance levels of 5% and 1% respectively

Table 2: Genotypic and Phenotypic correlation coefficient between seed yield per plant and other characters in cowpea in E2

Character	D/F	Days to 50% Flowering	Days to 75% Maturity	Plant Height (cm)	Branches/ Plant	Cluster/ Plant	Pods/ Plant	Pod Length (cm)	Seed/ Pod	Biological Yield/ Plant (g)	Harvest Index (%)	100-grain Weight (g)	Seed Protein Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	1.000	-0.213*	-0.713**	0.059	-0.493**	-0.441*	0.412**	-0.484**	0.064	0.065	0.245*	-0.023	-0.119
	P	1.000	0.277**	-0.314**	0.092	0.038	-0.006	0.090	0.086	0.046	0.001	0.131	-0.047	-0.007
Days to 75% Maturity	G		1.000	-0.556**	-0.137	-0.110	-0.319**	0.016	-0.517**	0.267*	-0.210*	0.442**	-0.462**	-0.001
	P		1.000	-0.242*	0.048	0.139	0.046	-0.097	-0.024	0.086	-0.009	0.214*	-0.251*	0.055
Plant Height (cm)	G			1.000	-0.034	0.276**	0.328**	-0.077	0.394**	0.109	0.083	-0.227*	-0.313**	0.268*
	P			1.000	-0.031	0.228*	0.257*	-0.072	0.316**	0.095	0.060	-0.219*	-0.301**	0.266*
Branches/ Plant	G				1.000	-0.602**	-0.410**	-0.089	0.213*	-0.023	-0.172	0.243*	-0.047	-0.210*
	P				1.000	-0.401**	-0.304**	-0.073	0.213*	-0.030	-0.128	0.244*	-0.056	-0.181
Cluster/ Plant	G					1.000	0.523**	0.150	-0.155	0.372**	0.224*	-0.069	-0.152	0.339**
	P					1.000	0.344**	0.031	0.035	0.231*	0.093	-0.032	-0.127	0.269*

Pods/ Plant	G						1.000	0.162	0.152	0.139	0.529**	-0.051	0.130	0.372**
	P						1.000	0.077	0.148	0.151	0.298*	-0.041	0.100	0.313**
Pod Length (cm)	G							1.000	0.100	0.014	-0.026	0.263*	0.235*	0.066
	P							1.000	0.106	-0.021	-0.057	0.191	0.221*	-0.006
Seed/ Pod	G								1.000	-0.091	-0.066	0.059	-0.120	-0.008
	P								1.000	-0.121	-0.003	0.067	-0.101	0.012
Biological Yield/ Plant (g)	G									1.000	0.187	0.400**	-0.161	0.878**
	P									1.000	0.094	0.368**	-0.146	0.817**
Harvest Index (%)	G										1.000	-0.179	0.042	0.393**
	P										1.000	-0.121	0.038	0.319**
100-grain Weight (g)	G											1.000	-0.276**	0.260*
	P											1.000	-0.280**	0.256*
Seed Protein Content (%)	G												1.000	-0.057
	P												1.000	-0.062

*and ** significance levels of 5% and 1% respectively

Table 3: Genotypic and Phenotypic correlation coefficient between seed yield per plant and other characters in cowpea in E3

Character	D/F	Days to 50% Flowering	Days to 75% Maturity	Plant Height (cm)	Branches/ Plant	Cluster/ Plant	Pods/ Plant	Pod Length (cm)	Seed/ Pod	Biological Yield/ Plant (g)	Harvest Index (%)	100-grain Weight (g)	Seed Protein Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	1.000	0.560**	0.155	0.105	0.056	0.192	0.106	0.292**	0.068	-0.198	0.288**	-0.549**	0.114
	P	1.000	0.148	0.058	0.056	-0.086	0.023	-0.016	0.158	0.006	-0.102	0.178	-0.303**	0.052
Days to 75% Maturity	G		1.000	-0.354**	0.106	-0.172	-0.040	0.303**	0.012	0.494**	-0.066	0.227*	-0.555**	0.207*
	P		1.000	-0.262*	0.082	-0.004	-0.027	0.120	0.052	0.295**	0.030	0.170	-0.382**	0.164
Plant Height (cm)	G			1.000	-0.038	0.057	0.368**	-0.530**	0.259*	-0.073	-0.141	-0.359**	0.040	0.088
	P			1.000	-0.034	0.059	0.318**	-0.407**	0.215*	-0.069	-0.119	-0.355**	0.038	0.076
Branches/ Plant	G				1.000	-0.408**	-0.048	0.165	0.204	0.186	-0.137	0.104	-0.058	-0.230*
	P				1.000	-0.312**	-0.048	0.173	0.162	0.173	-0.082	0.097	-0.029	-0.216*
Cluster/ Plant	G					1.000	0.402**	0.075	0.235*	0.334**	0.006	0.038	0.006	0.155
	P					1.000	0.311**	0.133	0.145	0.257*	-0.058	0.032	0.024	0.157
Pods/ Plant	G						1.000	-0.396**	-0.036	0.187	-0.004	-0.092	0.004	0.094
	P						1.000	-0.280**	-0.050	0.163	-0.060	-0.075	0.041	0.086
Pod Length (cm)	G							1.000	0.339**	0.251*	-0.042	0.679**	0.047	0.139
	P							1.000	0.247*	0.191	-0.018	0.536**	0.046	0.146
Seed/ Pod	G								1.000	0.118	-0.219*	0.146	-0.021	-0.017
	P								1.000	0.120	-0.116	0.130	-0.006	0.013
Biological Yield/ Plant (g)	G									1.000	0.313**	0.244*	-0.099	0.740**
	P									1.000	0.194	0.246*	-0.066	0.646**
Harvest Index (%)	G										1.000	-0.141	0.244*	0.361**
	P										1.000	-0.114	0.142	0.261**
100-grain Weight (g)	G											1.000	-0.337**	0.433**
	P											1.000	-0.318**	0.416**
Seed Protein Content (%)	G												1.000	-0.098
	P												1.000	-0.070

*and ** significance levels of 5% and 1% respectively

Table 4.7: Genotypic and Phenotypic correlation coefficient between seed yield per plant and other characters in cowpea over pooled

Character	D/F	Days to 50% Flowering	Days to 75% Maturity	Plant Height (cm)	Branches/ Plant	Cluster/ Plant	Pods/ Plant	Pod Length (cm)	Seed/ Pod	Biological Yield/ Plant (g)	Harvest Index (%)	100-grain Weight (g)	Seed Protein Content (%)	Seed Yield/ Plant (g)
Days to 50% Flowering	G	1.000	1.174**	-0.107	0.335**	0.042	0.160	0.141	-0.631**	0.722**	-0.601**	0.977**	-1.427**	0.511**
	P	1.000	0.288**	-0.004	0.049	0.053	0.047	-0.049	0.016	0.112	-0.151	0.127	-0.120	0.064
Days to 75% Maturity	G		1.000	-0.343**	0.200	-0.119	-0.173	0.126	-0.235*	0.447**	-0.242*	0.448**	-0.573**	0.224*
	P		1.000	-0.097	0.119	0.044	-0.015	-0.016	-0.029	0.257*	-0.177	0.215*	-0.276**	0.115
Plant Height (cm)	G			1.000	0.004	0.132	0.328**	-0.419**	0.296**	0.078	-0.065	-0.284**	-0.085	0.205
	P			1.000	-0.005	0.106	0.214*	-0.258*	0.230*	0.085	-0.048	-0.234*	-0.073	0.182
Branches/ Plant	G				1.000	-0.488**	-0.419**	0.112	0.168	0.037	-0.291**	0.230*	-0.034	-0.215*
	P				1.000	-0.373**	-0.247*	0.085	0.143	0.025	-0.184	0.206	-0.021	-0.197
Cluster/ Plant	G					1.000	0.759**	0.035	0.076	0.381**	0.046	-0.022	-0.085	0.327**
	P					1.000	0.438**	0.041	0.069	0.271**	-0.014	-0.024	-0.071	0.263*
Pods/ Plant	G						1.000	-0.134	-0.062	0.348**	0.072	-0.079	0.082	0.412**
	P						1.000	-0.108	-0.005	0.241*	0.042	-0.086	0.058	0.284**
Pod Length (cm)	G							1.000	0.303**	0.219*	-0.076	0.580**	0.192	0.148
	P							1.000	0.241*	0.135	-0.063	0.419**	0.153	0.102
Seed/ Pod	G								1.000	0.043	-0.028	0.106	-0.056	0.003
	P								1.000	-0.008	-0.010	0.082	-0.035	0.016
Biological Yield/ Plant (g)	G									1.000	-0.048	0.484**	-0.138	0.877**
	P									1.000	-0.181	0.384**	-0.093	0.730**
Harvest Index (%)	G										1.000	-0.228*	0.057	0.323**
	P										1.000	-0.177	0.002	0.241*
100-grain Weight (g)	G											1.000	-0.262*	0.359*
	P											1.000	-0.242*	0.331*
Seed Protein Content (%)	G												1.000	-0.094
	P												1.000	-0.091

*and ** significance levels of 1% & 5%, respectively

Conclusion

The present study revealed that genotypic and phenotypic positive correlation much emphasis should give on biological yield per plant, harvest index, 100-grain weight, seeds per pod and clusters per plant. Hence, improving one or more traits could result in high seed yield in cowpea.

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