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Genetic variability and character association studies for yield attributes in cowpea (*Vigna unguiculata* L., Walp)

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Abstract

Cowpea [*Vigna unguiculata* (L.) Walp.], is a legume and one of the most ancient crops known to man and grown in tropical and subtropical regions having a high nutritional value. Despite of its importance, the utilization of genetic diversity and germplasm characterization in cowpea breeding program is lacking. Adequate information on the relationship between yield components and seed yield is, however, crucial for the development of better-quality varieties to improve farmer's field yield. Therefore, eleven morphological characters were analysed for genetic variability and correlation studies in thirty-three cowpea genotypes. Data collected on plant vigour indices, yield components and seed yield were analysed for variance components, Pearson correlation coefficient and structural equation modelling for path analysis. The genotype exhibited significant variation for all yield components including seed yield. In addition, the variance estimates indicated that substantial variations recorded were mostly genetic with high heritability values. Importantly, all seed yield components were significantly correlated with each other and to total seed yield. Harvest index, however, recorded highest coefficient values ($r=0.91$; $p<0.001$; 3.58^{**}) followed by number of pod per plant ($r=0.61$; $p<0.001$; 1.36^{**}) and pod length ($r=0.28$; $p<0.001$; 5.30^{**}) for both Pearson correlation and path analysis, respectively, suggesting its importance as a yield component with highest direct effect on seed yield and should be a core selection index in cowpea breeding.

Keywords: Cowpea, correlation, path analysis, seed yield, variability

Introduction

The world is facing major critical situations of malnutrition in poor developing countries and prevalence of chronic diseases in well-off people in developed countries. Legumes are well-known for their protein-richness, of which cowpea has gained more attention due to its remarkable nutritional profile and nutraceutical properties that make it unique among other pulses (Dhanasekar *et al.* 2021) [9]. Cowpea is known as “the poor man’s meat” because of its protein-rich nature complemented by its less expensive and affordable access to rural poor people (Dugje *et al.* 2022) [10], and also because the protein content is approximately equal to certain meat types (18-25%). Cowpea is inherently tolerant to drought and heat and has the ability to fix nitrogen even in very poor soils. It is regarded as a key protein source for the urban and poor rural people and plays an important role in fighting malnutrition. Both grain and leaves are edible products of cowpea that are rich and cheap sources of high-quality protein.

The fruits are consumed at all stages of growth and young leaves are often used for soups. It also has digestible and non-digestible carbohydrates, potassium, and very low lipid and sodium content. Cowpea leaves are a nutritious food source, with an abundance of protein and minerals, digestible and non-digestible carbohydrates, and potassium but low lipids and sodium (Kamara *et al.* 2010) [14]. Leaves show higher nutritional content than grains. Nutritional analysis of diverse cowpea genotypes on the basis of grain mineral elements and crude protein content is essential in the identification of potential candidate parental genotypes to develop nutritionally enhanced cowpea cultivars.

Worldwide cowpea occupied 14.9 million hectares with production of 8.9 million tonnes (FAOSTAT, 2021) [3].

In India, it is cultivated mainly in Rajasthan, Maharashtra, Karnataka, Gujarat, Tamil Nadu, Andhra Pradesh and Madhya Pradesh. In India area under this crop was 55,800 hectares with a production of 35,600 tonnes with productivity of 638.6 kg per ha (INDIASTAT, 2021). Cultivation of cowpea is economic as it requires low input and has short maturity. As compared to crops like cereals, cowpea offers better chances of crop production under adverse conditions of moisture stress and low fertility but the present-day cultivars exhibit lower productivity, non-synchronous flowering and fruiting, unresponsive to high doses of inputs like fertilizers, irrigation, tillage, etc and unstability in production (Sharma *et al.* 2022) [26-27]. Non-suitability to various cropping systems, lodging and shattering susceptibility, long duration, complete or partial absence of genetic resistance of major insect pests and diseases which cause considerable economic loss. Development of cultivars with early maturity, acceptable grain quality and resistance to pests and diseases has significantly increased the yield and cultivated area.

Variance component analysis and correlation analysis has remained an important tool for assessing genetic variability among individuals in a population (Burton, 1952; Johnson *et al.* 1955; Allard 1960) [6, 13, 2] to determine the relationship between plant characters (Sharma and Sridevi 2016) [28]. Studies on genetic variability and phenotypic stability (Patel *et al.* 2021 and Sharma *et al.* 2022) [26-27] and correlation analysis nonetheless is an important tool for determining the relationships between plant characters; however, correlation coefficients can be misleading if the correlation between two traits is a consequence of the indirect effect of other traits (Bizeti *et al.* 2004) [15]. Path analysis on the other hand is an excellent platform for studying interrelated components of complex traits in plants (Singh and Chaudhary 1977) [29], because it partitions the effect into component parts: (i) direct effect, which is a standardized partial regression coefficient for the predictor variable and, (ii) indirect effect, which involve the product of a correlation coefficient between two predictor variables (Dewey and Lu 1959). The goal of this study is to apply correlation and path analysis to plant data from 33 cowpea genotypes in order to determine yield components that are critical for selection and improvement of cowpea.

Materials and Methods

Total thirty-three diverse genotypes of cowpea employed in the present study were procured from Pulses Research Station, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India and used for the variability and correlation analysis. The seeds were sown in a Randomized Block Design (RBD) with three replications in July, 2023. Each genotype was accommodated in a single row of 4 m length with a spacing 45 cm between row and 15 cm between plants. All the recommended crop production and protection practices were followed to raise the good crop. The land selected for the experiment is sandy loam. Five competitive plants per genotype were randomly selected for recording observations on eleven characters, namely days to flowering, days to maturity, number of branches per plant, plant height (cm), number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), harvest index (%), protein content (%) and seed yield per plant (g) in each replication and averages were worked out for statistical analysis. The mean values for all the characters

and genotypes were used for the construction of dendrogram. According to Panse and Sukhatme's descriptions, the data of different characters were examined (1978) and GCV and PCV by method suggested by Burton (1952) [6]. Following Hazel's (1943) [12] method, the genotypic and phenotypic correlations were calculated (1943). Analysis of path coefficients was performed using the Wright (1921) [33] recommended methodology.

Results and Discussion

Genetic variability, heritability and genetic advance

Genetic variability represents diversity of alleles, genes, and genetic traits present within a population. GCV (Genotypic Coefficient of Variation), measures the genetic variability or variation due to genetic factors within a population. PCV (Phenotypic Coefficient of Variation), measures the total variation in a trait observed within a population, including both genetic and environmental factors. Variability parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_b), and genetic advance as a percentage of mean (GA % of mean), were calculated based on variance components and mean values. All these parameters are presented in Table 1. For several traits such as number of pod per plant (26.53, 29.65), plant height (19.38, 20.08), Seed yield per plant (27.52, 29.79), harvest index (34.50, 40.44), both GCV and PCV estimates were high. The elevated GCV values, coupled with slightly higher PCV values, indicate substantial variation among the genotypes. Therefore, straightforward selection methods would be effective for further enhancing this crop. Similar findings were reported by Gerrano *et al.* (2015) [11], Ravi (2015) [22], and Sarath and Reshma, (2017) [25] Lal *et al.*, (2018) [15].

Heritability is a statistical measure that quantifies the proportion of phenotypic variation in a trait within a population that is attributable to genetic factors. Genetic advance is a term used in plant breeding and genetics to measure the progress made in improving a particular trait through selective breeding. It represents the average increase in the trait value achieved by selecting and breeding individuals from the population with the highest trait values. It provides breeders with valuable information on the potential gains that can be achieved through selection for specific traits in breeding programs. High heritability, along with a high genetic advance as a percentage of the mean, were noted for traits such as plant height (93.13, 38.53), number of pod per plant (80.07, 48.90), pod length (97.47, 23.56), 100-seed weight (90.45, 40.45), harvest index (72.74, 60.61) and seed yield per plant (85.36, 52.39). This suggests favourable potential for improvement through selection, as these traits are primarily influenced by additive genetic action. Therefore, a straight forward selection approach would be beneficial for enhancing these characteristics. These results are similar to the findings of Gerrano *et al.* (2015) [11], Ravi (2015) [22] and Sanjeev *et al.* (2016) [23].

High heritability values in yield contributing characters are useful while making selection. It indicated that the variation in these characters was mainly under genetic control and was less influenced by environment but selection based on this factor alone may limit the progress, as the same is also prone to environmental changes. High genetic variations combined with high heritability could provide effective

selection of phenotypic trait for further improvement in cowpea through hybridization. Mittal *et al.* (2010) [18] advocated that it is necessary to estimate broad sense heritability in conjunction with the genetic advance.

Correlation coefficients analysis

The result of correlation analysis indicated that the absolute values of genotypic correlation coefficient were slightly higher than corresponding phenotypic correlation coefficient values for almost interrelationships among 11 studied traits (Table 2). In the present study, the seed yield per plant exhibited highest and positive significant correlation at both genotypic and phenotypic levels with harvest index (0.911, 0.801), followed by number of pod per plant (0.612, 0.523), number of seed per pod (0.345, 0.229), pod length (0.288, 0.256), number of branches per plant (0.259, 0.093) and 100-seed weight (0.314, 0.277). If the selection is made on any of the component traits, simultaneous selection of the all the traits could be achieved. The concurrent results were reported by Aliyu and Makinde (2016) [1], Srinivas *et al.* (2017) [30], Lal *et al.* (2018) [15], for number of branches per plant; by Vidya and Oommen (2002) [34] and Aliyu and Makinde (2016) [1], Lazaridi *et al.* (2017) [35] and Srinivas *et al.* (2017) [30] for number of pods per plant and number of seeds per pod. Whereas, seed yield per plant has shown negative and significant correlations with days to 50% flowering (-0.520, -0.433) and days to maturity (-0.688, -0.428) and protein content (-0.570, -0.379) at genotypic level. Similarly, the negative and significant correlation between the days to 50% flowering and seed yield per plant was reported by Arora *et al.* (2010) [4], Ushakumari *et al.* (2010) [32], Manggoel *et al.* (2012) [16], Udensi *et al.* (2012) [31], Chattopadhyay *et al.* (2014) [31] and Patel *et al.* (2021) [20-21]. It also might be due to high rate of photosynthesis at early stages as compared to the reproductive stages of the plant growth which leads to high seed yield per plant in early flowering genotypes. It indicated that seed yield can be increased whenever there is an increase in characters that showed positive associations with seed yield and vice versa

for characters that showed negative correlations. Hence, characters *viz.*, number of pod per plant, number of branches per plant, 100-seed weight, number of seeds per pod and harvest index could be considered as criteria for selection for higher seed yield as these were mutually and directly associated with seed yield.

Path coefficient analysis

Correlation coefficients reveal the extent and nature of association between yield and its contributing characters but does not exhibit the direct and indirect effects of different contributing characters on yield per se performance. When more variables are considered in correlation, their indirect associations become more complicated, less obvious and somewhat perplexing. In this situation, path coefficient analysis provides an effective means of splitting direct and indirect cause of association and also provides an opportunity of critical evaluation of that specific cause acting to produce a given correlation and also measures the relative importance of each causal factor. In present study, path coefficients were calculated based on genotypic correlation coefficient. The residual effect value was 0.337 (Table 3), the estimates of residual effect reflect the adequacy and appropriateness of the characters chosen for path analysis. Among all the traits under study, harvest index (3.58), pod length (5.30), number of pods per plant (1.36) number of branches per plant (0.48) reflected high direct and positive effect of on seed yield per plant. This suggested that direct selection based on these traits would result in higher breeding efficiency for improving seed yield per plant. Thus, these traits might be estimated as the most important component traits for seed yield per plant. These results were in agreement with earlier findings Udensi *et al.* (2012) [31], Chattopadhyay *et al.* (2014) [31], Sapara and Javia, (2014) [24], Meena *et al.* (2015) [17] and Srinivas *et al.* (2017) [30]. The harvest index, which showed highest direct effect, was also contributing to seed yield per plant indirectly through pod length, number of branches per plant, number of pods per plant.

Table 1: Seed yield genetic variation factors and their contributory traits

Sr. No.	Characters	Range	Mean	GCV (%)	PCV (%)	h ² (b.s) (%)	GA (%)	GA as percent of mean (%)
1	Days to flowering	34.33-50.33	39.87	8.064	9.312	74.99	5.736	14.386
2	Days to maturity	57.33- 71	64.75	3.981	5.359	55.16	3.944	6.091
3	Number of primary branch per plant	3.66-4.93	4.38	5.291	10.942	23.37	0.231	5.27
4	Plant height	40.80-77.53	53.42	19.384	20.086	93.13	20.589	38.537
5	Number of pod per plant	9.1-39.93	26.22	26.532	29.651	80.07	12.825	48.909
6	Number of seed per pod	8.0-16.20	12.77	12.911	16.533	60.98	2.654	20.769
7	Pod length	11.42-18.48	14.62	11.589	11.738	97.47	3.447	23.569
8	100-seed weight	7.0-17.86	12.33	20.649	21.712	90.45	4.991	40.455
9	Harvest index	6.66-27.86	14.50	34.50	40.449	72.74	8.79	60.618
10	Protein content	17.92-21.44	19.82	3.768	5.201	52.48	1.115	5.624
11	Seed yield per plant	15.0-55.20	37.16	27.528	29.795	85.36	19.469	52.393

Where,

GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variance, respectively. h² (b.s) (%), GA and

GAM are broad sense heritability, genetic advance and genetic advance expressed as percent of mean, respectively.

Table 2: Different characters' phenotypic and genotypic correlation coefficients

		DF	DM	NPB	PH	NPP	NSP	PL	HSW	HI	PC	SYP
DF	rg	1.000										
	rp	1.000										
DM	rg	0.829**	1.000									
	rp	0.600**	1.000									
NPB	rg	-0.352**	-0.203	1.000								
	rp	-0.161	-0.120	1.000								
PH	rg	0.312**	0.155	-0.128	1.000							
	rp	0.264*	0.113	-0.014	1.000							
NPP	rg	-0.428**	-0.558**	-0.262*	0.112	1.000						
	rp	-0.331**	-0.386**	-0.062	0.124	1.000						
NSP	rg	-0.524**	-0.528**	-0.228*	-0.347**	0.332**	1.000					
	rp	-0.443**	-0.398**	-0.071	-0.276**	0.262*	1.000					
PL	rg	-0.450**	-0.581**	0.149	-0.252*	0.111	0.765**	1.000				
	rp	-0.400**	-0.427**	0.066	-0.245*	0.093	0.617**	1.000				
HSW	rg	-0.365**	-0.416**	0.406**	-0.357**	-0.059	0.036	0.472**	1.000			
	rp	-0.305**	-0.299**	0.158	-0.327**	-0.063	0.043	0.445**	1.000			
HI	rg	-0.511**	-0.551**	0.075	-0.371**	0.475**	0.317**	0.202	0.238*	1.000		
	rp	-0.441**	-0.339**	0.050	-0.289**	0.363**	0.195	0.182	0.206*	1.000		
PC	rg	0.287**	0.169	-0.554**	0.517**	0.013	0.156	-0.140	-0.538**	-0.596**	1.000	
	rp	0.152	0.116	-0.071	0.363**	0.042	0.173	-0.093	-0.333**	-0.404**	1.000	
SYP	rg	-0.520**	-0.688**	0.259*	-0.309**	0.612**	0.345**	0.288**	0.314**	0.911**	-0.570**	1.000
	rp	-0.433**	-0.428**	0.093	-0.245*	0.523**	0.229*	0.256*	0.277**	0.801**	-0.379**	1.000

*, ** significant at 0.05% and 0.01% level of significance, respectively

DF- days to flowering, DM- days to maturity, NPB- number of branches per plant, PH- plant height, NPP- number of pod per plant, NSP - number of seed per pod, PL – Pod length,

HSW - 100-seed weight, HI- harvest index, PC – protein content, SYP- seed yield per plant

Table 3: Effects of yield component on seed yield direct and indirect

	DF	DM	NPB	PH	NPP	NSP	PL	HSW	HI	PC	Genotypic correlation with SYP
DF	-2.08	2.43	-0.17	-0.68	-0.58	3.21	-2.38	0.36	-1.83	1.21	-0.520**
DM	-1.72	2.94	-0.09	-0.34	-0.76	3.23	-3.08	0.41	-1.97	0.71	-0.688**
NPB	0.73	-0.59	0.48	0.28	-0.35	1.39	0.79	-0.40	0.26	-2.33	0.259*
PH	-0.65	0.45	-0.06	-2.19	0.15	2.12	-1.33	0.35	-1.33	2.18	-0.309**
NPP	0.89	-1.64	-0.12	-0.24	1.36	-2.03	0.58	0.05	1.70	0.05	0.612**
NSP	1.09	-1.55	-0.11	0.76	0.45	-6.12	4.05	-0.03	1.13	0.66	0.345**
PL	0.93	-1.70	0.07	0.55	0.15	-4.68	5.30	-0.46	0.72	-0.59	0.288**
HSW	0.76	-1.22	0.19	0.78	-0.08	-0.22	2.50	-0.98	0.85	-2.27	0.314**
HI	1.06	-1.61	0.03	0.81	0.64	-1.94	1.07	-0.23	3.58	-2.51	0.911**
PC	-0.59	0.49	-0.26	-1.13	0.01	-0.95	-0.74	0.53	-2.13	4.22	-0.570**

(residual effect: 0.337)

*, ** significant at 0.05% and 0.01% level of significance, respectively

DF- days to flowering, DM- days to maturity, NPB- number of branches per plant, PH- plant height, NPP- number of pod per plant, NSP - number of seed per pod, PL - pod length, HSW – 100-seed weight, HI- harvest index, PC - protein content, SYP- seed yield per plant

Conclusion

The present investigation indicated the wide variation, coupled with high heritability and genetic advance as percent of mean, which exists in different characters of cowpea. It offers potential to evolve cowpea varieties through simple breeding methods. The improvement of seed yield in cowpea could be achieved on the basis of indirect selection of various characters like, number of pod per plant, harvest index, number of seeds per pod, pod length, number of branches per plant and 100-seed weight which were positively correlated with seed yield per plant. In addition, path analysis's results revealed high positively direct and indirect effects on seed yield related characters viz., harvest index, pod length, number of seeds per pod and number of pods per plant. Therefore, to obtain high seed yield, one

should consider these characters in cowpea breeding programme.

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