Original Research Article

Change the title

ESTIMATION OF CORRELATION AND PATH ANALYSIS FOR QUANTITATIVE TRAITS IN COWPEA (*Vigna unguiculata* (L.) Walp).

When you want to publish an article about Correlation & path studies, why do you write about Variability, heritability, GA & GA as % mean??

Abstract

R B

The experiment included 20 cowpea genotypes with three replications in a randomized block design. The study was carried out to estimate the genetic variability, genetic advance, correlation coefficient analysis and yield contributing traits and direct and indirect effect of yield component on yield through path analysis. The analysis of variance revealed the existence of all the traits, hence, the data on all the 17 traits which showed significant differences among the entries were subjected to further statistical analysis. Maximum GCV and PCV for biological yield and harvest index were recorded. There was a ~~High genetic advance as a percentage of the mean for 100 seed weight. The heritability of 100 seed weight was found to be high.~~ For biological yield, there was a significant genetic advance. At the phenotypic and genotypic levels, seed yield per plant had a high positive significant connection with Peduncle length, Number of Secondary Branches, Number of Seeds per Pod, Number of Pods per Plant, Biological yield, and Harvest index. Days to 50% Flowering, Number of Secondary Branches, Number of Seeds per Pod, Number of Pods per Plant, 100 seed weight ~~all~~ had a significant ~~beneficial~~ effect on seed yield per plant at both the phenotypic and genotypic levels. Genotypes IC 259106, EC 58905, IC 202797, KASHI KANCHAN, IC 202803 and IC 10854 were found to be superior for seed yield per plant.

existance of what??

positive

Key words: Cowpea, Variability, Genetic advance, Correlation, Path analysis

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is the world's oldest crop. It is ~~a~~ member of ~~the~~ Papilionaceae family and the subfamily Fabaceae, with chromosome number 2n = 22. Africa is its principal source of origin. It is widely farmed and used around the world. Cowpea is consumed in a variety of forms, including long green pods as a vegetable, seeds as ~~a~~ pulse, and foliage as milch animal feed. Gujarat, West Bengal, Tamil Nadu, Andhra Pradesh, Kerala, and Orissa are the top growing states in India for cowpea. Cowpea is also known as "poor man's

There were high heritability and high genetic advance as percentage of mean for 100 seed weight.

meat." The green has 84.6 percent hydration, 60.3 percent carbohydrates, 1.8% fat, and is high in vitamins and phosphorus **(Venkatesan *et al.* 2003)**. Cowpea is the most widely grown pulse in the world, accounting for 12.76 million ha with a total production of 7.56 million tonnes and a productivity of 750 kg per ha **(FAO 2013)**. In india, the cowpea is grown in an area about 3.9 million ha with a production of 2.21 million tones with a productivity of 625 kg per ha. During 2017 -2018 the total coverage under cowpea in Uttar Pradesh is 23.61lakh hectare with a production around 22.34 lakh tonnes **(Anonymous, 2018)**.Cowpea are farmed on around 3.9 million ha in India, with a yield of 625 kg per ha.

pod

I

of

Provide latest statistical figures for the year 2022

MATERIAL & AND METHODS

During *Zaid* - 2021, the current study on correlation and path analysis for yield and yield contributing character in cowpea was carried out at Naini Agricultural College, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj U.P. The experiment was carried out in a R randomised B block D design with 20 genotypes that were randomly ordered, reproduced three times, and divided into 60 plots. The gross area of the experiment ~~is~~ was 144.5 m^2 and plot size was 1 × 1 m. ~~The gross area of the experiment is 144.5 m^2 and plot size was 1 × 1 m.~~ The row to row spacing ~~is~~ was 60 cm and plant to plant spacing ~~is~~ was 30 cm. ~~The 5~~ A total number of five competitive plants from each of the replication were tagged and observation were taken from these tagged plants at various stages of the plant through out the growing stages. Data were recorded ~~from~~ for 17 characters viz, Days to 50% floweing, Days to 50% podding, Days to maturity, Petiole length, Peduncle length (cm), Number of primary branches, Number of secondary branches, Number of pods per cluster, Number of cluster per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Plant height (cm), Harvest index, Biological yield (g), Seed index (g)~~,~~ and Seed yield per plant (g)~~,~~ T the mean values were computed data were anlalysed for analysis of variance as suggested by **(Fisher, 1918)** and Coefficient of variance as well as Heritability (in broad sense), as suggested by **Burton and Devane (1953)**. The Genetic advance ~~were~~ was obtained by formula suggested by **Johnson *et al.* (1955)**. Phenotypic and Genotypic correlation and path coefficient of variation were computed as per the method given by **Dewey and Lu (1959)**.

RESULT AND DISSCUSSION

In this section, the genotypic and phenotypic coefficients of variation, heritability~~,~~ and genetic progress are all presented (Table- 1). All ~~of~~ the characters had a wide range of diversity. The phenotypic coefficient of variance was greater than the genotypic coefficient of variation for all traits studied. The phenotypic coefficient of variation (PCV) ranged from Days to 50% blooming (5.255) to Harvest index (36.978), with harvest index (36.978) having the highest PCV magnitude (24.961). Seed yield per plant was also found to be moderate. The genotypic coefficient of variation, which measures the level of genetic variation in a population, ranged from 0.384% to 18.703%. The traits, biological yield per plant (18.70%) and harvest index (16.40%) showed the highest genotypic coefficient of Variation. Penduncle length and pod length ~~have~~ had moderate values. **Sapara *et al.* (2014)** ~~discovered~~ recorded high PCV for pod length, while **Sapara *et al.* (2014)** and **Khanpara *et al.* (2016)** ~~discovered~~ recorded moderate PCV for pod length.

Give latest literatures

The estimation of good heritability is the best way to understand the transmission of character from parents to their offspring (Falconer 1981). High heritability ~~is~~ was observed for seed index (100 %) and seed yield per plant (88.22%) followed by days to maturity (82.56%), days to 50 % pod setting (72.6%), and number of cluster per plant (70.8%). High heritability alone may not lead to any conlusion unless ~~it will relate with the~~ genetic advance as percent mean is measured (Johson and Robinson, 1955). High heritability coupled with high genetic advance as percent of the mean was recorded for ~~the~~ seed yield per plant. These findings were in accordance to the findings of **Nwosu *et al.* (2013)** and **Sapara *et al.*(2014)**. The high heritability were also reported by **Suganthi and Miurugan (2007).**

in which crop?

give the result in which crop they quoted?

The genotypic and phenotypic correlation coefficients were computed among 17 characters in (Table -3). ~~The~~ N number pods per cluster, pod length, number of primary branches, number of seedss per pod, number of cluster per plant, number of pods per plant, biological yield, seed index and seed yield per plant exhibited significance both at genotypic and phenotypic level. ~~Hence~~ therefore these ~~above~~ characters appeared as greatest important associates of seed yield per plant and also very important for future aspects. Similarly the same result were also observed by **Kanimoli *et al.* (2015)** and **Ramesh *et al.* (2001)**.

or Re write Clearly and neatly with more quotings

Path analysis is also ~~a~~ important aspects and statistical approach to separate and observed the correlation coefficient into direct and indirect effects of independent variables on the dependent variables in (Table-4). The results of the present study on path analysis is presented in ~~In the preesent study,~~ the path analysis correlation is carried out for 17 quantative characters of the cowpea. Path analysis revealed that ~~the~~ days to 50% flowering, number of secondary branches, number of seeds per pod, number of pods per plant, seed index at both genotypic and phenotypic level. Similar results were observed by **Suganthi and Murugan (2008) and Lingaraj (2009)**. By looking to the nature and the result of correlation coefficient and direct and indirect effects it can be conluded that the number of seeds per pod, number of pods per plant, seed index may be given consideration during selection for crop improvement.

Revealed what???

Why quoting 13-14 yrs old references??

Provide the conclusion part elaborately with latest literature.

Refer other correl. & path. anal. articles and write accordingly.

maturity of what?

Table 3: Genotypic and Phenotypic correlation coefficient of cowpea genotypes

Traits		Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant Height	Petiole Length	Peduncle Length	Number of Pods / Cluster	Pod Length	Number of Primary Branches	Number of Secondary Branches	Number of Seeds / Pod	Number of Cluster / Plant	Number of Pods / Plant	Biological Yield	Harvest Index	Seed index	Seed Yield / Plant
Days to 50% flowering	G	1	0.202	0.567	-0.036	-0.785	-0.1138*	0.985	-0.5957*	0.898	-0.5736*	-0.776	0.829	0.637	0.19	-0.906	0.7557**	0.257
	P	1	0.032	0.897	0.0349*	-0.232	0.074	-0.159	-0.291	-0.335	-0.019	-0.555	-0.0061*	-0.4072*	0.106	-0.266**	0.501	-0.108
Days to 50% pod setting	G		1	0.678	-0.168	-0.5006*	-0.147	-0.898	0.0601*	0.721	0.737	0.1689*	-0.55	-0.217	-0.3311*	0.127	-0.141	-0.662
	P		1	0.456	0.0353*	-0.385	-0.681	0.2902*	0.0683*	-0.0961**	-0.309	0.1305*	-0.02	0.188	-0.2612*	0.556*	-0.12	0.197
Days to maturity	G			1	0.987	-0.897	0.567	0.879	0.567	-0.678	-0.786	-0.678	0.789	0.678	0.987	0.346	0.567	0.867
	P			1	0.987	-0.897	0.567	0.879	0.567	-0.678	-0.786	-0.678	0.789	0.678	0.987	0.346	0.567	0.867
Plant Height	G				1	0.037	-0.246*	0.7867*	-0.489	0.344	0.933	-0.623	-0.493	0.2573*	-0.671	0.49	0.015	0.0585*
	P				1	0.1433*	-0.1038*	-0.07	-0.155	-0.086	-0.2529*	-0.241	-0.282	-0.2565*	-0.2767*	0.111	0.0092*	-0.3016*
Petiole Length	G					1	0.536	0.782	-0.1085*	-0.6892*	-0.557	-0.0303*	-0.533	-0.35	0.992**	-0.616	0.2451*	0.761
	P					1	0.5508*	-0.2329*	-0.13	0.026	0.097	-0.201	-0.211	-0.0158**	0.381	-0.2495*	0.4176*	-0.087
Peduncle Length	G						1	0.5896*	-0.246	-0.21	-0.7947*	-0.675	0.0798*	-0.4063*	0.628	-0.855	0.337	0.4086*
	P						1	-0.19	-0.1869*	0.0175*	0.344	-0.2944*	-0.1567**	0.139	0.3314*	-0.4774**	0.2519*	0.1354**
Number of Pods /Cluster	G							1	-0.6541*	0.0905*	0.563	0.437	0.493	-0.086	0.319	-0.935	0.184	0.567
	P							1	0.038	0.1589*	0.0304**	0.082	-0.362	0.361	-0.238	0.3103**	-0.204*	0.237
Pod Length	G								1	0.674	0.643	0.0213*	0.27	0.472	0.2814**	0.61	-0.33	0.985*
	P								1	-0.208	-0.1	0.415**	0.169	-0.0726*	0.049	0.288	-0.221	-0.1839*
Number of Primary Branches	G									1	-0.348	0.28	0.7454**	0.3366*	-0.35	-0.22	0.413*	0.108
	P									1	0.422	-0.109	0.043*	0.0059*	0.0207*	0.0816*	0.0903**	0.0159*
Number of Secondary Branches	G										1	0.1753*	0.8621*	-0.198	-0.514	-0.159	-0.351	0.0653**
	P										1	-0.058	-0.025	0.162	0.181	0.0728*	0.243	0.2717*
Number of Seeds / Pod	G											1	0.635	-0.9097*	-0.4372**	-0.258	0.567**	0.0032**
	P											1	0.2072**	0.2366**	-0.1564*	0.111	-0.311**	0.2521*
Number of Cluster / Plant	G												1	0.25	0.4941*	-0.773	0.493	0.3942*
	P												1	0.029	0.1993**	0.158	0.138	0.345
Number of Pods / Plant	G													1	-0.082	0.052	0.595	0.0178**
	P													1	0.006	0.411	-0.302*	0.8399*
Biological Yield	G														1	-0.267	0.3682*	0.554*
	P														1	-0.334	0.2759*	0.0984**
Harvest Index	G															1	-0.6	0.2319*
	P															1	-0.266	0.2955*
Seed index	G																1	0.687
	P																1	0.099
Seed Yield / Plant	G																	1
	P																	1