Investigation on Genetic Variability, Heritability, correlation Studies in Cowpea (*Vignaunguiculata L.*)

ABSTRACT

The field experiment was conducted during rabi season of 2022 at horticulture research farm, department of horticulture, naini agriculture institute, shuats, to **study on genetic variability, heritability, correlationstudies in cowpea(*Vignaunguiculata* L.)**were estimated among 14 cowpea genotypes for 19 qualitative traits. The High estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for number of seeds per plant, seed weight per plant, green pod yield per plant and pod yield per hectare. While moderate estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for pod length, number of peduncles per plant, number of pods per peduncle, plant height at both flowering and maturity stage.

Keywords: Correlation coefficient, *GCV, PCV, Heritability, Genetic Advance,*

UNDER PEER REVIEW

1.INTRODUCTION

Cowpea (vernacular name: Lobia), [botanically known as *Vignaunguiculata*(L.)is one of the well-known plants belonging to Fabaceae. It is a diploid selfpollinated dicot plant species with chromosome number 2n=2x=22 (**Arumuganathan and Earle, 1991**).

Cowpeas were originated and domesticated in Africa (**Gomez, 2017**) and are one of the oldest crops to be farmed. A second domestication event probably occurred in Asia, before they spread into Europe and the Americas. According to **FAOSTAT (2020)**, global production of Cowpea in 2019-2020 reached 89.16 tons per hectare. Cowpeas are extensively cultivated in India, particularly in Uttar Pradesh, Andhra Pradesh, Karnataka, and Tamil Nadu. In 2022, India produced approximately 3.14 million metric tons of cowpeas (***Source: NHB,*** **Ministry of Agriculture & Farmers Welfare, Government of India, 2021-22**). A plant breeder uses germplasm as the foundation for his breeding programme. Both quantitative and qualitative traits have genetic variability. Germplasm is the genetic resources of plants, animals, and microorganisms used in breeding and research programs to develop new varieties adapted to changing environmental conditions and meet food demands. Evaluating germplasm helps identify desirable traits for specific environments and production systems, aiding plant breeders in developing new varieties that are more resilient to stress factors. It also preserves crop genetic diversity, crucial for sustainable agriculture and food security. Examples of organizations utilizing germplasm evaluation for breeding programs include CIMMYT and IRRI, developing new varieties with improved yield potential, drought tolerance, and disease resistance. Germplasm is the fundamental material that a plant breeder requires to begin a breeding program, consisting of genetic diversity for quantitative and qualitative characteristics. Understanding the classification of cowpea germplasm for these traits is important for plant breeders to select and enhance the crop. Genetic variability and its quantification for economically important qualitative and quantitative traits are necessary for any crop improvement program. Knowledge of genetic advance and heritability assists breeders in selecting superior parents to start a successful breeding program. Therefore, identifying superior parents with better heritability and genetic advance for various traits is critical for any yield improvement program. (**Khan *et al.*, 2005**). Depicting character association for yield attributing traits is important in plant breeding and crop improvement programs as it provides valuable information for identifying important traits and selecting the best parents for breeding. A complex character, yield depends on several quantitatively inherited component characters. Therefore, prior to beginning any breeding programme, one should have a thorough understanding of the type and degree of genetic variability. Every crop improvement programme starts with genotype evaluation to determine the level of variability that already exists. For the assessment of the scope of potential improvement, knowledge of the degree of variation in the genetic material at hand and the role of the environment in the expression of plant characters is crucial. The presence of variability for various traits in the source population is a prerequisite for crop improvement because without heritable variability, breeding and selection efforts would be ineffective. Additionally, estimating genetic progress and heritability would provide the clearest picture possible of the level of improvement anticipated from selection and the validity of phenotypic-based selection (**Falconer, 1989**). Heritability estimation that accounts for genetic progress is more accurate than heritability estimation on its own. According to **Johnson *et al.* (1955)**, a study of estimated heritability in conjunction with genetic advancement would yield more accurate results than a heritability-only study. Keeping the objectives in mind, the current experiment tried to assess genetic variability and isolate the traits that could be reasonably attributed for a genetic improvement programme by manipulating genotypes.

2.MATERIALS AND METHODS

To comprehend the genetic variability, heritability, of Cowpea genotypes, the current study, was conducted. The present investigation was done to understand the genetic variability, heritability present among Cowpea genotypes. The investigation was carried out at Horticultural Research Farm (HRF), Department of Horticulture, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj during the *Rabi* season of 2022. The experiment was set up using a Randomized Block Design (RBD). The **Fisher and Yates, 1936** method was used to statistically analyses the data. **Johanson*et al.*,1955** formulae were used to calculate GCV and PCV. Heritability (in the broad sense) was eliminated by the formula **Burton and Devane** deduced (**1953**).

3.RESULTS AND DISCUSSION:

3.1. Analysis of variance

For the purposes of the experimental design, analysis of variance was performed on the mean sum squares data for 19 characters. Table 1 displays the variance analysis for the various characters that was calculated. For all the studied characters, the analysis of variance revealed highly significant differences (=0.01 & 0.05) among 14 genotypes, indicating that there is a sizable amount of genetic variation among the cowpea germplasms. Additionally, it demonstrated the range of mustard genetic improvement through selection. The data on the values of different characters and the analysis of variance showed significant differences among genotypes for all 19 characters indicating that the material has adequate genetic variability to support the breeding programme for improving the pod yield of cowpea. These results are in agreement with the studies conducted by **Dinesh *et al.*, (2017), Kalambe*et al.*, (2019)** in cowpea.

3.2. Genetic parameters from table 2, Genotypic coefficient of variation (GCV) ranged from 2.06% (number of seeds per pod) to 49.55% (pod yield per hectare). High GCV (>20%) was recorded for pod yield per hectare (49.55%) followed by seed weight per plant (31.86%), number of seeds per plant (21.56%) and green pod yield per plant (21.44%). Moderate GCV (10-20%) was recorded for plant height at flowering stage (19.81%) followed by number of pods per peduncle (17.04%), plant height at maturity (15.62%), dry pod weight (14.27%), number of peduncles per plant (14.14%) and pod length (11.39%). Low GCV (<10%) was recorded for number of nodes on main stem (9.24%) followed by number of pods per plant (8.61%), days to first pod formation (4.30%), days to first flowering (4.23%), days to 50% flowering (3.74%), TSS (3.28%), test weight (2.93%), days to 50% maturity (2.57%), and number of seeds per pod (2.06%). Phenotypic coefficient of variation (PCV) ranged from 2.15% (number of seeds per pod) to 49.58% (pod yield per hectare). High PCV (>20%) was recorded for pod yield per hectare (49.58%) followed by seed weight per plant (31.87%), number of seeds per plant (21.56%) and green pod yield per plant (21.45%). Moderate PCV (10-20%) was recorded for plant height at flowering stage (19.81%) followed by number of pods per peduncle (18.57%), plant height at maturity (15.63%), dry pod weight (15.22%), number of peduncles per plant (14.20%), pod length (12.85%), TSS (11.74%) and number of pods per plant (11.67%). Low PCV (<10%) was recorded for number of nodes on main stem (9.59%) followed by days to first pod formation (4.31%), days to first flowering (4.39%), days to 50% flowering (3.88%), test weight (3.08%), days to 50% maturity (2.67%), and number of seeds per pod (2.15%). GCV and PCV have different significances in the field of genetics. GCV, or Genotypic Coefficient of Variation, is a statistical measure used to quantify the variability in genotypic values within a population. It helps geneticists assess the extent of genetic diversity and the potential for selective breeding to improve desired traits. A high GCV suggests a wide range of genotypic values and indicates greater genetic variation, which can be beneficial for breeding programs. On the other hand, PCV, or Phenotypic Coefficient of Variation, measures the variability in phenotypic values within a population. It reflects the combined influence of genetic and environmental factors on a specific trait. PCV helps geneticists understand the degree of phenotypic variation and the potential contribution of genetic factors to the observed variability. This information is crucial for determining the heritability of traits and designing breeding strategies to enhance desired phenotypic characteristics. Both, High GCV and PCV was recorded for pod yield per hectare, seed weight per plant, number of seeds per plant and green pod yield per plant. Both, Moderate GCV and PCV was recorded for plant height at flowering stage, number of pods per peduncle, plant height at maturity, dry pod weight, number of peduncles per plant and pod length. These characters, in comparison to other characters, indicated the presence of high to moderate amount of genetic variability, thereby, suggesting a good scope for crop improvement, creating variability by hybridization followed by selection. Similar findings for high GCV and PCV were earlier reported by **Khanpara*et al.*, (2016); Kalambe*et al.*, (2019)** in cowpea. Low GCV and PCV was recorded for number of nodes on main stem, number of pods per plant, days to first pod formation, days to first flowering, days to 50% flowering, TSS, test weight, days to 50% maturity, and number of seeds per pod. Similar findings were reported by **Dinesh *et al*., (2017)** in cowpea.

3.3 Genetic variability

The heritability, which measures the genetic relationship between parent and offspring and is frequently used to predict the extent to which a character may be transmitted from parent to offspring, further reflects the genotypic coefficient of variation estimates, which reflect the overall amount of genotypic variability that is transmitted from parents to the progeny. Lush (1949) introduced the idea of heritability in a broad sense. In general, high heritability alone cannot lead to enough genetic progress to allow for sufficient improvement through selection. According to Burton (1952), a character with a high GCV along with a high heritability will be useful in selection because they will provide a better idea of the expected efficiency of selection. The results of heritability for all the 14 characters are also presented in table 3.

The estimates of heritability (%) in broad sense for 19 characters studied, ranged from 54.50 % for number of pods per plant to 100% for plant height at flowering, number of seeds per plant and green pod yield per plant. High heritability (broad sense) (>60%) was recorded for plant height at flowering, number of seeds per plant and green pod yield per plant with (100%) followed by pod yield per hectare (99.99%), seed weight per plant and plant height at maturity with (99.93%), days to first pod formation (99.50%), number of peduncles per plant (99.20%), number of nodes on main stem (92.80%), days to 50% maturity (92.72%), days to first flowering and days to 50% flowering with (92.70%), number of seeds per pod (91.75%), test weight (90.90%), dry pod weight (87.92%), number of pods per peduncle (84.20%), pod length (78.64%) and TSS (78.00%). Moderate heritability (broad sense) (30-60%) was observed for number of pods per plant (54.50%) with lowest value. Similar results for high heritability for plant height, number of seeds per plant, green pod yield and days to first pod formation was reported earlier by **Patel *et al*., (2016)** in cowpea. High heritability for days to first flowering, days to 50% flowering, days to 50% maturity, number of peduncles per plant, number of pods per peduncle, number of seeds per pod, dry pod weight was concluded earlier by**Kalambe*et al.* (2019)** in cowpea. Moderate heritability was also observed for number of pods per plant were earlier also concluded by **Patel *et al.* (2016)**. Heritability estimates generally influenced by the type of genetic material, sample size, method of sampling, conduct of the experiment, method of calculation and effect of linkage, etc. **Johanson*et al*. (1995)** had pointed out that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection.

In the present study, high estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for number of seeds per plant, seed weight per plant, green pod yield per plant and pod yield per hectare. While moderate estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for pod length, number of peduncles per plant, number of pods per peduncle, plant height at both flowering and maturity stage. A high GCV indicates a wide range of genotypic values and reflects significant genetic diversity within a population. When combined with high heritability, which measures the proportion of phenotypic variation attributed to genetic factors, it suggests that a substantial portion of the observed variation is genetically controlled. Furthermore, a high genetic advance as a percent of the mean implies that selection based on the observed trait values can lead to a considerable improvement in subsequent generations. It indicates that the selection process can effectively target and amplify the desired trait. These traits are governed by additive gene effects and therefore, may be improved through direct selection. Similar findings for number of seeds per plant, pod length and number of peduncles per plant were reported by **Dinesh *et al.* (2017), Kalambe*et al.* (2019)** in cowpea. Similar findings for seed weight per plant, pod yield and number of pods perpeduncles and plant height were reported by **Kalambe*et al.***

(2019) in cowpea.

3.4. Character association Phenotypic Correlation coefficient analysis revealed that pod yield per hectare exhibited highly significant and positive correlation with plant height at flowering stage, plant height at maturity stage, number of nodes on main stem, days to first pod formation, number of peduncles per plant, number of pods per peduncle, number of pods per plant, dry pod weight, number of seeds per pod, number of seeds per plant, seed weight per plant, test weight and green pod yield per plant. Pod yield per hectare showed significant negative correlation with days to first flowering, days to 50% flowering, days to 50% maturity and TSS. Genotypic Correlation coefficient analysis revealed that pod yield per hectare exhibited highly significant and positive correlation with plant height at flowering stage, plant height at maturity stage, number of nodes on main stem, days to first pod formation, number of peduncles per plant, dry pod weight, pod length, number of seeds per pod, number of seeds per plant, seed weight per plant, test weight and green pod yield per plant. Pod yield per hectare showed significant negative correlation with days to first flowering, days to 50% flowering, days to 50% maturity, number of pods per peduncle, number of pods per plant and TSS.

At genotypic level, Maximum positive direct effects on pod yield per hectare was mainly depicted by number of nodes on main stem (0.123), days to first flowering (0.349), number of peduncles per plant (0.096), number of seeds per plant (0.751), seed weight per plant (0.452), test weight (0.199) while negative direct effects were mainly due to plant height at flowering stage (-0.046), plant height at maturity stage (-0.097), days to first pod formation (-0.046), days to 50% flowering (-0.490), number of pods per peduncle (0.034), number of pods per plant (-0.022), dry pod weight (-0.112), pod length (-0.052), number of seeds per pod (-0.169). Similar reporting was earlier concluded by **Kalambe*et al.*, (2019), Reshma*et al.*, (2019)**in cowpea.

4.CONCLUSION

The current study found that out of 14 genotypes of cowpea, 2 genotypes namely, Lalima and KashiKanchan exhibited substantially higher yield and performed better for other desirable traits as compared to other genotypes.Therefore, these genotypes may be promoted for cultivation as well as in future breeding programme to develop superior varieties for Agro-climatic zones of Prayagraj. High estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for number of seeds per plant, seed weight per plant, green pod yield per plant and pod yield per hectare. While moderate estimate of GCV along with high heritability coupled with high genetic advance as percent of mean was recorded for pod length, number of peduncles per plant, number of pods per peduncle, plant height at both flowering and maturity stage. These traits are governed by additive gene effects and therefore, may be improved through direct selection.

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Table 1 Analysis of Variance (ANOVA) for 19 characters in cowpea.

Sl. No.	Source	Mean Sum of Squares		
		Replication (df=2)	**Treatment/genotypes (df=13)**	**Error (df=26)**
1	**Plant height at flowering (cm)**	14.39	692.72**	0.007
2	**Plant height at maturity (cm)**	14.05	661.08**	0.037
3	**Number of nodes on main stem**	8.29	4.36**	0.110
4	**Days to first flowering**	11.31	6.05**	0.154
5	**Days to 50% flowering**	11.14	6.019*	0.154
6	**Days to first pod formation**	12.97	7.21**	0.011
7	**Days to 50% maturity**	11.14	6.02**	0.155
8	**Number of peduncles per plant**	12.81	17.02*	0.048
9	**Number of pods per peduncle**	4.23	2.07**	0.122
10	**Number of pods per plant**	2530.36	176.24*	38.34
11	**Dry pod weight (g)**	0.48	0.49**	0.021
12	**Pod length (cm)**	5.29	16.02**	1.329
13	**Number of seeds per pod**	2.46	1.55**	0.045
14	**Number of seeds per plant**	2119.33	32709.21**	2.363
15	**Seed weight per plant (g)**	27.43	785.06**	0.140

16	**Test weight (g)**	616.96	49.33*	1.586
17	**T.S.S. (°Brix)**	0.25	0.24**	0.192
18	**Green pod yield per plant (g)**	23.55	5027.25*	0.677
19	**Pod yield per hectare (kg/ha)**	7436.52	1544989.97**	661.194

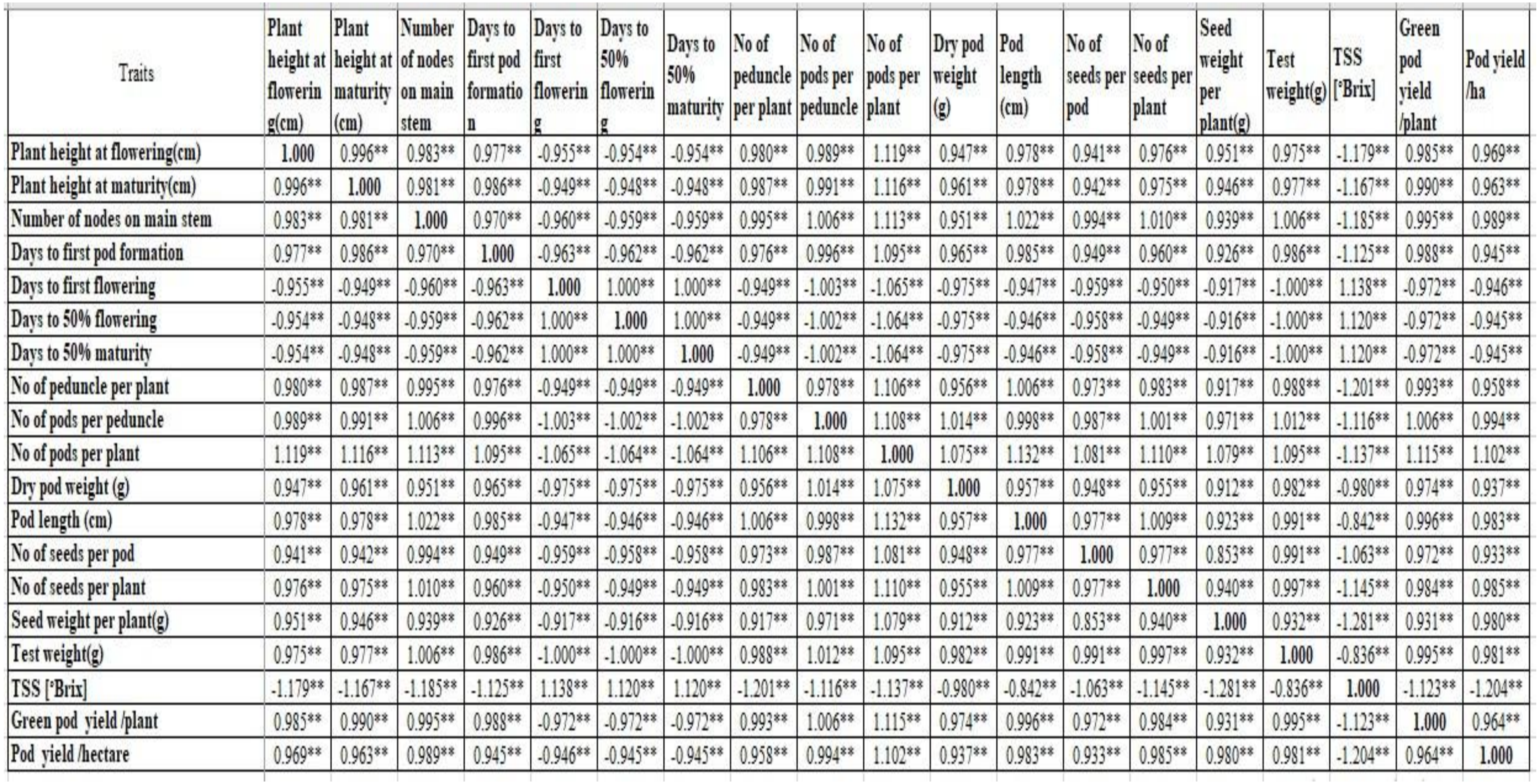
****, * Significant at 1% and 5 % level of significance respectively**

Table 2.Genetic Parameters for 19 characters of 14 cowpea genotype.

Characters	Mean	Range	GCV	PCV	H^2 (Heritability in broad sense)	Genetic advancement 5%	Genetic advancement as % mean 5%
Plant height at flowering (cm)	76.70	50.19-96.43	19.81	19.81	100.0	31.30	40.81
Plant height at maturity (cm)	94.99	69.59-114.16	15.62	15.63	99.93	30.57	32.18
Number of nodes on main stem	12.88	11.37-14.93	9.24	9.59	92.80	2.36	18.33
Days to first flowering	36.00	30.21-35.65	4.23	4.39	92.70	2.78	8.39
Days to 50% flowering	33.13	34.42-39.86	3.74	3.88	92.70	2.77	7.42
Days to first pod formation	37.34	33.35-38.28	4.30	4.31	99.50	3.18	8.84

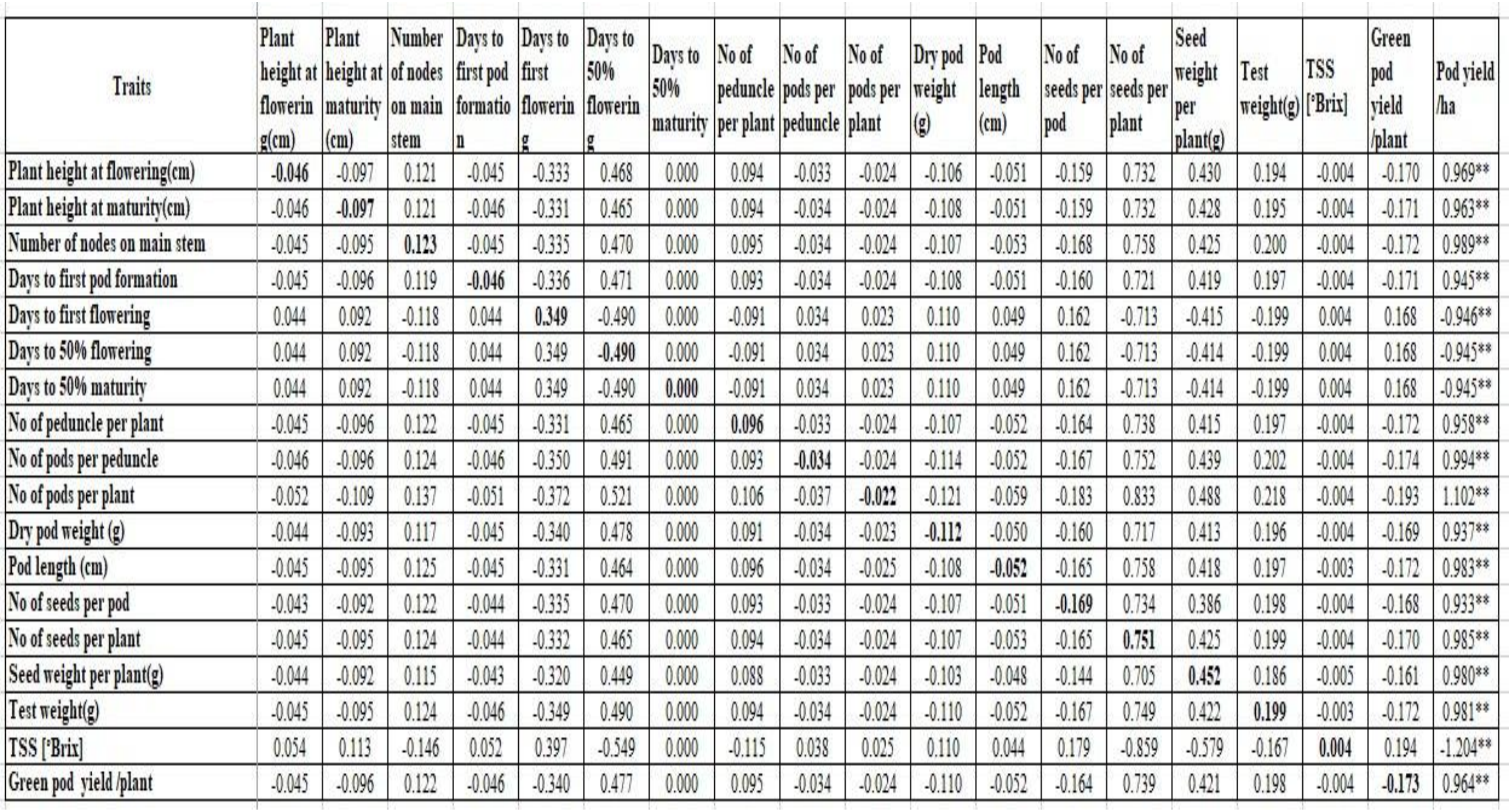
Days to 50% maturity	54.34	51.42-56.86	2.57	2.67	92.72	2.77	5.10
Number of peduncles per plant	16.82	13.22-20.20	14.14	14.20	99.20	4.87	29.00
Number of pods per peduncle	4.73	3.54-6.34	17.04	18.57	84.20	1.52	32.21
Number of pods per plant	78.67	66.01-89.30	8.61	11.67	54.50	10.31	13.10
Dry pod weight (g)	2.76	2.05-3.44	14.27	15.22	87.92	0.76	27.58
Pod length (cm)	19.40	16.84-20.08	11.39	12.85	78.64	4.03	20.81
Number of seeds per pod	34.32	33.39-35.77	2.06	2.15	91.75	1.39	4.07
Number of seeds per plant	484.16	352.42-652.82	21.56	21.56	100.0	215.07	44.42
Seed weight per plant (g)	50.76	28.67-72.77	31.86	31.87	99.93	33.31	65.62
Test weight (g)	135.72	129.94-143.82	2.93	3.08	90.90	7.83	5.77
T.S.S. (°Brix)	1,447.88	3.09-4.31	3.28	11.74	78.00	0.07	1.89
Green pod yield per plant (g)	190.84	128.40-256.47	21.44	21.45	100.0	84.30	44.17
Pod yield per hectare (kg/ha)	3.88	561.89-2500.39	49.55	49.58	99.99	1477.05	102.01

Table 3 Correlation coefficient between different characters of Cowpea Phenotypic correlation coefficient (above diagonal) and Genotypic correlation coefficient (below diagonal)



Traits	Plant height at flowering(cm)	Plant height at maturity (cm)	Number of nodes on main stem	Days to first pod formation	Days to first flowering	Days to 50% flowering	Days to 50% maturity	No of peduncle per plant	No of pods per peduncle	No of pods per plant	Dry pod weight (g)	Pod length (cm)	No of seeds per pod	No of seeds per plant	Seed weight per plant(g)	Test weight(g)	TSS [°Brix]	Green pod yield /plant	Pod yield /ha
Plant height at flowering(cm)	**1.000**	0.996**	0.983**	0.977**	-0.955**	-0.954**	-0.954**	0.980**	0.989**	1.119**	0.947**	0.978**	0.941**	0.976**	0.951**	0.975**	-1.179**	0.985**	0.969**
Plant height at maturity(cm)	0.996**	**1.000**	0.981**	0.986**	-0.949**	-0.948**	-0.948**	0.987**	0.991**	1.116**	0.961**	0.978**	0.942**	0.975**	0.946**	0.977**	-1.167**	0.990**	0.963**
Number of nodes on main stem	0.983**	0.981**	**1.000**	0.970**	-0.960**	-0.959**	-0.959**	0.995**	1.006**	1.113**	0.951**	1.022**	0.994**	1.010**	0.939**	1.006**	-1.185**	0.995**	0.989**
Days to first pod formation	0.977**	0.986**	0.970**	**1.000**	-0.963**	-0.962**	-0.962**	0.976**	0.996**	1.095**	0.965**	0.985**	0.949**	0.960**	0.926**	0.986**	-1.125**	0.988**	0.945**
Days to first flowering	-0.955**	-0.949**	-0.960**	-0.963**	**1.000**	1.000**	1.000**	-0.949**	-1.003**	-1.065**	-0.975**	-0.947**	-0.959**	-0.950**	-0.917**	-1.000**	1.138**	-0.972**	-0.946**
Days to 50% flowering	-0.954**	-0.948**	-0.959**	-0.962**	1.000**	**1.000**	1.000**	-0.949**	-1.002**	-1.064**	-0.975**	-0.946**	-0.958**	-0.949**	-0.916**	-1.000**	1.120**	-0.972**	-0.945**
Days to 50% maturity	-0.954**	-0.948**	-0.959**	-0.962**	1.000**	1.000**	**1.000**	-0.949**	-1.002**	-1.064**	-0.975**	-0.946**	-0.958**	-0.949**	-0.916**	-1.000**	1.120**	-0.972**	-0.945**
No of peduncle per plant	0.980**	0.987**	0.995**	0.976**	-0.949**	-0.949**	-0.949**	**1.000**	0.978**	1.106**	0.956**	1.006**	0.973**	0.983**	0.917**	0.988**	-1.201**	0.993**	0.958**
No of pods per peduncle	0.989**	0.991**	1.006**	0.996**	-1.003**	-1.002**	-1.002**	0.978**	**1.000**	1.108**	1.014**	0.998**	0.987**	1.001**	0.971**	1.012**	-1.116**	1.006**	0.994**
No of pods per plant	1.119**	1.116**	1.113**	1.095**	-1.065**	-1.064**	-1.064**	1.106**	1.108**	**1.000**	1.075**	1.132**	1.081**	1.110**	1.079**	1.095**	-1.137**	1.115**	1.102**
Dry pod weight (g)	0.947**	0.961**	0.951**	0.965**	-0.975**	-0.975**	-0.975**	0.956**	1.014**	1.075**	**1.000**	0.957**	0.948**	0.955**	0.912**	0.982**	-0.980**	0.974**	0.937**
Pod length (cm)	0.978**	0.978**	1.022**	0.985**	-0.947**	-0.946**	-0.946**	1.006**	0.998**	1.132**	0.957**	**1.000**	0.977**	1.009**	0.923**	0.991**	-0.842**	0.996**	0.983**
No of seeds per pod	0.941**	0.942**	0.994**	0.949**	-0.959**	-0.958**	-0.958**	0.973**	0.987**	1.081**	0.948**	0.977**	**1.000**	0.977**	0.853**	0.991**	-1.063**	0.972**	0.933**
No of seeds per plant	0.976**	0.975**	1.010**	0.960**	-0.950**	-0.949**	-0.949**	0.983**	1.001**	1.110**	0.955**	1.009**	0.977**	**1.000**	0.940**	0.997**	-1.145**	0.984**	0.985**
Seed weight per plant(g)	0.951**	0.946**	0.939**	0.926**	-0.917**	-0.916**	-0.916**	0.917**	0.971**	1.079**	0.912**	0.923**	0.853**	0.940**	**1.000**	0.932**	-1.281**	0.931**	0.980**
Test weight(g)	0.975**	0.977**	1.006**	0.986**	-1.000**	-1.000**	-1.000**	0.988**	1.012**	1.095**	0.982**	0.991**	0.991**	0.997**	0.932**	**1.000**	-0.836**	0.995**	0.981**
TSS [°Brix]	-1.179**	-1.167**	-1.185**	-1.125**	1.138**	1.120**	1.120**	-1.201**	-1.116**	-1.137**	-0.980**	-0.842**	-1.063**	-1.145**	-1.281**	-0.836**	**1.000**	-1.123**	-1.204**
Green pod yield /plant	0.985**	0.990**	0.995**	0.988**	-0.972**	-0.972**	-0.972**	0.993**	1.006**	1.115**	0.974**	0.996**	0.972**	0.984**	0.931**	0.995**	-1.123**	**1.000**	0.964**
Pod yield /hectare	0.969**	0.963**	0.989**	0.945**	-0.946**	-0.945**	-0.945**	0.958**	0.994**	1.102**	0.937**	0.983**	0.933**	0.985**	0.980**	0.981**	-1.204**	0.964**	**1.000**

Table 4. Genotypic path coefficient showing direct (bold) and indirect effect of various characters on green pod yield per plant.



Traits	Plant height at flowering(cm)	Plant height at maturity (cm)	Number of nodes on main stem	Days to first pod formation	Days to first flowering	Days to 50% flowering	Days to 50% maturity	No of peduncle per plant	No of pods per peduncle	No of pods per plant	Dry pod weight (g)	Pod length (cm)	No of seeds per pod	No of seeds per plant	Seed weight per plant(g)	Test weight(g)	TSS [°Brix]	Green pod yield /plant	Pod yield /ha
Plant height at flowering(cm)	**-0.046**	-0.097	0.121	-0.045	-0.333	0.468	0.000	0.094	-0.033	-0.024	-0.106	-0.051	-0.159	0.732	0.430	0.194	-0.004	-0.170	0.969**
Plant height at maturity(cm)	-0.046	**-0.097**	0.121	-0.046	-0.331	0.465	0.000	0.094	-0.034	-0.024	-0.108	-0.051	-0.159	0.732	0.428	0.195	-0.004	-0.171	0.963**
Number of nodes on main stem	-0.045	-0.095	**0.123**	-0.045	-0.335	0.470	0.000	0.095	-0.034	-0.024	-0.107	-0.053	-0.168	0.758	0.425	0.200	-0.004	-0.172	0.989**
Days to first pod formation	-0.045	-0.096	0.119	**-0.046**	-0.336	0.471	0.000	0.093	-0.034	-0.024	-0.108	-0.051	-0.160	0.721	0.419	0.197	-0.004	-0.171	0.945**
Days to first flowering	0.044	0.092	-0.118	0.044	**0.349**	-0.490	0.000	-0.091	0.034	0.023	0.110	0.049	0.162	-0.713	-0.415	-0.199	0.004	0.168	-0.946**
Days to 50% flowering	0.044	0.092	-0.118	0.044	0.349	**-0.490**	0.000	-0.091	0.034	0.023	0.110	0.049	0.162	-0.713	-0.414	-0.199	0.004	0.168	-0.945**
Days to 50% maturity	0.044	0.092	-0.118	0.044	0.349	-0.490	**0.000**	-0.091	0.034	0.023	0.110	0.049	0.162	-0.713	-0.414	-0.199	0.004	0.168	-0.945**
No of peduncle per plant	-0.045	-0.096	0.122	-0.045	-0.331	0.465	0.000	**0.096**	-0.033	-0.024	-0.107	-0.052	-0.164	0.738	0.415	0.197	-0.004	-0.172	0.958**
No of pods per peduncle	-0.046	-0.096	0.124	-0.046	-0.350	0.491	0.000	0.093	**-0.034**	-0.024	-0.114	-0.052	-0.167	0.752	0.439	0.202	-0.004	-0.174	0.994**
No of pods per plant	-0.052	-0.109	0.137	-0.051	-0.372	0.521	0.000	0.106	-0.037	**-0.022**	-0.121	-0.059	-0.183	0.833	0.488	0.218	-0.004	-0.193	1.102**
Dry pod weight (g)	-0.044	-0.093	0.117	-0.045	-0.340	0.478	0.000	0.091	-0.034	-0.023	**-0.112**	-0.050	-0.160	0.717	0.413	0.196	-0.004	-0.169	0.937**
Pod length (cm)	-0.045	-0.095	0.125	-0.045	-0.331	0.464	0.000	0.096	-0.034	-0.025	-0.108	**-0.052**	-0.165	0.758	0.418	0.197	-0.003	-0.172	0.983**
No of seeds per pod	-0.043	-0.092	0.122	-0.044	-0.335	0.470	0.000	0.093	-0.033	-0.024	-0.107	-0.051	**-0.169**	0.734	0.386	0.198	-0.004	-0.168	0.933**
No of seeds per plant	-0.045	-0.095	0.124	-0.044	-0.332	0.465	0.000	0.094	-0.034	-0.024	-0.107	-0.053	-0.165	**0.751**	0.425	0.199	-0.004	-0.170	0.985**
Seed weight per plant(g)	-0.044	-0.092	0.115	-0.043	-0.320	0.449	0.000	0.088	-0.033	-0.024	-0.103	-0.048	-0.144	0.705	**0.452**	0.186	-0.005	-0.161	0.980**
Test weight(g)	-0.045	-0.095	0.124	-0.046	-0.349	0.490	0.000	0.094	-0.034	-0.024	-0.110	-0.052	-0.167	0.749	0.422	**0.199**	-0.003	-0.172	0.981**
TSS [°Brix]	0.054	0.113	-0.146	0.052	0.397	-0.549	0.000	-0.115	0.038	0.025	0.110	0.044	0.179	-0.859	-0.579	-0.167	**0.004**	0.194	-1.204**
Green pod yield /plant	-0.045	-0.096	0.122	-0.046	-0.340	0.477	0.000	0.095	-0.034	-0.024	-0.110	-0.052	-0.164	0.739	0.421	0.198	-0.004	**-0.173**	0.964**