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Genetic variability of seed yield and its components in grain cowpea (*Vigna unguiculata* (L.) Walp.) under coconut based farming systems

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Abstract

Thirty three grain cowpea genotypes were evaluated for yield and yield contributing characters under coconut based farming system. The genotypes showed significant difference for maturity period, yield and yield components. Phenotypic coefficient of variation was found to be higher than genotypic coefficient of variation for all the characters considered. Highest magnitude of PCV and GCV was observed for seed yield per plant. High GCV with correspondingly high values of PCV was observed for number of primary branches per plant, number of pods per plant, 100 seed weight and harvest index. All characters recorded high estimates of heritability. High heritability coupled with high genetic advance was observed for number of primary branches per plant, height of plant, number of pods per plant, number of seeds per pod, 100 seed weight, crop duration and harvest index indicating additive gene action for these characters and scope for improvement of these characters by selection.

Keywords: grain cowpea, coconut based farming system, GCV, PCV, heritability, genetic advance

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp) (2n=22) is a versatile food legume belonging to the family Fabaceae, also known as “poor man’s meat” due to the high protein content in seeds and leaves.

The diminishing per capita availability of land and ever increasing labour charges are the major constraints to agricultural production. In such a scenario, the small and marginal farmers rely upon strategies such as homestead farming where the available land area and family labour can be utilised for economic and food security. Coconut is the most dominant and important tree crop in the homesteads of Kerala^[4]. Intercrops can be raised in coconut gardens where the trees are less than 20 years and older than 40 years of age. Pulses are important food crop for nutritional security, sustainable crop production and soil health. Besides being a rich and cheapest source of dietary protein, it also plays a key role in improving and sustaining soil productivity on account of inherent capacity to fix atmospheric nitrogen, addition of huge amount of organic matter through roots and leaves fall and deep penetrating root system. Consequently, they remained an integral component of cropping systems especially in rainfed areas since time immemorial. Cowpea is an ideal crop among pulses which can be cultivated as intercrop in coconut gardens. One of the major limitations in popularizing grain cowpea among the small and marginal farmers is the non-availability of varieties suited to the coconut based homesteads.

Assessment of variability present in the population is the primary step in any breeding programme. If ample variability is present, with the aid of genetic parameters viz., coefficients of variation, heritability and genetic advance it can be partitioned into heritable and non-heritable components and effective selection for elite genotypes can be carried out. In this context, evaluation of grain cowpea genotypes was conducted to assess the genetic variability for yield and its components under coconut based homesteads.

Materials and Methods

The study was undertaken at Farming Systems Research Station, Sadanandapuram, Kottarakara during December, 2019 – March, 2020. Thirty three grain cowpea genotypes were evaluated in coconut based homestead garden where coconuts are of age 30 – 40 years, in randomized block design replicated thrice. The seeds were sown on raised beds of (3 x 1.5) m² size at a spacing 30 cm between rows and 15 cm within rows. The genotypes were evaluated for growth, yield and quality characters such as days to 50% flowering, number of primary branches per plant, height of plant (cm), number of pods per plant, number of seeds per pod,

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100 seed weight (g), seed yield per plant, crop duration (days), harvest index and total protein content of seeds (%). The light intensity in the experimental field was recorded and the shade intensity was worked out.

The data recorded on yield and quality characters were subjected to analysis of variance as suggested by Panse and Sukhatme^[11] and genetic parameters (GCV, PCV, heritability and genetic advance as percent of mean) were worked out.

Results

The light intensity in the experimental field was measured using light intensity meter at 11.45 am. The average light intensity in the field was found to be 0.719 W/m² resulting in shade intensity of 33.49 per cent.

The analysis of variance revealed significant differences among the thirty three grain cowpea genotypes for all the characters studied under coconut based homesteads (table 1). Wide range of variation was observed for all the characters depicting the existence of maximum variability for the traits. Days to 50% flowering varied from 37 to 64, number of primary branches from 4.22 to 10.73, height of plant (cm) from 31.78 to 59.47, number of pods per plant from 2.33 to 20.8, number of seeds per pod from 9.17 to 16.07, 100 seed weight (g) from 5.7 to 18.79, seed yield per plant (g) 1.87 to 26.55, crop duration from 47.00 to 105.67, harvest index from 0.18 to 0.77 and protein content (%) from 17.68 to 26.57.

Highest mean value for number of primary branches and height of plant (cm) were exhibited by the genotype KYLMVU-3. Genotype IC 39853 recorded highest mean for number off pods per plant, CHESCP-32 for number of seeds per pod, Pant lobia-4 for 100 seed weight (g) and CHESCP-03 for harvest index. The variety Hridya and genotype KYLMVU-10 were early flowering as indicated by the minimum days to 50% flowering and also showed lowest crop duration in the coconut based homesteads. The grain cowpea varieties Sreya and Subhra recorded highest seed yield per plant (g) and highest seed protein content (%) respectively under coconut based homesteads.

The genetic parameters were estimated for the characters and presented in table 2.

Table 1: Analysis of variance of yield and yield contributing characters of grain cowpea

Characters	Mean Sum of Square		
	Replication	Genotype	Error
Days to 50% flowering	144.364	84.413**	9.853
No. of primary branches per plant	0.084	9.147**	0.551
Height of plant (cm)	12.281	147.055**	17.548
No. of pods per plant	21.260	64.673**	2.691
No. of seeds per pod	2.416	9.631**	0.605
100 Seed weight (g)	0.067	26.717**	0.253
Crop duration (days)	28.313	466.669**	8.063
Harvest Index	0.087	0.076**	0.010
Protein Content (%)	0.877	15.347**	0.3
Seed yield per plant (g)	20.159	111.075**	5.128

** Significant at 1% level

Genotypic and Phenotypic coefficients of Variation

Coefficient of variation gives information on nature and magnitude of variation and also knowledge on whether the variations are due to genetic factors or environmental influence. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were categorised as suggested by Sivasubramanian and Menon^[14] as low (less than 10%), moderate (10-20%) and high (more than 20%).

The GCV values ranged from 6.85 to 59.41. Highest GCV was recorded for seed yield per plant (g) (59.41). High GCV was observed for number of primary branches per plant (24.76), number of pods per plant (49.36), 100 seed weight (g) (25.36) and harvest index (32.37). GCV was moderate for days to 50% flowering (10.29), height of plant (cm) (14.31), number of seeds per pod (12.99) and crop duration (14.52) whereas it was low for protein content (%) (6.85).

The PCV values ranged from 7.06 to 63.61. Highest PCV was observed for seed yield per plant (g) (63.61) followed by number of primary branches per plant (27.04), number of pods per plant (52.48), 100 seed weight (g) (25.72) and harvest index (39.40). Days to 50% flowering (12.16), height of plant (cm) (16.67), number of seeds per pod (14.24) and crop duration (14.89) exhibited moderate PCV. Lowest PCV was noted for protein content (%) (7.06). PCV was higher than GCV for all the characters studied.

Table 2: Genetic parameters of yield and yield contributing characters of grain cowpea

Character	Range	Mean	PCV	GCV	H ² (%)	GAM (%)
Days to 50% flowering	37-64	48.45	12.16	10.29	71.61	17.93
No. of primary branches/plant	4.22-10.73	6.84	27.04	24.76	83.86	46.71
Height of plant (cm)	31.78-59.47	45.92	16.67	14.31	71.1	24.85
No. of pods per plant	2.33-20.8	9.21	52.48	49.36	88.48	95.64
No. of seeds per pod	9.17 - 16.07	13.35	14.24	12.99	83.26	24.42
100 seed weight (g)	5.7 - 18.79	11.71	25.72	25.36	97.22	51.50
Crop duration (days)	47 - 105.67	85.17	14.89	14.52	94.9	29.15
Harvest index	0.18 - 0.77	0.46	39.40	32.37	67.50	54.78
Protein content (%)	17.68 - 26.57	22.67	7.06	6.85	94.35	13.72
Seed yield per plant (g)	1.87 - 26.55	9.84	63.61	59.41	87.22	96.18

Heritability and Genetic advance

For selection to be effective, the variability present in the population should be carried over to future generations. Heritability and genetic advance give an idea about how much of the variability is heritable and also the superiority of the selected individuals over base population. Heritability and genetic advance as per cent of mean were categorized as suggested by Johnson *et al.*^[5]. The heritability (broad sense) values for studied characters ranged from 67.50% to 97.22%. Heritability was high for all the characters studied and highest

value was observed for 100 seed weight (g) while lowest was for harvest index.

High genetic advance (as per cent of mean) was exhibited by all the characters except days to 50% flowering (17.93%) and protein content (13.72%) which exhibited moderate genetic advance. Highest GAM estimates were noted for seed yield per plant (g) (96.18%) followed by number of pods per plant (95.64%), harvest index (54.78%), 100 seed weight (g) (51.5%), number of primary branches per plant (46.71%), crop duration (29.15%), height of plant (cm) (24.85%) and number of seeds per plant (24.42%).

Discussion

The significant difference exhibited by the genotypes indicates the presence of substantial amount of variability for the characters studied.

For all the characters studied PCV was higher than GCV whereas the difference between PCV and GCV was low for most of the traits, indicating higher genetic variability. This suggests the scope for improvement of these characters through hybridization followed by selection. The PCV and GCV estimates were in conformity with the findings of Girish^[3] for number of primary branches, number of pods per plant and seed yield per plant; Manggoel *et al.*^[8] for seed yield per plant, 100 seed weight and number of pods per plant; Annasaheb^[2] for days to 50% flowering, harvest index and seed yield per plant; Kakde^[6] for protein content; Thouseem *et al.*^[15] for days to 50% flowering, height of plant, number of seeds per pod and crop duration and Nkoana *et al.*^[9] for days to 50% flowering and number of seeds per pod.

For all the characters high heritability was estimated which indicates the highly heritable nature of these characters and the minimum influence of environment in its expression. The high heritability estimates recorded for days to 50% flowering, height of the plant, number of primary branches, number of pods per plant, number of seeds per pod, seed yield per plant and 100 seed weight was in consonance with the reports of Girish^[3] and Manggoel *et al.*^[8]. In addition to the above characters, high heritability was reported for harvest index and protein content by Annasaheb^[2]. The findings were also supported by the observations of Ajayi *et al.*^[1] for number of primary branches, number of pods per plant, number of seeds per plant and 100 seed weight; Sharma *et al.*^[13] for height of the plant, number of primary branches, number of pods per plant, 100 seed weight, seed yield per plant and harvest index and Yadav and Rajasekhar^[17] for days to 50% flowering, grain yield per plant, 100 seed weight and number of pods per plant in cowpea.

Genetic advance is the measure of genetic gain under selection. The GAM estimates obtained were in conjunction with the reports of Girish^[3] for height of the plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant; Tigga^[16] for seed yield per plant; Kakde^[6] for height of the plant, number of pods per plant and seed yield per plant, Sharma *et al.*^[13] for number of pods per plant, 100 seed weight, seed yield per plant and harvest index; Purohit *et al.*^[12] for days to 50% flowering and protein content in cowpea.

According to Johnson *et al.*^[5], selection based on heritability estimates along with genetic gain is more effective than heritability estimates alone. In the present study, high heritability coupled with high genetic advance was observed for number of primary branches per plant, height of the plant, number of pods per plant, number of seeds per pod, 100 seed weight, crop duration, harvest index and seed yield per plant (g). It was in agreement with the findings of Ajayi *et al.*^[1] for number of primary branches per plant, number of pods per plant, number of seeds per plant and 100 seed weight; Sharma *et al.*^[13] for height of the plant, number of primary branches per plant, 100 seed weight, seed yield per plant and harvest index and Thouseem *et al.*^[15] for length of the stem, number of seeds per pod and 100 seed weight. High heritability coupled with moderate genetic advance was exhibited by the traits days to 50% flowering and protein content which were supported by the reports of Nwosu *et al.*^[10], Kouam *et al.*^[7] and Purohit *et al.*^[12].

Characters exhibiting high heritability along with high GAM are most likely governed by additive gene action and hence direct phenotypic selection may be effective for their improvement whereas characters showing moderate GAM may be governed by non-additive gene action. Hence can be improved by heterosis breeding.

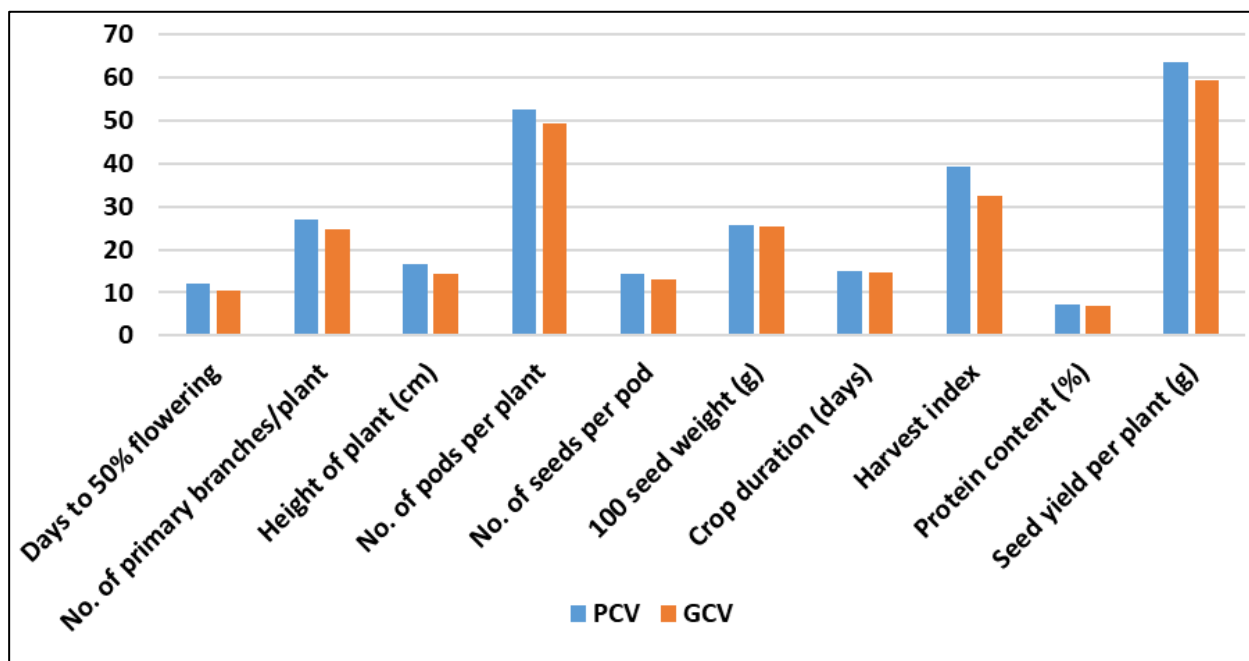


Fig 1: PCV and GCV of ten characters in grain cowpea

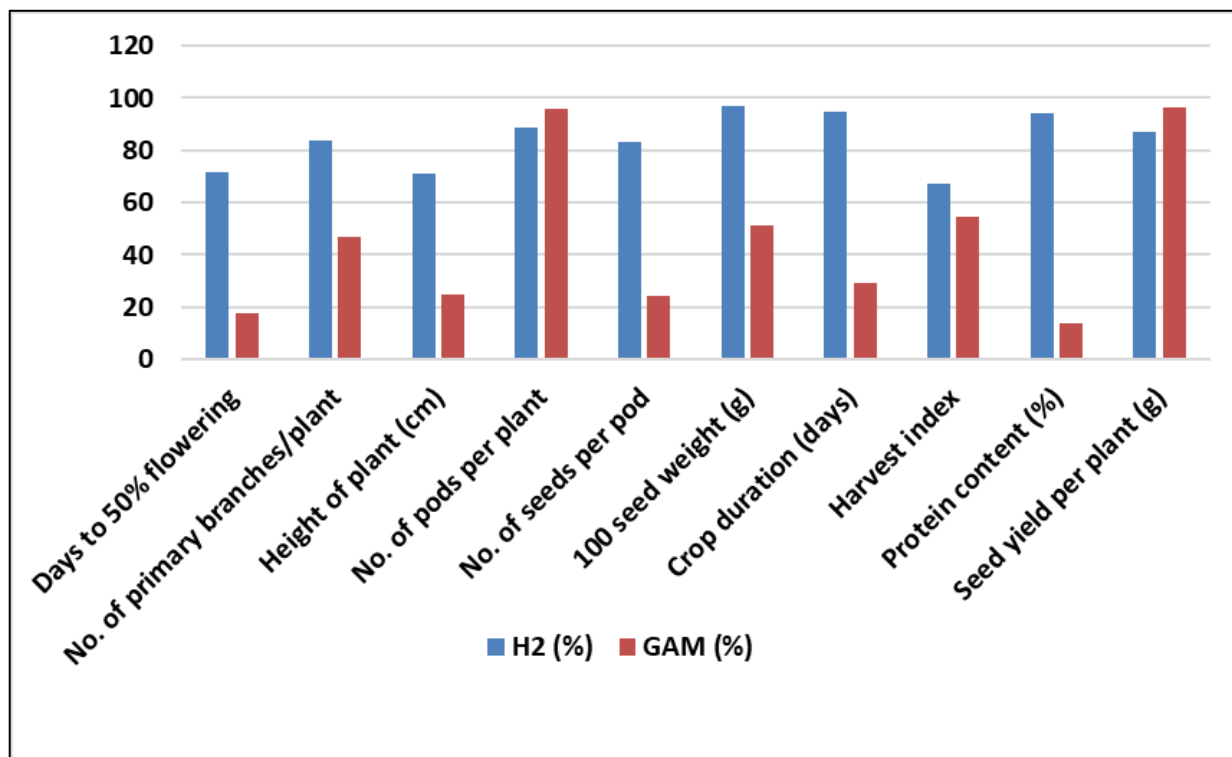


Fig 2: Heritability and Genetic advance (as per cent of mean) of ten characters in grain cowpea

Conclusion

Based on the present evaluation, it can be concluded that considerable variability was present among the genotypes for all the characters studied along with high values of genetic parameters for most of the characters. Hence the genotypes can be used in future breeding programs for improvement of these traits in grain cowpea under coconut-based homesteads.

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