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Study of Genetic Variability Parameters in F_3 Generation of Interspecific Hybrids in Cowpea [*Vigna* spp.]

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ABSTRACT: A cross has been made between grain-type cowpea (*Vigna unguiculata* ssp. *unguiculata*) and yard long bean (*Vigna unguiculata* ssp. *sesquipedalis*) and the obtained fifteen families each having three progenies along with two check varieties were subjected to variability studies. Analysis of variance revealed significant variation between families and within the progeny for all the twelve characters, justifying the selection of genotypes for the study. Plant height showed a higher estimate of phenotypic and genotypic variance. The phenotypic coefficient of variation (PCV) was higher in magnitude over the respective genotypic coefficient of variation (GCV) for all the characters under study. The estimates of PCV and GCV were high for plant height, pod length, number of pods per plant and hundred seed weight. High heritability coupled with genetic advance as percent of mean (GAM) was observed for characters plant height, pod length, number of pods per plant, hundred seed weight, seed yield per plant, number of clusters per plant, number of branches per plant, number of seeds per pod and number of pods per cluster which suggest that these characters are governed by additive genes and can be subjected to direct selection for the development of better progeny in the future.

Keywords: Cowpea, Inter-specific Hybrids, Families, GAM, Heritability, PCV, GCV Progenies.

INTRODUCTION

Cowpea (*Vigna* spp.) 2n = 22 is grown in the semi-arid tropics covering Africa, Asia, Europe, United States and Central and South America (Rachie, 1985; Singh, 2005). It is native to central Africa, where nearly all wild variants can be found. It is a multifunctional legume grown for food, fodder, vegetable, green manure, and a cover crop to prevent soil erosion and improve soil fertility through nitrogen fixation (Timko and Singh 2008; Goncalves *et al.*, 2016). Its dry edible grains are rich in protein (20–32%) with high amounts of essential amino acids (lysine and tryptophan), minerals (zinc, iron, Ca), vitamins (thiamine, folic acid and riboflavin) and fibers (6%) with low fat (< 1%) (Sebetha *et al.*, 2014; Boukar *et al.*, 2015). It is resilient to high temperature and limited water stresses and grows well on poor soil with a wide range of soil pH thus making it a good choice for resource-poor small-scale farmers for their sustenance (Carvalho *et al.*, 2017). Approximately 6,991,174 tonnes of dry cowpea grains are produced annually across the world on about 12,316,878 ha (FAOSTAT, 2016). Cowpea is extensively grown in southern India, particularly in the states of Andhra Pradesh, Karnataka, Tamil Nadu and Maharashtra. States like Kerala and Karnataka cultivate vegetable cowpea extensively while in Tamil Nadu and Maharashtra it is cultivated in very few pockets only (Nene, 2006; Pande *et al.*, 2012; Rajpoot and Rana, 2016). In Maharashtra cowpea occupies about 11,800-hectare area with a productivity of 390 Kg/ha (Nagare *et al.*, 2010; Anonymous, 2014). It is grown for all the purposes *i.e.*, grain, vegetable and fodder under two seasons Kharif and Rabi in all types of soils in different regions of this state (Rajemahadik *et al.*, 2018). In the Konkan region 1,300-hectare area is under cowpea with 410 Kg/ha productivity (Anonymous, 2014). Improvement of cowpea has largely been through conventional breeding methods, which usually involve interspecific crosses, *i.e.*, crosses between different species (Amusa *et al.*, 2022). An attempt has been made by crossing grain type cowpea (*Vigna unguiculata* ssp. *unguiculata*) and yard long bean (*Vigna unguiculata* ssp. *sesquipedalis*) in the hope of generating the desired variability in advance segregating generations. This study aimed to compare the nature and extent of variability for yield and yield contributing characters in the F_3 population of different crosses of cowpea.

MATERIALS AND METHODS

Experimental details: The experiment was conducted in 'Compact Family Block Design' as suggested by Panse and Sukhatme (1967); Premnarain *et al.*, (1979) with three replications to study progeny differences within the fifteen F_3 families each having three progenies along with two check varieties with a spacing of 30 × 20 cm at Educational and farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during rabi 2018-19 (Table 1).

Table 1: List of Experimental material.

Sr. No.	Genotypes
F_3 family population:	
F1	Konkan safed × Konkan wali
F2	Konkan safed × Arkagarima
F3	Konkan safed × UBA-1
F4	Konkan sadabahar × UBA-1
F5	Pusadophasali × UBA-1
F6	Pusadophasali × DPL-YB-5
F7	PCP-9723 × Arkagarima
F8	ACP-109 × Arkagarima
F9	ACP-109 × DPL-YB-5
F10	PCP-97102 × UBA-1
F11	V-585 × Konkan wali
F12	ACP-1264 × Konkan wali
F13	ACP-1264 × UBA-1
F14	ACP-1264 × DPL-YB-5
F15	PCP-97100 × Arkagarima
F16	KONKAN SAFED
F17	KONKAN SADABAHAR

Cultural practices: All recommended practices were carried out as and when required to maintain a good crop stand as per standard recommendation. Irrigation was provided as and when required.

Observations recorded: Observations were recorded from five randomly selected plants from each progeny per replication for 12 characters like plant height (cm), number of branches per plant, days to first flowering, days to maturity, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), hundred seed weight (g), harvest index (%) and seed yield per plant (g) and average was taken for analysis. Further to test the homogeneity of progenies within the families, data is subjected to Bartlett's test for homogeneity of variances.

Genetic variability parameter *viz.*, mean, variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) as suggested by Burton and De Vane (1953), heritability (h^2) as suggested by Lush (1949), and genetic advance as suggested by Johnson *et al.* (1955) for all the characters were calculated by following standard procedures with the help of INDOSTAT software.

RESULTS AND DISCUSSION

The analysis of variance between families and within the progeny revealed significant variation for all the characters studied (Table 3 and 4). Similar results were reported by Moalafi *et al.* (2010) for number of pods per plant and Santos *et al.*, (2014) for all the characters except hundred seed weight. Bartlett's test explained the significant difference present between the error variances of individual families for all the characters except for days to first flowering, number of pods per plant and number of seeds per pod (Table 2).

Seed yield per plant had significant variation between the progenies of family Konkan safed × UBA-1, Konkan sadabahar × UBA-1, Pusadophasali × UBA-1, PCP-9723 × Arkagarima, ACP-109 × Arkagarima, ACP-109 × DPL-YB-5, ACP-1264 × Konkan wali, ACP-1264 × DPL-YB-5 and PCP-97100 × Arkagarima. This indicated the best criterion for the selection of seed yield per plant both in families and progenies. Similar results were recorded by Bernardo *et al.* (2018) for genetic variability within the progenies. Genetic variability helps to choose a potential cross since variability indicates the extent of recombination for initiating effective selection.

Table 2: Bartlett's test for homogeneity of different characters.

Sr. No.	Characters	Degrees of freedom	Chi-square value
1.	Plant height	16	37.106**
2.	No. of branches per plant	16	31.461*
3.	Days to first flowering	16	15.888
4.	Days to maturity	16	103.227**
5.	No. of clusters per plant	16	95.994**
6.	No. of pods per cluster	16	49.633**
7.	No. of pods per plant	16	19.039
8.	Pod length	16	87.184**
9.	No. of seeds per pod	16	22.626
10.	Hundred seed weight	16	133.537**
11.	Harvest index	16	32.554**
12.	Seed yield per plant	16	47.996**

*Significant at 5% level **Significant at 1% level

Table 3: Analysis of variance among all families (Mean Sum of Squares).

Source of variation	d.f	PH	BPP	DFF	DM	NCP	NPC	NPP	PL	NSP	HSW	SYPP	HI
Replication	2	9.50	2.12 **	7.30	82.23	7.00	0.066	115.79 *	0.14	1.59	0.30	20.01 *	4.20 *
Families	16	2,012.23**	2.58 **	59.76 **	586.28**	73.52 **	0.873**	731.95**	127.27**	20.19 **	59.02**	97.31 **	142.46 **
Error	32	34.72	0.26	2.94	25.13	6.05	0.037	22.60	1.30	0.55	1.00	4.00	1.07
Bartlett's test	16	37.106**	31.461*	15.888	103.227**	95.994**	49.633**	19.039	87.184**	22.626	133.537**	47.996**	32.554**

*Significant at 5% level **Significant at 1% level

Table 4: Analysis of variance for progenies within family (Mean Sum of Squares).

Source of variation	d.f	PH	BPP	DFF	DM	NCP	NPC	NPP	PL	NSP	HSW	SYPP	HI
		Konkan safed × Konkan wali											
Replication	2	15.018**	0.023	4.333**	1.366	9.930**	0.013	11.348*	6.334**	0.023	0.756*	3.891**	0.939
Progenies	2	1.854	0.003	16.333**	4.698*	0.463**	0.003	1.988	4.320*	0.163	0.344	0.228	0.127
Error	4	0.354	0.027	0.167	0.370	0.008	0.017	1.104	0.262	0.092	0.056	0.092	1.300
		Konkan safed × Arkagarima											
Replication	2	6.786**	0.004	3.111	1.606*	12.841**	0.022	15.475	4.213	0.881	1.063	8.280**	0.453
Progenies	2	0.017	0.008	0.111	0.751	0.568	0.020	8.041	21.283*	0.748	1.233	0.049	0.610
Error	4	0.254	0.021	4.444	0.110	0.221	0.014	3.078	2.869	0.151	4.653	0.137	0.589
		Konkan safed × UBA-1											
Replication	2	75.554**	0.012*	10.111*	3.613**	0.938**	0.001	25.448*	0.175	0.101	1.604**	6.024**	0.623
Progenies	2	0.375	0.002	3.444	0.640	0.218*	0.002	6.321	2.870**	0.351	0.517*	0.295*	1.199
Error	4	0.302	0.002	1.111	0.173	0.018	0.002	1.421	0.082	0.098	0.047	0.042	0.226
		Konkan sadabahar × UBA-1											
Replication	2	113.492**	0.934**	2.111	0.495	3.070**	0.008	23.590**	2.493**	0.068	1.442**	6.601**	0.222
Progenies	2	60.063**	0.021	1.778	4.853*	1.030**	0.029	8.973*	0.173	0.601*	0.074	3.625**	17.908**
Error	4	0.010	0.011	1.444	0.306	0.035	0.014	1.198	0.091	0.083	0.033	0.106	0.278
		Pusadophasali × UBA-1											
Replication	2	0.702	1.000*	0.778	1.895	3.648**	0.028	24.373*	0.489	0.114	0.226	7.759**	0.231
Progenies	2	0.387	0.043	2.111	2.404	3.134**	0.285**	2.613	0.033	2.341**	0.089	10.504**	18.909**
Error	4	1.705	0.013	0.611	1.119	0.051	0.013	1.582	1.042	0.051	0.448	0.096	0.090
		Pusadophasali × DPL-YB-5											
Replication	2	4.756	0.893	0.778	1.392	4.623**	0.002	37.124*	0.023	0.090	1.267**	3.554	0.827
Progenies	2	4.530	0.083	0.111	15.738**	0.343**	0.062*	3.893	0.119	3.630**	1.416**	0.141	1.541
Error	4	1.436	0.057	0.611	0.344	0.002	0.006	4.546	0.099	0.030	0.030	1.091	0.245
		PCP-9723 × Arkagarima											
Replication	2	0.051	0.028	3.444	6.520*	3.623**	0.234	34.915**	0.582	0.070	0.987**	3.590**	3.526
Progenies	2	6.774*	0.028	1.778	2.280	0.763**	0.008	0.288	0.259	1.003**	0.084*	4.493**	6.472
Error	4	0.394	0.008	1.278	0.560	0.037	0.094	0.458	0.310	0.013	0.009	0.021	2.799
		ACP-109 × Arkagarima											
Replication	2	30.561**	0.008	1.444	21.127	1.141	0.007	46.908**	0.167	0.063	1.357*	2.791**	0.236
Progenies	2	81.451**	0.074	0.444	20.831	2.741	0.012	0.274	13.595**	1.710*	2.491**	4.431**	0.233

Error	4	0.404	0.033	0.778	3.323	1.093	0.004	0.670	0.030	0.213	0.106	0.029	0.334
		ACP-109 × DPL-YB-5											
Replication	2	63.476**	0.010	4.111	3.128*	1.028*	0.000	46.208**	0.036	0.074	1.392**	3.489**	3.231
Progenies	2	57.577**	0.160	19.444*	42.031**	0.801	0.002	5.248*	26.758**	2.568**	0.011	2.277**	2.751
Error	4	0.905	0.030	1.778	0.436	0.134	0.004	0.546	0.023	0.108	0.032	0.084	0.666
		PCP-97102 × UBA-1											
Replication	2	50.948**	0.008	1.778	17.970**	0.955	0.000	26.973**	0.115*	4.068**	1.235**	2.147	1.432*
Progenies	2	3.805	0.231	0.778	1.653	2.054	0.002	2.773	0.037	1.724**	0.224*	2.943	2.973**
Error	4	0.927	0.059	1.444	0.449	1.561	0.004	1.272	0.010	0.053	0.021	0.695	0.116
		V-585 × Konkan wali											
Replication	2	0.141	0.008	13.778*	4.000	42.954**	0.002	24.949**	0.072	0.821**	1.144**	6.482**	3.207**
Progenies	2	18.591**	0.404**	0.111	0.053	0.431	0.007	4.698**	0.298*	1.254**	0.048	0.020	1.014
Error	4	0.667	0.009	1.944	2.753	0.834	0.049	0.237	0.025	0.043	0.012	0.010	0.169
		ACP-1264 × Konkan wali											
Replication	2	83.141**	0.854	6.333	68.550	1.954	0.314**	33.888*	0.105	0.583**	0.916**	6.062**	3.943*
Progenies	2	51.005**	0.528	0.333	5.564	1.574	0.135*	6.361	0.004	0.203**	0.007	0.959*	1.702
Error	4	0.512	0.141	2.667	17.419	0.411	0.008	4.248	0.144	0.007	0.003	0.039	0.311
		ACP-1264 × UBA-1											
Replication	2	41.744**	0.351*	0.333	321.936***	6.484**	0.017	41.611**	0.082*	0.730*	0.839**	10.467**	1.407
Progenies	2	0.610	0.031	0.333	4.164	5.748**	0.069	1.213	0.345**	0.063	0.003	0.838	2.223
Error	4	0.198	0.044	1.167	0.692	0.006	0.029	1.023	0.010	0.068	0.003	0.209	0.630
		ACP-1264 × DPL-YB-5											
Replication	2	67.168**	0.974**	0.444	29.937	7.390**	0.003	39.630**	0.128	2.031*	0.999**	9.977**	0.010
Progenies	2	1.271**	0.001	1.778	14.271	2.010**	0.001	11.170*	3.048**	0.288	0.073**	0.860**	1.479
Error	4	0.019	0.029	0.944	35.818	0.030	0.004	1.000	0.049	0.254	0.022	0.042	1.498
		PCP-97100 × Arkagarima											
Replication	2	11.167**	1.141**	0.111	0.163	3.134	0.013*	43.282**	5.922*	0.670*	0.998	2.337*	0.342
Progenies	2	0.935*	0.001	2.111	0.658	9.458*	0.006	11.441**	0.481	1.773**	2.953	1.788*	0.106
Error	4	0.115	0.029	1.778	0.285	1.146	0.002	0.544	0.360	0.083	0.029	0.140	0.362
		Konkan safed (Check 1)											
Replication	2	0.363	0.042	0.333	0.360	0.004	0.000	0.653	0.001	0.048	0.023	0.505	0.395
Progenies	2	0.016	0.020	1.333	0.640	0.048	0.001	2.263	0.002	0.111	0.247	0.479	0.097
Error	4	0.372	0.015	0.667	0.140	0.014	0.002	0.727	0.003	0.021	0.036	0.079	0.087
		Konkan sadabahar (Check 2)											
Replication	2	0.017	0.012	1.000	0.190	0.090	0.000	1.074	0.057	0.014	0.044	0.001	0.288
Progenies	2	0.001	0.010	0.333	0.751	0.070	0.001	1.404	0.294	0.074	0.462	0.222	0.081
Error	4	0.093	0.002	0.333	0.318	0.040	0.001	2.718	0.090	0.033	0.166	0.032	0.102

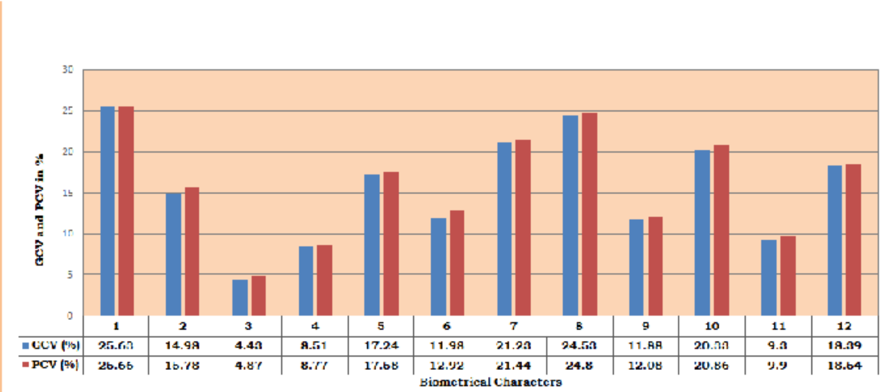
Significant at 5% level **Significant at 1% level

PH - Plant height, NBP -No. of branches per plant, DFF -Days to first flowering, DM -Days to maturity,
NCP - No. of clusters per plant, NPC -Number of pods per cluster, NPP -No. pods per plant, PL -Pod length,
NSP -No. of seeds per pod, HS -Hundred seed weight, SYPP -Seed yield, HI - Harvest index.
W

In the present study, the crosses exhibited a maximum range of variation for the character's plant height (37 to 98 cm), days to first flowering (55 to 66 days), days to maturity (77 to 114 days), number of clusters per plant (8 to 26), number of pods per plant (18 to 68), pod length (7.7 to 33.2 cm), number of seeds per pod (7 to 25), hundred seed weight (7.52 to 19.16 g), harvest index (30.33 to 50.88 %) and seed yield per plant (10.13 – 29.96 g). Similar results were reported by Patel *et al.* (2016); Nair *et al.,* (2018) for these characters. The high range of values indicated the good scope for the selection of suitable basic material for breeders for further improvement.

The mean values for each character play an important role in selection. In the case of days to first flowering and days to maturity, lower mean values enabled the identification of several short-duration segregants. The lower mean values for these characters were observed by the families ACP-1264 × UBA-1 (56.00 days) and Konkan safed × Arkagarima (80.42 days) respectively out of 15 families. The cross-combination ACP-109 × DPL-YB-5 and PCP-97102 × UBA-1 reported a maximum number of pods per cluster. Pusadophasali × DPL-YB-5 (22.50, 56.27 and 17.76 g) had the highest number of clusters per plant, number of pods per plant and hundred seed weight. The cross Konkan safed × Arkagarima (24.62 cm, 16.64, 47.77% and 24.30 g) recorded maximum pod length, number of seeds per pod, harvest index and seed yield per plant among all the crosses. The estimates of phenotypic, genotypic and environmental variance revealed that phenotypic variance was higher in magnitude than the genotypic variance for all the characters. The magnitude of phenotypic and genotypic variances was closer to each other for the majority of the characters thus indicating the lesser role of environment in the expression of these characters.

The character's plant height (25.66%), pod length (24.80%), number of pods per plant (21.44%) and hundred seed weight (20.86%) exhibited maximum PCV estimates (Table 3). High values of GCV were registered for plant height (25.63 %), pod length (24.53%), number of pods per plant (21.23%) and hundred seed weight (20.33%) (Ugale *et al.*, 2020; Tambitkar *et al.*, 2021). The characters seed yield per plant (18.39%), number of clusters per plant (17.24%), branches per plant (14.98%), number of pods per cluster (11.98%) and number of seeds per pod (11.88%) exhibited moderate GCV and low GCV estimates were reported for harvest index (9.30%), days to maturity (8.51%) and days to first flowering (4.43%) (Fig. 1). Similar results were recorded by Prasad *et al.* (2015); Patel *et al.* (2016); Dinesh *et al.* (2017). The environmental influence was minimum for the expression of most of the traits which is evident from the narrow difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates.



	1	2	3	4	5	6	7	8	9	10	11	12
■ GCV (%)	25.63	14.98	4.43	8.51	17.24	11.98	21.23	24.53	11.88	20.33	9.3	18.39
■ PCV (%)	25.66	15.78	4.87	8.77	17.68	12.92	21.44	24.8	12.08	20.86	9.9	18.64

1. Plant height (cm)	2. Number of branches per plant	3. Days to first flowering
4. Days to maturity	5. Number of clusters per plant	6. Number of pods per cluster
7. Number of pods per plant	8. Pod length (cm)	9. Number of seeds per pod
10. Hundred seed weight (g)	11. Harvest index (%)	12. Seed yield per plant (g)

Fig. 1. Genotypic and phenotypic coefficient of variation for twelve characters in cowpea.

High heritability was recorded for all the characters under study (Table 5, Fig. 2). The genetic advance ranged from 0.59 to 30.4 between the character's number of pods per cluster and plant height respectively. High heritability estimates along with high genetic advance as percent of mean was noticed in plant height (99.8%, 52.74%), pod length (97.8%, 49.98%), number of pods per plant (98.1%, 43.31%), hundred seed weight (95.0%, 40.8%), seed yield per plant (98.4%, 37.59%) number of clusters per plant (96.1%, 34.81%), number of branches per plant (90.2%, 29.31%), number of seeds per pod (96.6%, 24.05%) and number of pods per cluster (86.0%, 22.89%). The high heritability coupled with genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression (Pramanik *et al.*, 2021). Hence seed yield per plant can be improved by selection in further generations. Similar result was reported by Shanko *et al.* (2014); Dinesh *et al.* (2017); Kumar *et al.* (2017); Sabale *et al.* (2018); Manju Devi and Jayamani (2018). High heritability with low genetic advance as percent of mean for days to first flowering (82.9%, 8.32%) indicates that character may be controlled by non-additive gene action. Similar results were recorded by Udensi *et al.* (2012); Saidaiah *et al.* (2021); Manohara *et al.* (2021).

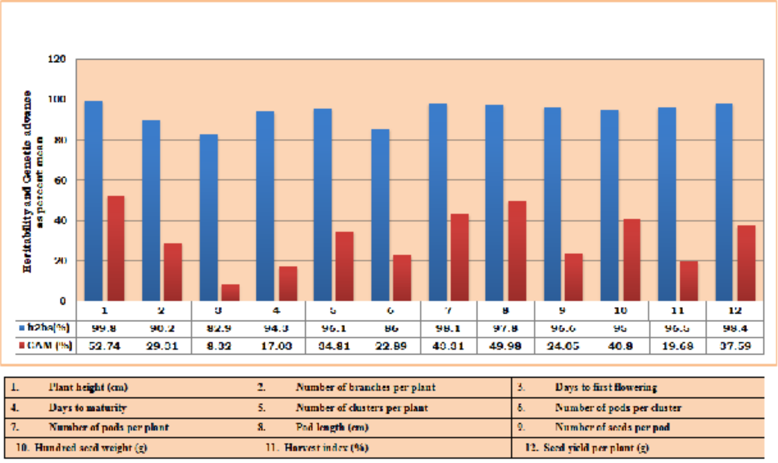


Fig. 2. Heritability and genetic advance as percent of mean for twelve characters in cowpea.

Table 5: Estimation of genetic variability parameters for twelve characters.

Sr. No.	Characters	Mean±S.E.(m)	Range	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
1.	Plant height	57.65±**2.78**	37-98	25.66	25.63	99.8	52.74
2.	No. of branches per plant	3.58±0.24	1-5	15.78	14.98	90.2	29.31
3.	Days to first flowering	58.03±0.81	55-66	4.87	4.43	82.9	8.32
4.	Days to maturity	93.18±2.36	77-114	8.77	8.51	94.3	17.03
5.	No. of clusters per plant	16.56±1.16	8-26	17.58	17.24	96.1	34.81
6.	No. of pods per cluster	41.76±2.24	18-68	12.92	11.98	86	22.89
7.	No. of pods per plant	2.59±0.09	1-3.5	21.44	21.23	98.1	43.31
8.	Pod length	15.50±0.54	7.7-33.2	24.8	24.53	97.8	49.98
9.	No. of seeds per pod	12.98±0.35	7-25	12.08	11.88	96.6	24.05
10.	Hundred seed weight	12.37±0.47	7.52-19.16	20.86	20.33	95	40.8
11.	Harvest index	40.87±0.49	30.33 - 50.88	9.9	9.3	96.5	19.68
12.	Seed yield per plant	17.85±0.94	10.13-29.96	18.54	18.39	98.4	37.59

CONCLUSION AND RECOMMENDATION

It is concluded that a wide range of variability exists among the families and within the progeny of the same family for all the characters under study. PCV was higher in magnitude over respective GCV. High heritability with high genetic advance as percentage of mean was observed for plant height, pod length, number of pods per plant, hundred seed weight, seed yield per plant, number of clusters per plant, number of branches per plant, number of seeds per pod and number of pods per cluster. Seed yield per plant showed positive and high significant correlation with harvest index, number of pods per plant, number of branches per plant, number of pods per cluster, hundred seed weight, pod length, number of clusters per plant and number of seeds per pod at both genotypic and phenotypic level. These characters should be used as selection criteria for genetic improvement of seed yield per plant in the cowpea population under study.

FUTURE SCOPE

A wide range of variability exists between families and within the progeny for the different quantitative characters, which could be used for systematic exploitation in segregants of cowpea. High heritability with high genetic advance as percentage of mean was observed for plant height, pod length, number of pods per plant, hundred seed weight, seed yield per plant, number of clusters per plant, number of branches per plant, number of seeds per pod and number of pods per cluster. The progenies of Konkan safed × Arkagarima, ACP-1264 × DPL-YB-5, ACP-1264 × UBA-1, PCP-97100 × Arkagarima and Pusadophasali × DPL-YB-5 were promising based on seed yield and yield attributing characters. These crosses along with their progeny can be promoted to F_4 generation for the selection of promising cultivars.

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Conflict of Interest. None.

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