The Pharma Innovation

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Assessment of yield criteria in interspecific crosses of cowpea (*Vigna* spp.)

Sudhamani Kalluru, SS Desai, VV Dalvi, AV Mane and UB Pethe

Abstract
Cowpea is a prospective climate-resilient food legume of the 21st century owing to its high protein content, nitrogen-fixing capacity, drought tolerance, and adaptability to harsh environments. Despite being in use for centuries, there is still a gap in obtaining maximum yield potential, primarily ascribed to the shortage of high-yielding cultivars. To this end, nine grain-type cowpea varieties (*Vigna unguiculata* ssp. *unguiculata*) and four-yard-long bean-type varieties (*Vigna unguiculata* ssp. *sesquipedalis*) were crossed to produce fifteen families each having three progeny in the F₃ generation. Using the compact family block design, the 15 families, parents and two checks were assessed for twelve yield component traits. Data subjected to multiple selections using Pearson's correlation, principal component, factor, path and cluster analyses revealed seed yield being directly controlled by branches per plant, harvest index, 100 seed weight and pod number per plant. These characteristics should serve as the primary selection criteria for the genetic enhancement of yield. Further, the progeny of the crosses *Konkan safed* x *Arka garima*, ACP-1264 x DPL-YB-5, ACP-1264 x UBA-1, PCP-97100 x *Arka garima*, and *Pusa dophasali* x DPL-YB-5 were the best performing lines which should be forwarded to the next generation.

Keywords: Correlation, families, grain-type cowpea, progenies, yard-long bean

1. Introduction
According to the Food and Agriculture Organization (FAO) estimates, by 2050, food production must grow by 70% to feed the 9.3 billion population and this will be highly challenging in view of the lack of adaptable varieties to climate change, new pests and diseases labour shortage, over fertilization of the land, and a fewer availability of resources. Cowpea (*Vigna unguiculata* L.) is a versatile tropical legume that serves as an essential source of nutrition for most of the rural and tribal cultures in Asia, Africa, Europe and South America (Singh, 2005) [25]. It is native to central Africa, where nearly all wild variants can be found (Kumar *et al.,* 2021). Cowpea, with its high protein content, nitrogen-fixing capacity, drought tolerance, and adaptability to harsh environments, is a potential climate-resilient food legume for the 21st century. It is a multipurpose legume that can be used as a cover crop, food, fodder, vegetable and green manure that also prevents soil erosion by fixing nitrogen into the soil (Timko and Singh, 2008) [28]. Dry edible grains of cowpea are high in protein (20-32%), essential amino acids (lysine and tryptophan), minerals (zinc, iron, calcium), vitamins (thiamine, folic acid, and riboflavin), and fibre (6%) while being low in fat (1%). (Sebetha *et al.,* 2014; Boukar *et al.,* 2015) [23, 4]. Approximately 8.9 million tonnes of dry cowpea grains are produced annually across the world on about 15 million hectares (FAOSTAT, 2021) [10].

Even though cowpea has a lot of benefits, in India, its production has been hindered by its low yield, which is caused by a variety of factors, including the continuous use of inferior cultivars by the farmers and the timely emergence of new pests and diseases. Recent studies revealed the development of high-yielding varieties of cowpea having yield potential up to 4-6 t ha⁻¹ (Aliyu and Makinde, 2016) [2]. A standard procedure for increasing quality and yield in self-pollinated plants such as cowpea is to identify or interbreed genotypes with character combinations already existing in nature. Further, through multivariate analysis such as correlation, path analysis, principal component and factor analysis one can determine the characters directly or indirectly contributing to the yield increment. In this study, nine grain-type cowpea varieties (*Vigna unguiculata* ssp. *unguiculata*) and four-yard-long bean-type varieties (*Vigna unguiculata* ssp. *sesquipedalis*) were crossed to produce fifteen families each having three progeny in the F₃ generation. Multiple selection criteria were used to evaluate these F₃ progeny and two national check varieties in order to determine yield components important for cowpea selection and improvement.

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2. Materials and Methods
2.1 Experimental details
The experiment was laid out in the 'Compact Family Block Design' (Panse and Sukhatme, 1967 and Premnarain *et al.,* 1979) [20, 21] with three replications with a spacing of 30 x 20 cm at Educational and farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *Rabi*, 2018-19 (Table 1). By conventional recommendations, all advised actions were followed to maintain a good crop stand. When required, irrigation was provided. Observations were recorded from five randomly selected plants from each progeny per replication for various vigour (plant height, branches per plant, days to first flowering, days to maturity) and yield-related traits (cluster number per plant, pod number per cluster, pod number per plant, seed number per pod, pod length, 100 seed weight, harvest index and seed yield per plant).

2.2 Statistical analysis
A variety of statistical techniques were used to investigate the trade-off between the various vigour and yield contributing variables used in the screening process. A matrix of association between all parameters studied was created using correlation analysis. Using principal component analysis, a significant number of variables were divided into primary components (PCA). The first two main components best explain the variability in the data (Everitt & Dunn, 1992). A significant number of related variables are condensed by the factor analysis into a manageable number of factors. On the factor loading matrix, the varimax orthogonal rotation is performed. Path analysis was used to assess the direct and indirect effects of characteristics. Path coefficient analysis was performed using grain yield as a dependent characteristic and the other estimated characteristics as causative, based on the logical connections between grain yield and other attributes. The analyses were performed using IBM SPSS 22.0 (SPSS Inc., 2013).

3. Results
3.1 Correlations between vigour and yield component traits
Both phenotypic and genotypic correlation revealed branching and yield-contributing traits positively and significantly associated with seed yield per plant (Figure. 1). Plant height showed a negative non-significant relation with days to maturity, cluster number, pod number and seed weight. Early flowering is associated with the earliest pod maturity, as demonstrated by a strong and positive significant association between flowering and maturity. Similar results were observed by Santos *et al.,* (2014) [22]. Days to maturity revealed a significant negative correlation between pod length and the seed number per pod. Branching has a positive significant correlation with most of all the yield component traits. Most of all the yield contributing characters showed positive and significant associations between themselves.

The pod number recorded a positive and significant correlation with the cluster number per plant, pod number per cluster, harvest index, hundred seed weight and seed yield per plant at both genotypic and phenotypic levels. Indicating that seed yield may be obtained indirectly with selection for an increase in the pod number. Similar results were reported by Kalaiyarasi and Palanisamy, (2001) [13]; Deepa and Balan, (2006) [6] and Alege and Mustapha, (2007) [1].

3.2 Classifying the vigour and yield contributing traits into major components
Principal component analysis (PCA) results revealed that out of twelve components, the first four PCs explained most of the total variations present in the genotypes (Table 2). Principal components were selected by the eigenvalue >1 suggested by Brejda *et al.* (2000) [5]. The first four principal components with eigenvalue >1 contributed about 76.91% of the total variability among the progenies which were evaluated for various vigour and yield component traits. The remaining eight components contributed only 23.09%. The Principal Component PC1 contributed maximum variability of 37.33% followed by PC2 at 21.11%. PC3 recorded 9.99% variability. 8.48% variability was recorded by PC4.

The variables that have the strongest correlations with each component's principal component are used to interpret the results. Eigenvalues close to -1 or 1 indicate that the variable strongly influences the component. Values close to 0 indicate that the variable weakly influences the component. The important characteristics that contributed to the positive factor loading value for PC 1 were harvest index (0.4216), pod number (0.3999), seed yield per plant (0.3795), followed by the branches per plant (0.3511), pod number per cluster (0.2824). The trait days to first flowering (-0.2196) contributed to PC1 negatively. PC 2 was contributed positively by the trait's days to maturity (0.4504), pod number per plant (0.2193) while the seed number per pod (-0.4669), pod length (-0.4450) and plant height (-0.4100) contributed negatively. The PC3 related to the characters plant height (0.5359), days to fifty percent flowering (0.4504) and the pod number per cluster (0.4040) contributed positively whereas hundred seed weight (-0.5414) and seed yield per plant (-0.1227) contributed negatively. The first three principal component axes explained more than half of the total variability (68.42%). Hence, it indicated a high degree of correlation among the traits studied (Jain and Patel, 2016) [12]. As a whole, PCA could identify important characters responsible for the variability in a population. Similar studies were also reported by Sharifi *et al.,* (2018) [24] and Mofokeng *et al.,* (2020) [19].

Scree plot created a graph between eigenvalues and principal components to explain the percentage of variation connected with each principal component (Figure 2). Depending on how much the character contributes to the major component, the length of the vector is determined in the biplot (Figure 3). Additionally, the character vectors' angle reflects how the various variables are correlated. A positive correlation is shown if there is an acute angle of 90° between two trait vectors. The six vectors in the 1st quadrant *viz.,* seed yield per plant, harvest index, pod number per plant, branches per plant, cluster number per plant and pod number per cluster were highly correlated variables. These six variables have a substantial correlation with the first principal component according to the factor loading values. Similarly, the vectors in the 4th quadrant hundred seed weight, pod length, seed number per pod and plant height were highly correlated variables. If the angle between two traits is >90° (an obtuse angle), indicates a negative correlation. While if the angle is equivalent to 90°, indicates that no correlation between the characters. Most of the yield component characters were negatively correlated with plant height and days to first flowering. Days to maturity and seed number per pod do not correlate with the branches per plant, pod number per cluster,

cluster number per plant and pod number per plant.

The biplot graph clearly shows that the progeny of the cross Konkan safed x Arka Garima recorded the highest seed yield per plant. The third progeny of the cross Pusa dophasali x DPL-YB-5 coincides with the vectors of various yield component traits such as pod number, cluster number per plant, pod number per plant and seed yield per plant above the origin indicating a positive interaction (Figure 3). This concludes that by comparing the progeny of the fifteen families, the family progeny of Pusa dophasali x DPL-YB-5 and Konkan safed x Arka garima were superior for most of the yield component traits. Moreover, the progenies of the crosses ACP-109 x Arka Garima, ACP-109 x DPL-YB-5 and PCP-97102 x UBA-1G7 also had a positive interaction with those characters.

3.3 The reduction of vigour and yield contributing traits to factors

The factor analysis reduced the 12 vigour and yield contributing traits to four common factors that accounted for 74.33% of the total variability (Table 3). The first factor included about half recorded traits which include the branches per plant, cluster number per plant, pod number per cluster, pod number per plant, harvest index and seed yield per plant which accounted for 31.46% of the total variability. This factor had high positive loadings for the pod number per plant (0.916) followed by harvest index (0.904), seed yield per plant (0.742), branches per plant (0.732), cluster number per plant (0.669) and pod number per cluster (0.644). Thus, this factor can be considered the most important Second factor showed high positive loadings for the seed number per pod (0.885), plant height (0.786) and pod length (0.759). The third factor possessed high negative loadings of most of the yield-contributing traits and high positive loadings of days to fifty percent flowering (0.799) and days to maturity (0.752).

3.4 The relative importance of vigour and yield component traits on seed yield

Yield is a complicated concept that has a lot of constituent components that are interconnected with one another. Because of this interconnectedness, the contributing factors' direct link with yield is frequently impacted, rendering the correlation coefficients of the contributing components unreliable as selection indices. To determine the degree of linkage of component features with one another as well as yield, correlation is divided into direct and indirect effects. The path analysis reveals whether a character's link with yield is the result of a direct impact on yield or an outcome of an indirect impact via other features (Dewey and Lu, 1959) [7].

The phenotypic and genotypic path coefficient values for various characters are presented in Table 4. The harvest index (0.791) has the highest positive direct effect on seed yield per plant at both phenotypic and genotypic levels (Figure 5). At the genotypic level, the second highest was recorded by the branches per plant (0.508) followed by days to fifty percent flowering (0.479) and hundred seed weight (0.302). The lowest positive direct effects were recorded by the seed number per pod (0.045) and the pod number per plant (0.088) respectively. Days to maturity (-0.354) recorded the highest negative direct effect on seed yield per plant and was closely followed by the pod number per cluster (-0.318), pod length (-0.312), the cluster number per plant (-0.232) and plant height (-0.107).

Similarly, at the phenotypic level, the second highest positive direct effect was recorded by pod length (0.194) followed by the branches per plant (0.101), days to fifty percent flowering (0.082) and hundred seed weight (0.076). The highest negative direct effects were recorded by the cluster number per plant (-0.125). Even though harvest index and hundred seed weight showed positive direct effects on seed yield they were affected by negative indirect effects of most of the vigour traits. Interestingly, there exists a stable trade-off between the trait's cluster number per plant, pod number per cluster and pod number. The F_3 population had very low residual effects at both the genotypic and phenotypic levels, implying that the data were nearly full proof for concluding the traits studied.

4. Discussion

Exploring alternative secondary traits as screening tools to choose superior germplasm rather than grain yield is one of the key objectives of recent innovative breeding strategies. Establishing several efficient secondary selection characteristics and making their measurement simpler, quicker, and less expensive than the measurement of the key trait grain yield can help achieve this goal. It is essential to compare these features using more diverse materials to establish efficient secondary selection traits (Liu et al., 2011) [16]. The fifteen F_3 families along with their progeny used in this study represent exceptionally wide genetic diversity in different vigour and yield contributing traits. To identify which of these traits are effective and reliable as screening traits for evaluating the progeny lines, multiple statistical procedures were applied. The results of the principal component analysis (PCA) and factor analysis (FA) showed that all measured various vigour and yield component traits except plant height, days to fifty percent flowering and days to maturity and accounted for 37.33% and 31.46% of the total variability respectively (Tables 2 and 3). Based on PCA and FA, harvest index, pod number per plant, seed yield per plant, branches per plant, cluster number per plant, pod number per cluster and pod number could be nominated as screening criteria for evaluating cowpea progeny. Similar results were also reported in previous studies by Mofokeng et al., (2020) [19] and Sharifi et al., (2018) [24], which indicated a significant contribution to most of these traits.

Additionally, the findings showed that all of the characters had genotypic correlations that were generally stronger than their phenotypic counterparts. The genotypic correlations, which naturally link two variables, can therefore be used to improve crops in upcoming generations. The largest positive significant association was found between the character seed yield per plant and the harvest index, pod number, and branches per plant at both genotypic and phenotypic levels. Similar results were observed by Singh and Mehndiratta, (1968) [26] and Manggoel et al., (2012) [17]. These results indicate that several traits measured in this study could be strongly nominated as screening criteria instead of grain yield. Path analysis studies of the present investigation revealed that primary branches per plant, pod number, hundred seed weight and harvest index were the important yield components having a positive direct effect on the improvement of seed yield. Hence, the selection of genotypes based on these attributes would help improve seed yield potential. Similar results were recorded by Singh and Mehndiratta (1970) [27], Aman et al. (2000) [3], Meena et al. (2015) [18] and Dinesh et

al. (2017) [8]. Further, it was observed that traits *viz.*, plant height, days to maturity, number of clusters per pod, pod length and seed number per pod exhibited a negative direct effect on yield. Hence, it is difficult to go for simultaneous selection of these characters with seed yield. Days to maturity, the pod number per cluster and pod length had a positive direct effect on seed yield at the phenotypic level while having a high negative direct effect at the genotypic level. Similar results were observed by Kalaiyarasi and Palanisamy (2002) [14].

The measured vigour and yield attributing traits in the biplot graph revealed the family progeny of Pusa dophasali x DPL-YB-5 and Konkan safed x Arka garima were superior for most of the yield component traits. Moreover, the progenies of the crosses ACP-109 x Arka Garima, ACP-109 x DPL-YB-5 and PCP-97102 x UBA-1G7 also had a positive interaction with those characters.
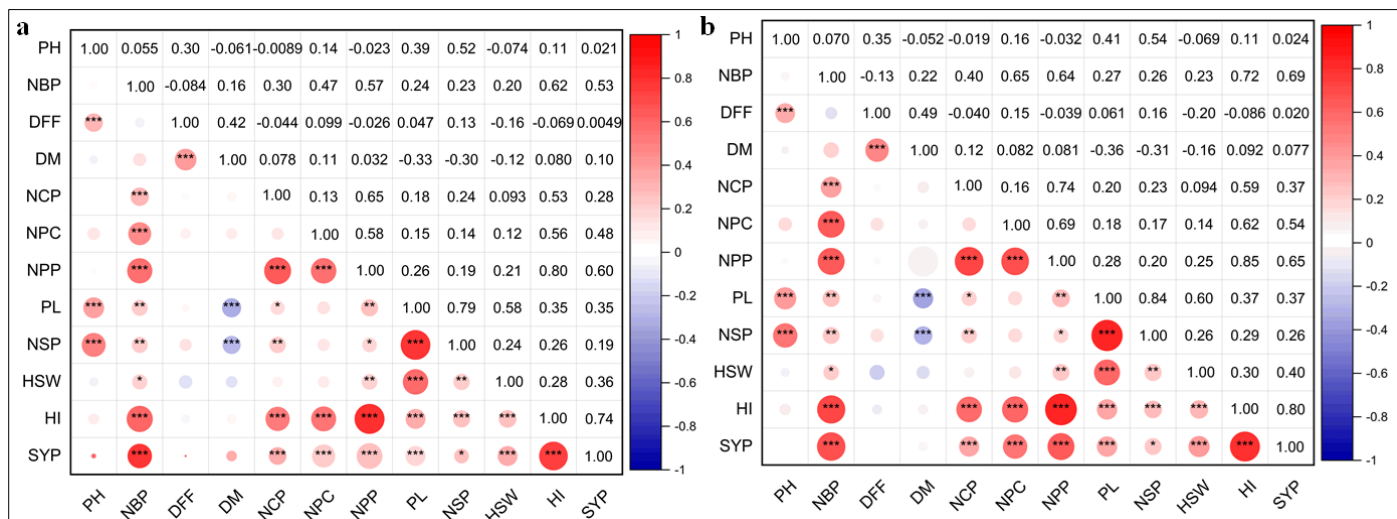
*Significant at *p*≤0.05 level; ** Significant at *p*≤0.01 level; *** Significant at *p*≤0.001 level; PH- Plant height (cm); NBP- Branches per plant; DFF- Days to first flowering; DM- Days to maturity; NCP- Clusters per plant; NPC- Pods per cluster; NPP- Pods per plant (g); PL- Pod length (cm); NSP- Seeds per pod; HSW- 100 seed weight, HI- Harvest index; SYP- Seed yield per plant.

Fig 1: Estimates of a) phenotypic; b) genotypic correlation between different characters in Cowpea
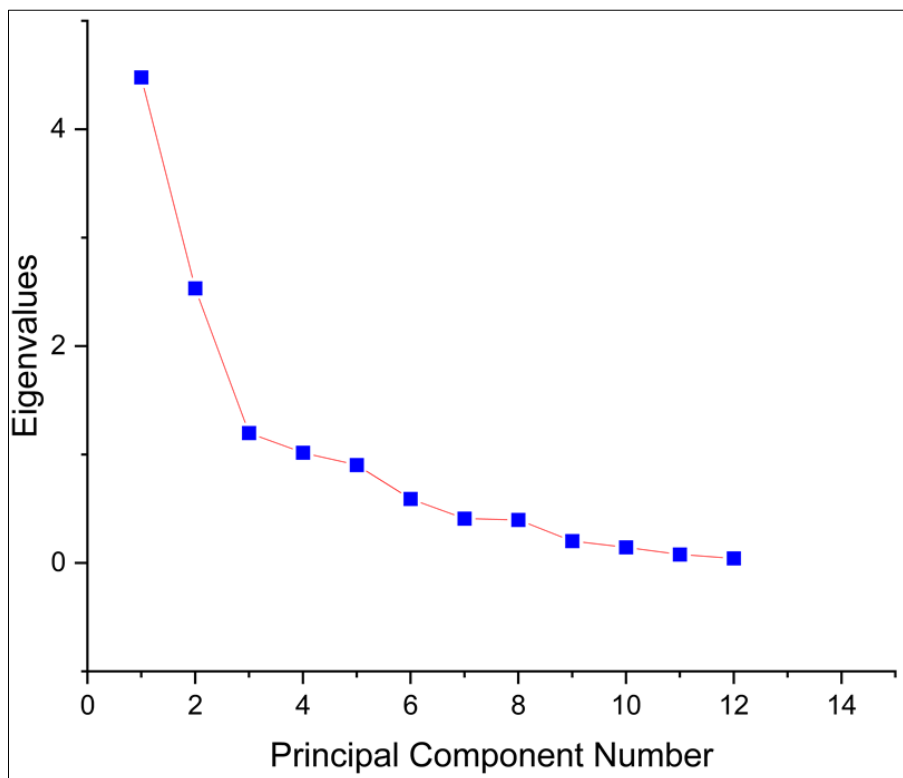
Fig 2: Scree plot depicting eigenvalues between various principal components
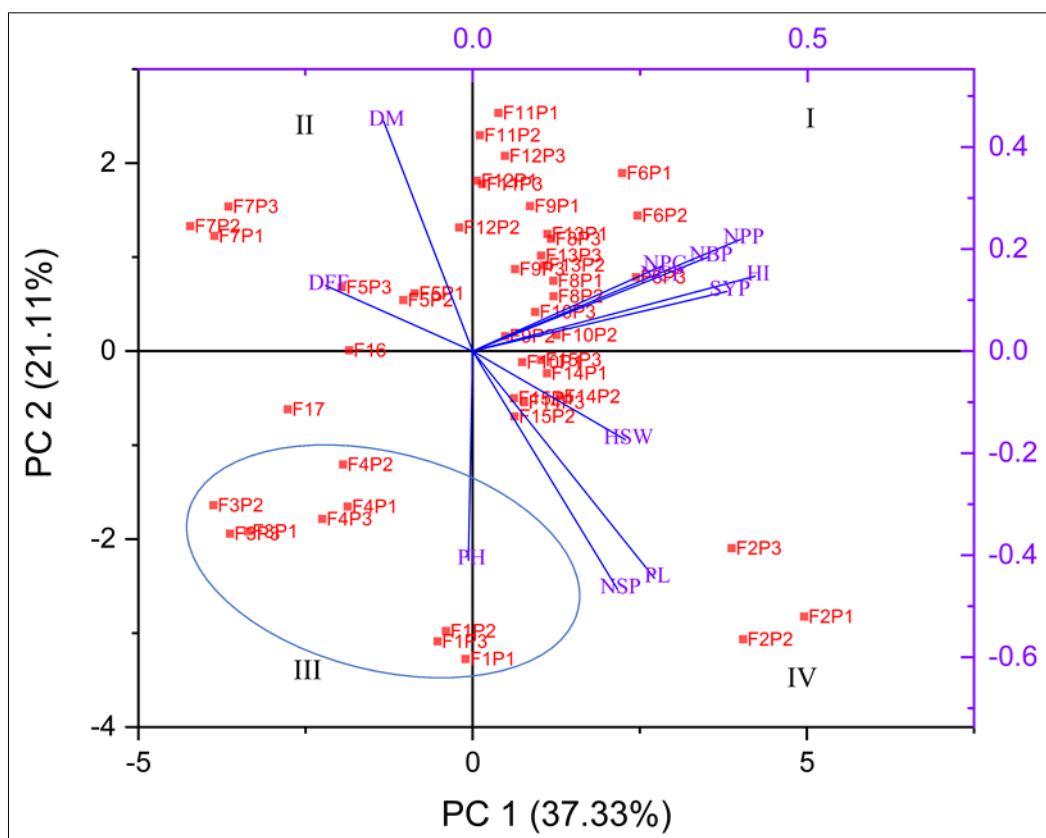
F1-15- Families; P1-3- Progenies (details given in Table 1); PH- Plant height (cm); NBP- Branches per plant; DFF- Days to first flowering; DM- Days to maturity; NCP- Clusters per plant; NPC- Pods per cluster; NPP- Pods per plant (g); PL- Pod length (cm); NSP- Seeds per pod; HSW- 100 seed weight, HI- Harvest index; SYP- Seed yield per plant.

Fig 3: PCA biplot of the progeny data showing loading values of each variable

Table 1: List of Experimental material

S. No.	Genotypes
F1	Konkan safed x Konkan wali
F2	Konkan safed x Arka garima
F3	Konkan safed x UBA-1
F4	Konkan sadabahar x UBA-1
F5	Pusa dophasali x UBA-1
F6	Pusa dophasali x DPL-YB-5
F7	PCP-9723 x Arka garima
F8	ACP-109 x Arka garima
F9	ACP-109 x DPL-YB-5
F10	PCP-97102 x UBA-1
F11	V-585 x Konkan wali
F12	ACP-1264 x Konkan wali
F13	ACP-1264 x UBA-1
F14	ACP-1264 x DPL-YB-5
F15	PCP-97100 x Arka garima
F16	KONKAN SAFED (check variety)
F17	KONKAN SADABAHAR (check variety)

Table 2: Eigenvalues, factor scores and contribution of the twelve principal component axes to variation

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
PH	-0.0063	-0.4100	0.5359	-0.0947	-0.1004	0.2334	0.5881	0.2688	0.1869	0.1061	-0.0042	-0.0832
NBP	0.3511	0.1845	0.1133	0.1464	-0.1365	0.5401	-0.1467	-0.4049	0.5315	-0.1639	0.0193	-0.0542
DFF	-0.2196	0.1286	0.4104	0.3104	0.6292	-0.2199	-0.2033	0.1664	0.3403	-0.1200	0.1642	0.0007
DM	-0.1330	0.4504	0.0414	0.0203	0.4105	0.5542	0.2519	-0.0252	-0.4441	0.1392	-0.1435	-0.0196
NCP	0.2783	0.1461	0.0169	-0.6754	0.3013	-0.1420	0.0651	-0.1172	0.2333	0.3217	0.0964	0.3857
NPC	0.2824	0.1666	0.4040	0.4505	-0.2088	-0.3048	0.1242	-0.3029	-0.2651	0.3093	0.0123	0.3415
NPP	0.3999	0.2193	0.1291	-0.1417	0.1076	-0.3493	0.1322	-0.0669	-0.0476	-0.0834	-0.2999	-0.7075
PL	0.2712	-0.4450	-0.0506	0.1097	0.3365	0.0483	-0.0852	-0.0422	-0.0723	-0.2130	-0.6647	0.3112

NSP	0.2160	-0.4669	0.1808	-0.0844	0.2127	0.1873	-0.4011	-0.1948	-0.3728	0.1933	0.4138	-0.2625
HSW	0.2277	-0.1735	-0.5414	0.3610	0.3116	-0.0669	0.4913	-0.1061	0.1395	0.0974	0.3260	-0.0729
HI	0.4216	0.1468	0.0791	-0.0758	-0.0233	0.0224	0.0910	0.3363	-0.2623	-0.6480	0.3547	0.2276
SYP	0.3795	0.1171	-0.1227	0.1964	-0.0690	0.1444	-0.2700	0.6793	0.1006	0.4582	-0.0871	-0.0312
Eigen value (root)	4.4796	2.5327	1.1987	1.0178	0.9041	0.5911	0.4100	0.3971	0.2028	0.1452	0.0782	0.0429
Variance proportion	37.33%	21.11%	9.99%	8.48%	7.53%	4.93%	3.42%	3.31%	1.69%	1.21%	0.65%	0.36%
Proportion cumulative	37.33%	58.44%	68.42%	76.91%	84.44%	89.37%	92.78%	96.09%	97.78%	98.99%	99.64%	100.00%

PH- Plant height (cm); NBP- Branches per plant; DFF- Days to first flowering; DM- Days to maturity; NCP- Clusters per plant; NPC- Pods per cluster; NPP- Pods per plant (g); PL- Pod length (cm); NSP- Seeds per pod; HSW- 100 seed weight, HI- Harvest index; SYP- Seed yield per plant.

Table 3: Rotated (Varimax rotation) factor loadings for different vigour and yield component traits in Cowpea progeny lines

Traits	Factor1	Factor2	Factor3	Factor4
PH	-.026	.786	.282	-.128
NBP	.732	.041	.071	.167
DFF	-.059	.305	.799	-.115
DM	.181	-.327	.752	-.096
NCP	.669	.150	-.260	-.418
NPC	.644	.049	.291	.170
NPP	.916	.062	-.095	-.063
PL	.231	.759	-.195	.479
NSP	.182	.885	-.129	.110
HSW	.219	.130	-.213	.808
HI	.904	.131	-.026	.110
SYP	.742	.042	.103	.398
% of Variance	31.464	18.691	13.010	11.168
Cumulative %	31.464	50.155	63.165	74.334

PH- Plant height (cm); NBP- Branches per plant; DFF- Days to first flowering; DM- Days to maturity; NCP- Clusters per plant; NPC- Pods per cluster; NPP- Pods per plant (g); PL- Pod length (cm); NSP- Seeds per pod; HSW- 100 seed weight, HI- Harvest index; SYP- Seed yield per plant.

Table 4: Path analysis for different characters at the phenotypic and genotypic levels in Cowpea

Characters	PH	NBP	DFF	DM	NCP	NPC	NPP	PL	NSP	HSW	HI	SYP
PH	-0.103	0.005	0.025	-0.002	0.001	0.008	-0.0001	0.076	-0.055	-0.006	0.070	0.021
	-0.107	0.035	0.166	0.018	0.004	-0.052	-0.003	-0.127	0.024	-0.021	0.085	0.024
NBP	-0.006	0.101	-0.006	0.006	-0.038	0.029	0.0020	0.046	-0.025	0.015	0.408	0.532**
	-0.007	0.508	-0.062	-0.077	-0.092	-0.207	0.056	-0.083	0.012	0.069	0.570	0.687**
DFF	-0.032	-0.008	0.082	0.016	0.005	0.006	-0.0001	0.013	-0.016	-0.010	-0.036	0.020
	-0.037	-0.065	0.479	-0.174	0.009	-0.048	-0.003	-0.019	0.007	-0.060	-0.068	0.020
DM	0.006	0.016	0.033	0.039	-0.010	0.007	0.0001	-0.065	0.031	-0.009	0.053	0.102
	0.006	0.111	0.236	-0.354	-0.027	-0.026	0.007	0.114	-0.014	-0.047	0.073	0.077
NCP	0.001	0.030	-0.003	0.003	-0.125	0.008	0.0022	0.035	-0.025	0.007	0.348	0.281**
	0.002	0.201	-0.019	-0.042	-0.232	-0.051	0.065	-0.063	0.010	0.028	0.469	0.368**
NPC	-0.014	0.047	0.008	0.004	-0.017	0.061	0.0020	0.029	-0.014	0.009	0.368	0.483**
	-0.017	0.330	0.072	-0.029	-0.037	-0.318	0.060	-0.055	0.008	0.042	0.489	0.545**
NPP	0.002	0.058	-0.001	0.001	-0.081	0.035	0.0034	0.051	-0.021	0.016	0.532	0.596**
	0.003	0.328	-0.019	-0.029	-0.172	-0.219	0.088	-0.089	0.009	0.075	0.675	0.651**
PL	-0.040	0.024	0.006	-0.013	-0.022	0.009	0.0009	0.194	-0.083	0.044	0.235	0.354**
	-0.044	0.135	0.029	0.129	-0.047	-0.056	0.025	-0.312	0.038	0.181	0.293	0.373**
NSP	-0.053	0.023	0.012	-0.011	-0.030	0.008	0.0007	0.153	-0.106	0.018	0.175	0.190*
	-0.058	0.130	0.076	0.110	-0.053	-0.054	0.017	-0.262	0.045	0.077	0.227	0.256**
HSW	0.008	0.020	-0.011	-0.005	-0.012	0.007	0.0007	0.113	-0.025	0.076	0.185	0.358**
	0.007	0.116	-0.096	0.056	-0.022	-0.044	0.022	-0.187	0.012	0.302	0.240	0.405**
HI	-0.011	0.062	-0.004	0.003	-0.066	0.034	0.0028	0.069	-0.028	0.021	0.662	0.745**
	-0.011	0.366	-0.041	-0.033	-0.137	-0.197	0.075	-0.115	0.013	0.091	0.791	0.802**

Note: Values in Italics are genotypic path correlation values.
Underlined figures showed direct effects; *Significant at 5% level; **Significant at 1% level; PH- Plant height (cm); NBP- Branches per plant; DFF- Days to first flowering; DM- Days to maturity; NCP- Clusters per plant; NPC- Pods per cluster; NPP- Pods per plant (g); PL- Pod length (cm); NSP- Seeds per pod; HSW- 100 seed weight, HI- Harvest index; SYP- Seed yield per plant.

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6. Declarations

Conflict of interest: The authors declare that they do not have any conflict of interest.

7. Ethical approval

This is an observational study. The University's Research

Ethics Committee has confirmed that no ethical approval is required.

8. Consent to participate
Informed consent was obtained from all individual participants included in the study.

9. Consent to publish
No ethical approval is required as there is no personal data of the authors in the article.

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