



Research Article

Identification of selection indices for the yield enhancement in cowpea (*Vigna unguiculata* (L.) Walp.) under sodic condition

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Abstract

The experiment was conducted at sodic soils to determine the relationship and degree of direct and indirect effects of yield and yield contributing traits in 57 cowpea accessions along with checks CO (CP) 7, VBN 1 and VBN 3. The association analysis showed that clusters number per plant, pod numbers per cluster, length of the pod, seeds per pod and hundred seed weight were positively correlated with seed yield. Path analysis indicated that the number of clusters per plant revealed a highly positive direct effect on single plant yield at genotypic level followed by pod length, pods number per cluster and seeds per pod. Principal Component Analysis (PCA) revealed first four PCs together contributed 67.33 per cent of variability. A total of 12 genotypes occupied the first quadrant showed better performance for five characters namely 100 seed weight, seed yield per plant, the number of clusters per plant, the number of pods per cluster and plant height. These selected genotypes namely IC 201075, EC 101989, EC 724750, EC 725166, CO 7, EC 724707, EC 121879, EC 101940, EC 101913, EC 724767, EC 107181 and EC 101928 could be used as donors or elite genotypes in cowpea yield improvement programmes.

Key words: Correlation, cowpea, path analysis, PCA, sodicity

INTRODUCTION

Pulses are the chief source of nutrition for millions of people around the world. Among the pulses, cowpea (*Vigna unguiculata* (L.) Walp.) is a widely adapted, drought tolerant and nutritious crop. Cowpea seeds are rich in antioxidants, folic acid, phenols and other essential minerals (Da Silva *et al.*, 2018). It is a versatile crop covering an area of 14.4 million hectares with production and productivity of 8.9 million tonnes and 616.3kg/, respectively (FAOSTAT, 2019). In India, cowpea is mainly cultivated in Karnataka, Gujarat, Maharashtra, Kerala and Tamil Nadu (Nguyen *et al.*, 2019). Grain yield is the major limiting factor in cowpea production. This is mainly due to the lack of high yielding cultivars, poor crop management

practices, a decline in soil fertility. The relationship between yield and yield contributing characters through association studies will help in determining the yield components. The trait association helps the breeder to formulate selection strategies for the genetic improvement of yield in cowpea. PCA transforms the complex set of data into a smaller number of constituents and provides information about the relevance of each variable and its contribution to the total variation. With this background, the present investigation was carried out to study the principal component analysis and character association for yield components in cowpea genotypes in sodic conditions.

MATERIALS AND METHODS

Fifty-seven cowpea genotypes along with three checks namely CO (CP) 7, VBN 1 and VBN 3 were raised in a randomized block design with two replications at experimental fields of Anbil Dharmalingam Agricultural College and Research Institute, Trichy under sodic condition (EC 1.5 dSm⁻¹ and pH 8.75) during *Rabi*, 2020 (**Table 1**). Observations on ten biometrical traits namely plant height (cm), days to 50 per cent flowering, days to maturity, the number of primary branches per plant, the number of clusters per plant, the number of pods per cluster, pod length (cm), the number of seeds per pod, 100 seed weight (g), seed yield per plant (g) were recorded from five randomly selected plants in each replication. Correlation at a genotypic and phenotypic level was analyzed as per Johnson *et al.* (1955), path analysis by Dewey and Lu (1959) using TNAU STAT statistical package and principal component analysis was computed using STAR 3.0 package

Table 1. List of cowpea germplasm accessions used in the study

S.No	Accessions	S.No	Accessions
1	IC 201075	31	EC 724763
2	IC 202777	32	EC 724767
3	IC 202784	33	EC 724771
4	IC 219580	34	EC 725103
5	IC 249133	35	EC 725109
6	IC 249141	36	EC 725110
7	IC 337931	37	EC 725166
8	IC 390252	38	EC 725170
9	EC 101896	39	EC 725171
10	EC 101910	40	EC 725173
11	EC 101928	41	EC 725174
12	EC101939	42	EC 725176
13	EC 101940	43	EC 725177
14	EC 101977	44	EC 100087
15	EC 101989	45	EC 101913
16	EC 107181	46	EC 14420
17	EC 121879	47	EC 607968
18	EC 16473	48	EC 723658
19	EC 16955	49	EC 723761
20	EC 201075	50	EC 724468
21	EC 273741	51	EC 724707
22	EC 514422	52	EC 724750
23	EC 528415	53	EC 724774
24	EC 528425	54	EC 723739
25	EC 723650	55	EC 724763-A
26	EC 723660	56	EC 723946
27	EC 723668	57	EC 723980
28	EC 723890	58	VBN 1
29	EC 724303	59	VBN 3
30	EC 7243312	60	CO (CP) 7

RESULTS AND DISCUSSION

In the current study, the character association at a phenotypic and genotypic level between yield component traits (**Table 2**) varied from being significantly positive to significantly negative besides being non-significant for many character pairs. These results revealed the existence of a proper balance between yield and its component traits.

The genotypic character association were slightly higher than the values of correlation coefficients at the phenotypic level indicating that there may be a high degree of relationship among the traits. The genotypic and phenotypic correlation coefficients between the character pair were generally identical in direction. This could be because of the existence of genes with similar and small effects.

In the present study, the number of clusters per plant (0.701,0.700) followed by the number of pods per cluster (0.553,0.531), pod length (0.395,0.390), the number of seeds per pod (0.365,0.337) and hundred seed weight (0.320,0.320) was recorded highly positive correlation with seed yield. The results are in agreement with Manggoel *et al.* (2012), Kumar *et al.* (2016), Kalambe *et al.* (2019), Gupta *et al.* (2019), Rukhsar *et al.* (2020) and Ceritoglu *et al.* (2020).

The traits days to 50 per cent flowering (-0.435, -0.424) and days to maturity (-0.401, -0.384) recorded significantly negative correlation with seed yield, which indicates the photosynthetic rate could be faster in early flowering genotypes which helps in the rapid accumulation of dry matter in the seeds than the late flowering genotypes. These results were akin with earlier findings of Walle *et al.* (2018) and Nguyen *et al.* (2019).

These correlation findings revealed that an increase in the clusters number per plant, pods number per plant, length of pod, seeds number per pod and weight of hundred seeds will increase the seed yield in cowpea.

The correlation study only provides information on the association and do not give any information about their direct or indirect contribution towards yield. Consequently, the correlation results alone are sometimes misleading. Hence, path coefficient analysis was done to partition the correlation into direct and indirect effects (**Table 3**).

The trait, the number of clusters per plant showed the highest direct effect (0.550) followed by the number of pods per cluster (0.422) and the number of seeds per pod (0.184) by establishing a significantly positive association and highly positive direct effect on seed yield per plant. These observations were on par with Thorat and Gadewar, (2013), Meena *et al.* (2015), Gupta *et al.* (2019), Yadav and Rajasekhar, (2019), Tambitkar *et al.* (2020), Rukhsar *et al.* (2020) and Snehal *et al.* (2021).

Table 2. Genotypic and phenotypic correlation coefficient of yield and yield components in cowpea genotypes

Traits		DFF	DMM	PH	NPB	NCP	NPC	PL	NSP	HSW	SYP
DFF	G	1.000	0.958**	0.153	0.099	-0.259**	-0.120	-0.468**	-0.385**	-0.128	-0.435**
	P	1.000	0.915**	0.147	0.105	-0.253	-0.117	-0.454**	-0.336**	-0.127	-0.424**
DMM	G		1.000	0.198	0.178	-0.243	-0.083	-0.402**	-0.387**	-0.081	-0.401**
	P		1.000	0.189	0.163	-0.234	-0.068	-0.380**	-0.353**	-0.080	-0.384**
PH	G			1.000	0.125	-0.012	0.252	0.126	0.133	0.084	0.124
	P			1.000	0.120	-0.010	0.241	0.123	0.116	0.083	0.123
NPB	G				1.000	0.158	0.037	-0.202	-0.150	-0.043	0.016
	P				1.000	0.150	0.032	-0.196	-0.149	-0.044	0.016
NCP	G					1.000	0.184	0.135	0.110	0.077	0.701**
	P					1.000	0.177	0.132	0.105	0.077	0.700**
NPC	G						1.000	0.024	0.047	0.065	0.553**
	P						1.000	0.027	0.068	0.061	0.531**
PL	G							1.000	0.650**	0.243	0.395**
	P							1.000	0.602**	0.241	0.390**
NSP	G								1.000	-0.007	0.365**
	P								1.000	-0.004	0.337**
HSW	G									1.000	0.320*
	P									1.000	0.320*
SYP	G										1.000
	P										1.000

** Significant at 1% level

DFF-Days to 50% flowering, DMM-Days to maturity, PH- Plant height, NPB- Number of primary branches, NCP- Number of clusters per plant, NPC- Number of pods per cluster, PL- Pod length, NSP- Number of seeds per pod, HSW- Hundred seed weight, SYP- Seed yield per plant

Table 3. Direct (bold) and indirect effects of yield components on seed yield at genotypic level in cowpea genotypes

Traits	DFF	DMM	PH	NPB	NCP	NPC	PL	NSP	HSW	Genotypic correlation coefficient
DFF	0.029	-0.122	-0.002	-0.008	-0.143	-0.051	-0.047	-0.071	-0.028	-0.435**
DMM	0.028	-0.128	-0.002	-0.001	-0.134	-0.035	-0.040	-0.071	-0.018	-0.401**
PH	0.005	-0.025	-0.010	-0.001	-0.006	0.107	0.013	0.024	0.019	0.124
NPB	0.003	-0.023	-0.001	-0.007	0.087	0.016	-0.020	-0.028	-0.010	0.016
NCP	-0.008	0.031	0.001	-0.001	0.550	0.078	0.013	0.020	0.017	0.701**
NPC	-0.004	0.011	-0.002	-0.003	0.101	0.422	0.002	0.009	0.014	0.553**
PL	-0.014	0.051	-0.001	0.002	0.074	0.010	0.099	0.120	0.054	0.395**
NSP	-0.011	0.050	-0.001	0.001	0.061	0.020	0.065	0.184	-0.002	0.365**
HSW	-0.004	0.010	-0.008	0.003	0.042	0.027	0.024	-0.001	0.222	0.320

DFF-Days to 50% flowering, DMM-Days to maturity, PH- Plant height, NPB- Number of primary branches, NCP- Number of clusters per plant, NPC- Number of pods per cluster, PL- Pod length, NSP- Number of seeds per pod, HSW- Hundred seed weight

The characters, days to 50 per cent flowering showed positively low value (0.029) and days to maturity showed low with negative (-0.128) direct effect on yield even though it shows highly significant negative correlation with yield. The negative correlation of these characters on yield may be due to negative indirect effects on yield via other characters.

The PCA analysis revealed that out of eleven Principal Components (PC), four (with eigenvalue more than 1) exhibited major variation among the genotypes for all the characters studied (Table 4).

The first four PCs together contribute 67.33 per cent of variability. Per cent contribution of all the characters to variation is presented in Table 5. The characters positively associated with PC1 were days to 50 per cent flowering, days to maturity and the number of primary branches per plant. The traits number of seeds per pod and pod length were positively correlated with PC2. In PC3, all the traits showed positive loadings except the number of primary branches, the number of clusters per plant and

Table 4. Principal components showing Eigenvalues, Percentage of variation and Cumulative percentage

Principal components	Eigen values	Percentage of variation	Cumulative percentage
PC 1	3.2557	29.60	29.60
PC 2	1.7871	16.25	45.84
PC 3	1.3342	12.13	57.97
PC 4	1.0287	09.35	67.32
PC 5	0.9235	08.40	75.72
PC 6	0.8758	07.96	83.68
PC 7	0.7803	07.09	90.77
PC 8	0.5227	04.75	95.53
PC 9	0.3302	03.00	98.53
PC 10	0.1097	01.00	99.53
PC 11	0.0522	00.47	100.00

seed yield per plant. The characters viz., the number of seeds per pod, plant height, the number of primary branches plant, the number of pods per cluster and pod length expressed positive loading effects in PC4. Similar findings were already reported by Nkoana *et al.* (2019), Mofokeng *et al.* (2020), Mahalingam *et al.* (2020), Vijayakumar *et al.* (2020) and Ashinie *et al.* (2020).

Scree plot illustrates the contribution of PC to the total divergence (Fig. 1.) which indicated that PC1 contributes 29.6 per cent to the overall variation with an eigenvalue of 3.26. Hence, the genotypes selection based on characters from the first principal component could be effective for capturing the total diversity present in the cowpea germplasm. Biplot analysis explains the relationship between the traits and genotypes that perform better for the characters studied (Fig. 2.). The serial numbers in the biplot represent the corresponding genotypes which are listed in Table 1. The length of the vector is directly proportional to its contribution towards the variation. The maximum vector length was observed for seed yield per plant followed by days to 50 per cent flowering, days to maturity and pod length.

In the biplot analysis, an acute angle (<90°) between vectors specifies the positive correlation between traits, whereas an obtuse angle (>90°) specifies a negative correlation and a right angle (90°) specifies zero correlation. Among the traits, pod length, the number of seeds per pod, hundred seed weight, the number of clusters per plant, the number of pods per cluster and plant height expressed a positive association with seed yield. The genotypes located near the vectors within the same quadrant would perform better for the traits involved. The genotypes in the same quadrant namely, IC 201075, EC 101989, EC 724750, EC 725166, CO 7, EC 724707, EC 121879, EC 101940, EC 101913, EC 724767, EC 107181 and EC 101928 showed better performance for five characters namely hundred seed weight, seed yield per plant, the number of clusters per plant, the number of pods per cluster and plant height.

Table 5. Per cent contribution of ten traits to the principal components

Traits	PC1	PC2	PC3	PC4
DFF	0.4525	-0.2138	0.2595	-0.0433
DMM	0.4352	-0.2511	0.2990	-0.0717
PH	-0.0164	-0.3076	0.6076	0.1850
NPB	0.0878	-0.3766	-0.1974	0.1720
NPCP	-0.2856	-0.3470	-0.2724	-0.1721
NPC	-0.1818	-0.4598	0.0809	0.1100
PL	-0.3840	0.1721	0.3554	0.0989
NSP	-0.3438	0.1774	0.3351	0.3880
HSW	-0.1631	-0.1055	0.2310	-0.7509
SYP	-0.4369	-0.3736	-0.0173	-0.1285

DFF-Days to 50% flowering, DMM-Days to maturity, PH- Plant height, NPB- Number of primary branches, NCP- Number of clusters per plant, NPC- Number of pods per cluster, PL- Pod length, NSP- Number of seeds per pod, HSW- Hundred seed weight, SYP- Seed yield per plant

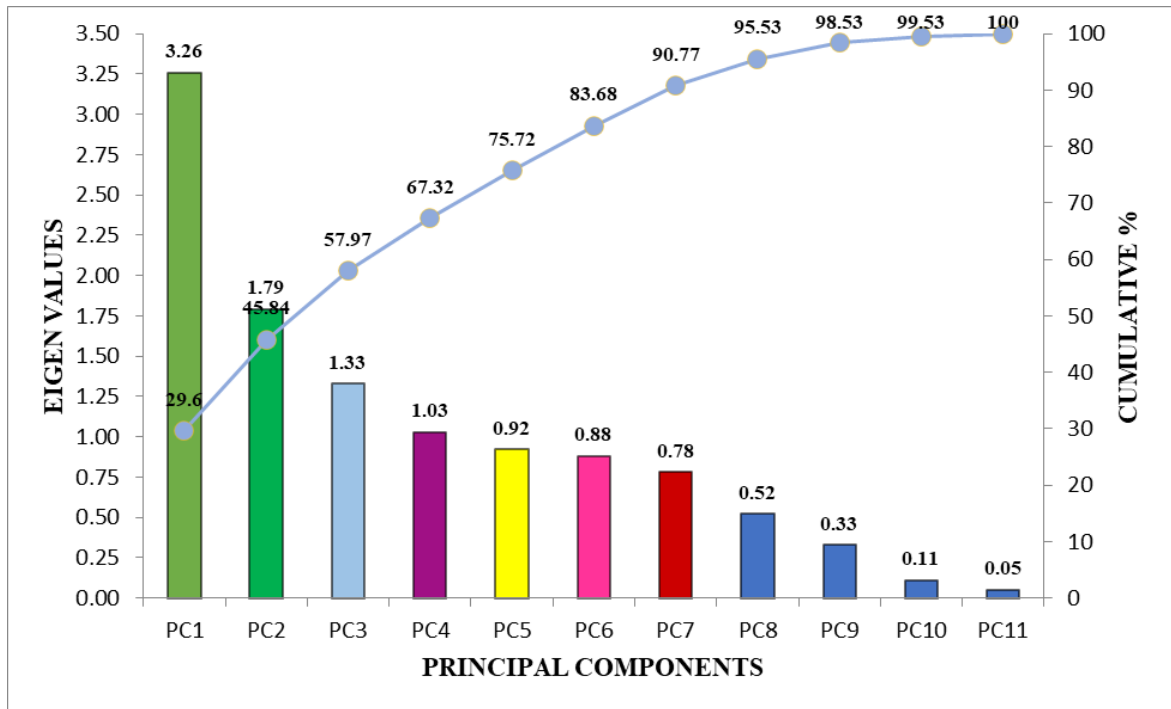


Fig. 1. Scree plot diagram

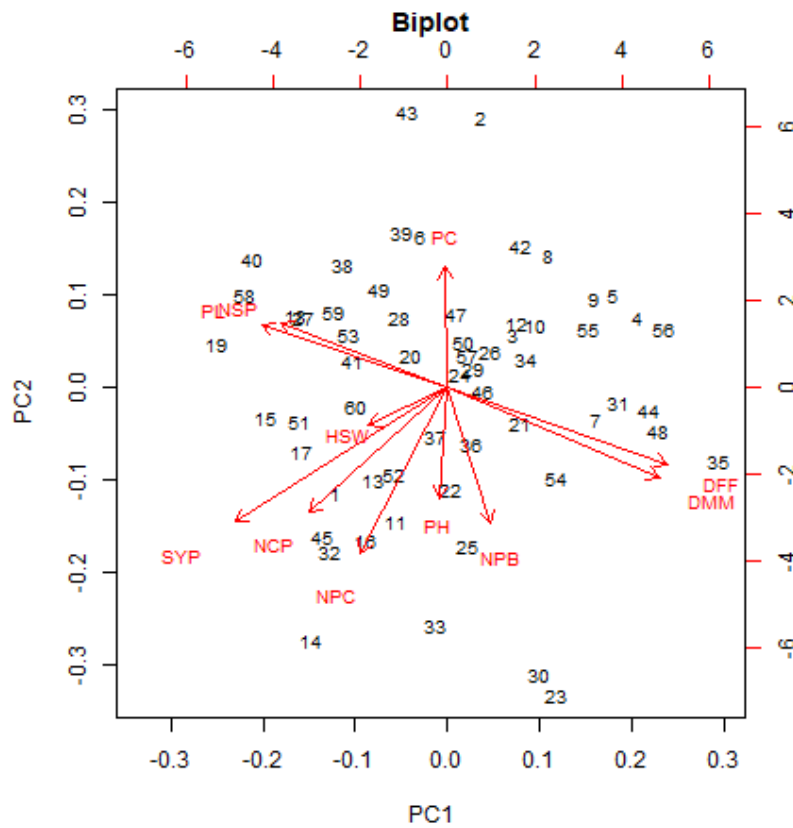


Fig. 2. Principal component biplot of PC1 and PC2

Selection is the earliest and oldest method of improvement in self-pollinated crops like cowpea. If the presence of sufficient variability and the character showing high heritability with high genetic gain, the direct selection is practised. But for polygenic traits like yield, indirect selection for yield component traits will be beneficial. Therefore, an association between seed yield and component traits were established in the current study. A comprehensive consideration of the analysis on character association led to the inference that for achieving yield improvement in cowpea genotypes, selection has to be towards the higher side for clusters number per plant, pods number per cluster and towards intermediate level for seeds number per pod and length of the pod. By comparing PCA and correlation studies, it is concluded that the traits namely hundred seed weight, seed yield per plant, number of clusters per plant and number of pods per cluster will be considered for improvement of yield in cowpea. The selected 12 genotypes could be used as donors or elite genotypes in yield enhancement programmes.

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