

PRINCIPAL FACTOR AND CLUSTER ANALYSIS FOR SEED YIELD AND BACTERIAL LEAF BLIGHT RESISTANCE IN ADVANCED F₄ PROGENIES OF CLUSTERBEAN

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SUMMARY

Principal factor and hierarchical cluster analysis were carried out in 36 advanced F₄ progenies of clusterbean. The study was done on 11 traits, which identified five principal components explaining 78.93 per cent variability. The first PC explained 28.76 per cent of total variation. The second, third, fourth and fifth principal components explained 18.19, 11.83, 10.78 and 9.38 per cent variation, respectively. Using principal factor (PF) scores, all the progenies were plotted for PF I and PF III which cumulatively explained 40.59 per cent variability. Factor I was designated as yield factor and factor III was designated as bacterial leaf blight disease factor. The hierarchical cluster analysis (UPGMA with city block distances) classified these progenies into five clusters. Cluster II consisted of maximum number of progenies i. e. 15. Clusters I, III, IV and V included 12, 7, 1 and 1 progenies, respectively.

Key words : Principal factor, hierarchical analysis, principal components, clusterbean

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.], popularly known as guar, is one of the most important **kharif** legumes grown for seed, green fodder, vegetable and green manuring . Its seed is also used for extraction of gum. Due to its importance as guar gum, it has emerged as new industrial crop of export value. Germplasm forms the base material for any crop improvement programme therefore, systematic characterization and evaluation of germplasm for various characters are of paramount importance (Ordas *et al.*, 1994). Moreover, accumulations of different desirable traits spread over the diverse genotypes into one or few genotypes are important for rapid advancement of yield of any crop. It was suggested that the use of multivariate techniques could resolve several phenotypic measurements even of large collections into fewer, more interpretable and more easily visualized dimensions. Therefore, present investigation was undertaken for evaluation, categorization and computation of principal components in advanced F₄ progenies of clusterbean to determine the degree of similarity among the progenies and relative importance of the principal factors and characters evolved in them.

MATERIALS AND METHODS

A set of 36 advanced F₄ progenies of cross HG 563 x PNB in clusterbean was evaluated in randomized block design with three replications during the **kharif** season, 2010 in research area of Forage Section. The planting was done in row of 3 m length and spacing between and within rows was 45 and 10 cm, respectively. All the recommended package and practices were followed to raise the good crop.

The data were recorded on per plot basis for days to 50 per cent flowering to maturity. The data of bacterial leaf blight disease were recorded by using 0-9 scale and then disease index was calculated using formulae as suggested by Gandhi (1984). For remaining eight characters i. e. plant height, branches/plant, pods/plant, seeds/pod, 100-seed weight, seed yield/plant, gum content (%) and crude protein content (%). Observations were recorded on random sample of six competitive plants and were averaged.

$$\text{Bacterial blight index (\%)} = \frac{\text{Sum of all numerical ratings}}{\text{Total no. of plants/leaves observed} \times 9} \times 100$$

Principal factor and cluster analysis were carried out using computer programme SPSS. Principal factor analysis was carried out using principal component method for factor extraction as it does not require assumption of normal distribution of population. For deciding number of principal components to be retained, suggestion of dropping those principal factors with eigen roots less than one, was followed, as the initial factors loading was not clearly interpretable, the factor axes were rotated using varimax rotation. Principal factor scores were calculated using Anderson-Rubin method as given in SPSS. Scatter plots were drawn using two main principal factors in order to identify the most distinct accessions in different clusters.

Un-weighted pair-group method using arithmetic averages (UPGMA) method of hierarchical cluster analysis was utilized with city block distances to classify the rescaled distances. Based on the method suggested by the Romesburg (1990) the dendrogram was constructed.

RESULTS AND DISCUSSION

The first five principal components (PC) showed eigen values more than one and they altogether explained 78.93 per cent cumulative variability (Table 1). The first PC explained 28.76 per cent of total variation. The second, third, fourth and fifth principal components explained 18.19, 11.83, 10.78 and 9.38 per cent variation, respectively. The first PC accounted for maximum proportion of total variability in the set of all

TABLE 1
Total variance explained by different principal components in cross HG 563 x PNB

Principal component	Eigen value	Per cent variability	Cumulative % variability
1	3.16	28.76	28.76
2	2.00	18.19	46.96
3	1.30	11.83	58.79
4	1.19	10.78	69.56
5	1.03	9.38	78.93

variables and the remaining ones accounting for progressively lesser and lesser amount of variation.

Initially the data were analyzed without any rotation but it failed to load all the variables meaning thereby that it could not provide much information regarding the idea of correlation between the variables and the principal factors. To select the relevant characters in various principal factors, the correlation values (0.6) were considered as relevant for that principal factor. Factor's loading of different variables obtained through varimax rotations is presented in Table 2. The first principal factor showed high loading of characters pods/plant, branches/plant, plant height, seed yield/plant and gum content on first factor and this factor can be interpreted as seed yield factor. The second factor showed high loading of days to 50 per cent flowering and days to maturity and factor third had high loading of seeds per pod and bacterial leaf blight disease incidence. Forth principal factor exhibited high loading

TABLE 2
Factor loading of different characters with respect to different principal factors for cross HG 563 × PNB

Character/ Principal factor	PF-I	PF-II	PF-III	PF-IV	PF-V
Pods/plant	0.903*	0.059	-0.052	-0.235	-0.054
Branches/plant	0.865*	-0.071	-0.089	0.061	-0.087
Plant height (cm)	0.699*	0.178	0.25	0.27	-0.010
Seed yield/plant (g)	0.653*	0.011	0.312	-0.418	0.057
Gum content	-0.584*	-0.23	0.122	0.064	-0.515
Days to 50% flowering	0.062	0.99*	-0.031	-0.067	-0.052
Days to maturity	0.062	0.99*	-0.031	-0.067	-0.052
Seeds/pod	0.028	-0.060	0.901*	0.107	0.111
Disease intensity (%)	-0.165	0.048	-0.511*	0.328	0.406
100-seed weight (g)	-0.022	-0.122	0.045	0.89*	-0.11
Crude protein content (%)	-0.069	-0.067	0.083	-0.122	0.876*

PF : Principal factor.

of 100-seed weight and fifth factor showed high loading of crude protein content. Among these principal factors, principal factor I can be interpreted as yield factor and principal factor III as bacterial leaf blight disease factor.

Using principal factor (PF) scores, all the progenies were plotted for PF I and PF III (Fig. 1) which cumulatively explained 40.59 per cent variability. The plot clearly indicated the separation of high yielding progenies towards the positive side of yield factor axis, whereas the progenies which had resistance towards bacterial leaf blight disease clustered towards the positive side of disease factor. The progenies which found place towards the positive end of the factors are supposed to be superior for those two factors. From forgoing discussion, it is concluded that these progenies may prove better parents in hybridization programme when both the factors are considered together.

The hierarchical cluster analysis using UPGMA method and city block distances identified five clusters. Cluster membership of different progenies is presented in Table 3. Cluster II consisted of maximum number of progenies i. e. 15. Clusters I, III, IV, and V consisted of 12, 7, 1 and 1 progenies, respectively. The association among the different

progenies is presented in the form of dendrogram (Fig. 2) prepared using rescaled distances. The resemblance coefficient between the progenies is the value at which their branches join. The dendrogram also showed the relative magnitude of resemblance among the different clusters.

In the present study, the mean performance of different clusters calculated for different characters revealed wide range of variation among the clusters with respect to these traits. Cluster-wise mean and general means for the characters studied have been presented in Table 4. Highest number of branches/plant (7.14) was shown by progenies of cluster I. Highest bacterial leaf blight disease incidence (28.49) was shown by progenies of cluster II. The progenies of cluster III had maximum number of seeds/pod (7.89), 100-seed weight (3.58), bacterial leaf blight disease incidence (9.25) and gum content (30.08). The progenies of this cluster also recorded lowest number of pods/plant (70.72) and crude protein content (23.42) and took minimum days to 50 per cent flowering (41.67) and days to maturity (96.67). Progenies of cluster IV showed highest plant height (112.72) and number of pods/plant (92.17). The progenies of this cluster also

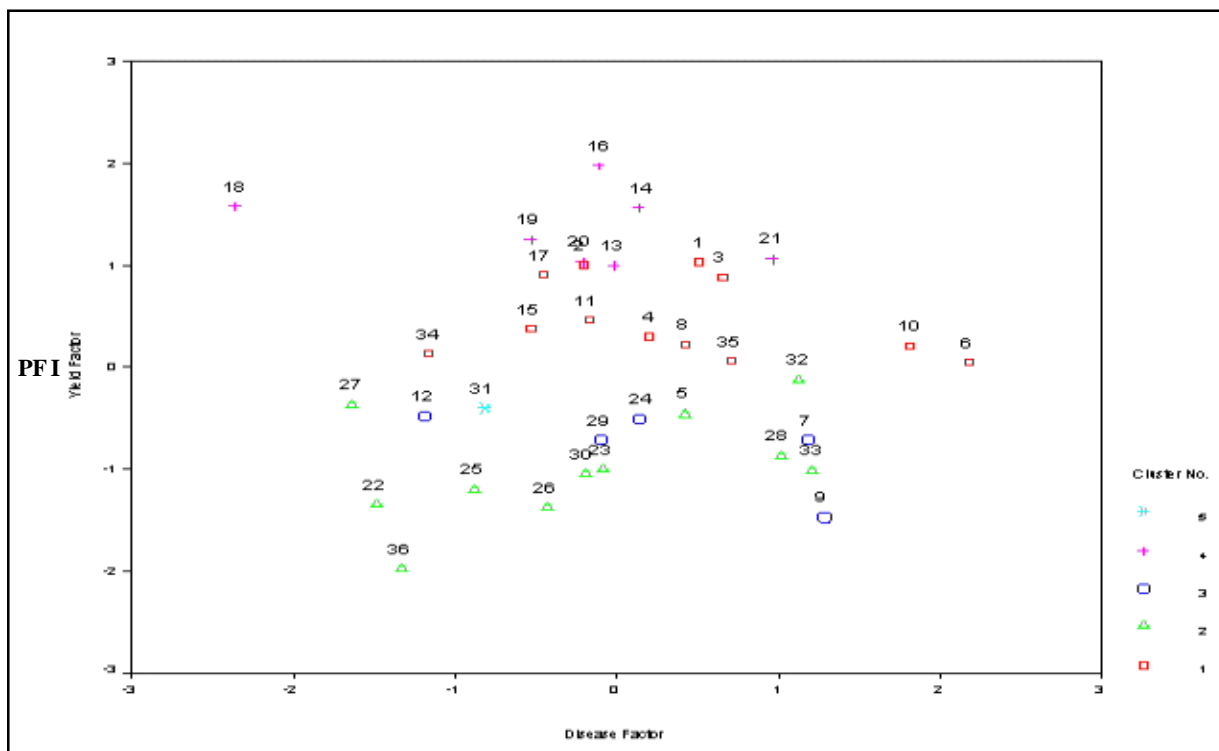


Fig. 1. Location of all progenies based on PF scores w.r.t. yield factor and disease resistance factor in cross HG 563 x PNB.

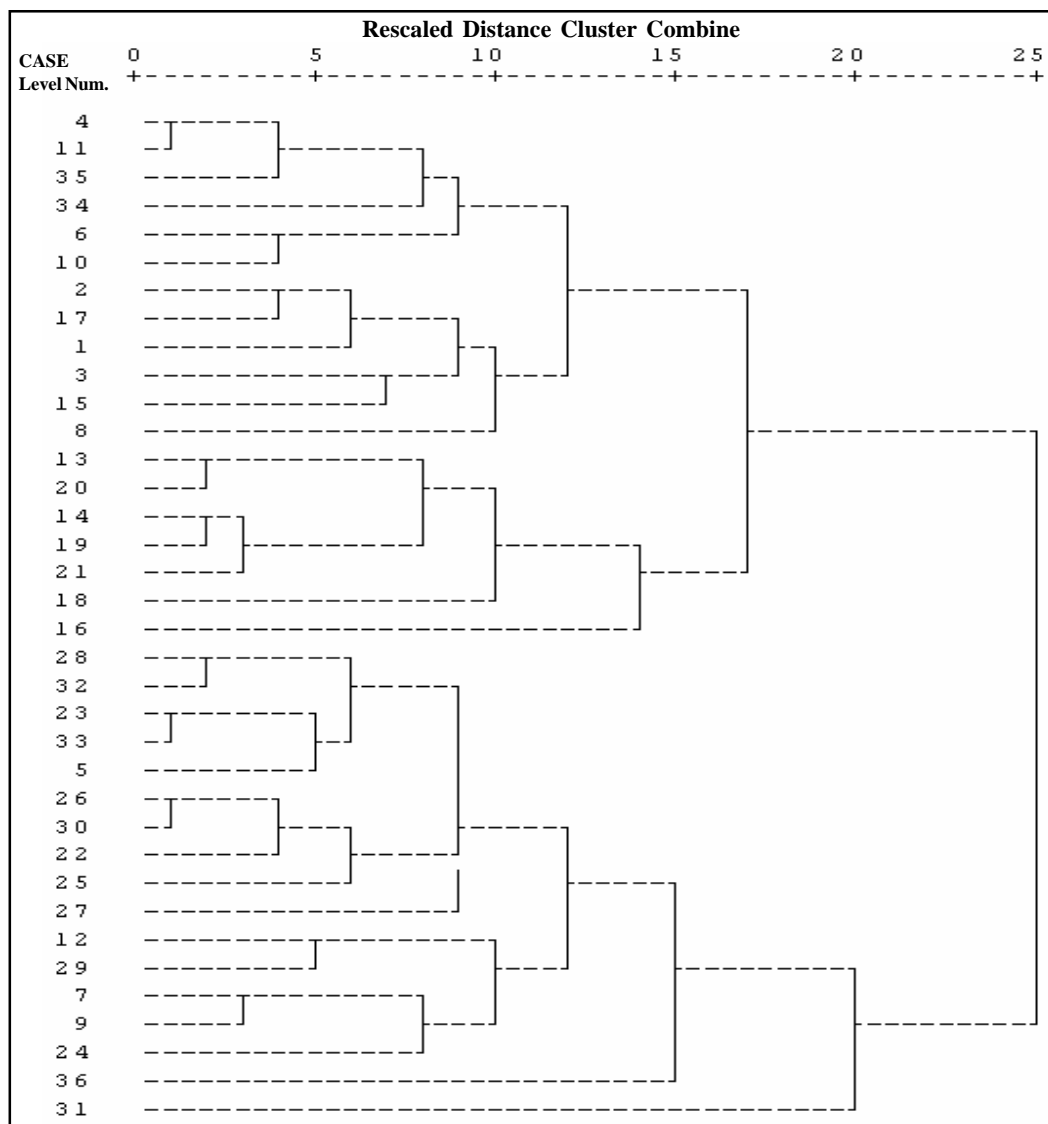


Fig. 2. Dendrogram portraying clustering patterns of different progenies for cross HG 563 x PNB.

TABLE 3
Cluster membership profile of different F_4 generation progenies
of cross HG 563 \times PNB

Cluster	No. of progenies	Progenies
I	12	1, 2, 3, 4, 6, 8, 10, 11, 15, 17, 34, 35
II	15	5, 7, 9, 12, 22, 23, 24, 25, 26, 27, 28, 29, 30, 32, 33
III	7	13, 14, 16, 18, 19, 20, 21
IV	1	31
V	1	36

had lowest number of seeds/pod (7.22) and 100-seed weight (3.29). The hybridization among the diverse parents is likely to produce heterotic hybrids and desirable transgressive segregants in further generations. To assess the diversity, inter and inter-cluster distances were calculated which are presented in Table 5. The maximum intra-cluster distance (28.67) was observed for cluster II followed by cluster III (27.71) and minimum for clusters IV (0.00) and V (0.00). The maximum inter-cluster distance (108.54) was found between clusters III and IV. Singh *et al.* (2003) and Arora *et al.* (2005) using cluster analysis in clusterbean found similar results. With the help of present study,

TABLE 4
Cluster mean for different characters in F₄ generation of cross HG 563 x PNB

Clusters	C I	C II	C III	C IV	C V	Mean
Plant height (cm)	94.92	96.96	92.22	112.72	83.09	95.98
Branches/plant	7.14	6.72	6.72	6.89	6.67	6.83
Pods/plant	87.87	85.98	70.72	92.17	73.26	82.00
Seeds/pod	7.67	7.63	7.89	7.22	7.27	7.54
100-seed weight (g)	3.47	3.40	3.58	3.29	3.40	3.43
Seed yield/plant (g)	22.41	20.69	20.79	21.99	18.02	20.78
Disease intensity (%)	14.85	28.49	9.25	9.62	12.21	14.88
Gum content (%)	29.73	29.77	30.08	30.05	29.65	29.86
Crude protein content (%)	23.71	23.76	23.42	23.73	23.81	23.69
Days to 50% flowering	46.88	45.44	41.67	45.33	48.22	45.51
Days to maturity	101.88	100.44	96.67	100.33	103.22	100.51

TABLE 5
Intra-cluster (diagonal) and inter-cluster distances for cross
HG 563 x PNB

Clusters	I	II	III	IV	V
I	22.87	53.92	42.35	44.08	78.73
II		28.67	83.09	51.13	41.89
III			27.71	108.54	72.43
IV				0.00	67.90
V					0.00

the F₄ progenies of cross HG 563 × PNB of clusterbean have been successfully classified based on various characters and also have been reduced into five principal factors only. This multivariate analysis has also enabled in identifying different progenies promising for different combinations of characters.

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