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Research Article

PRINCIPAL COMPONENT AND CLUSTER ANALYSES IN PIGEONPEA [*Cajanus cajan* (L.) MILLSP]

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ABSTRACT: Forty nine genotypes of pigeonpea representing the broad spectrum of variation were assessed for twelve characters using principal component analysis and cluster analysis. These genotypes were grouped into 8 clusters by using cluster analysis. Principal component analysis identified five principal components with eigen values more than one which contributed 80.10 per cent of the cumulative variance. The genotypes LRG-41 and SM-97, MRG-1001, WRG 51-Y, RST-16 and ICP 7035 were selected from the above analysis appeared to be desirable for inclusion in crossing programme aimed for improvement of pigeonpea.

Key words: Genetic divergence, Cluster analysis, Principal component analysis.

INTRODUCTION

Pigeonpea is one of the important pulse crops grown in India and consumed in diet as main source of protein. In any crop improvement programme genetic diversity is an essential pre-requisite for hybridization. Divergence studies indicated that geographical diversity is always not necessarily associated with the genetic diversity. Hence selection of parents for hybridization should be based more on genetic diversity rather than geographic diversity. Inclusion of diverse parents in hybridization helps in the isolation of superior recombinants. The divergence analysis by means of principal component analysis and hierarchical cluster analysis have been shown to be useful in selecting genetically distant parents for hybridization. The principal component technique has been applied in pigeonpea by Kalaimagal *et al.* (2008). Therefore, the present investigation is an attempt to study the genetic divergence in forty nine genotypes of pigeonpea based on principal component analysis and hierarchical cluster analysis.

MATERIAL AND METHODS

Forty nine genotypes of pigeonpea were grown in randomized block design with three replications during late *kharif* 2008-09 at Dry land farm of S.V.Agricultural College, Tirupati, Andhra Pradesh. Each genotype was sown in two rows of 3m length in each replication with a recommended spacing of 90×20 cm. the observations were recorded on five randomly selected plants of each genotype in each replication for the characters viz. plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and phenol content. The observations on days to 50% flowering and days to maturity were recorded on per plot basis and the mean values of twelve characters were used for statistical analysis. The protein content was estimated using the procedure suggested by Lowry *et al.* (1951) and the phenol content was estimated using the method suggested by Sadasivam and Manickam (1962). The data were statistically analyzed to study the genetic diversity by principal component analysis as described by Jackson (1991) and hierarchical cluster analysis as described by Anderberg (1993).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the forty nine genotypes of pigeonpea indicating that the existence of substantial genetic variability for all the characters under study.

Principal component analysis identified five principal components with eigen values more than one which contributed 80.10 per cent of cumulative variance (Table.2). The first principal component (PC1) contributed maximum towards variability (28.44) with high significant positive loading of number of secondary branches per plant (0.445) followed by number of pods per plant (0.431) and plant height (0.339). The second principal component (PC2) accounted 18.88 per cent of total variance and it reflected significant positive loading of days to maturity (0.336) followed by days to 50% flowering (0.287) and protein content (0.259).

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The third principal component (PC3) was characterized conspicuously by high loading of days to 50% flowering (0.435) followed by pod length (0.430) and seed yield per plant (0.361). Based on these first three principal components mean genotypic scores were computed (Table.3). Principal factor scores for all the forty nine genotypes were estimated for all three principal components and utilized to construct precise 2D and 3D plot (Fig.1&2). All the genotypes were plotted for PC1, PC2 and PC3 which cumulatively explained 71.46 per cent of variability accounted for all the characters (Table.2).

Table 1: Details of forty nine genotypes of pigeonpea

S. No.	Genotype	Source
1.	Palnadu (LRG-30)	RARS, Lam Farm, Guntur, Andhra Pradesh
2.	Rangabold (LRG-38)	RARS, Lam Farm, Guntur, Andhra Pradesh
3.	Abhaya (ICP-332)	ICRISAT, Hyderabad
4.	Lakshmi (ICP-85063)	ICRISAT, Hyderabad
5.	Asha (ICP-87119)	ICRISAT, Hyderabad
6.	MRG-66	ARS, Madhira, Andhra Pradesh.
7.	Maruti (ICP-8863)	ICRISAT, Hyderabad
8.	Rudrama-L	RARS, Warangal, Andhra Pradesh
9.	MRG-1001	ARS, Madhiram Andhra Pradesh.
10.	MRG-1004	ARS, Madhira, Andhra Pradesh.
11.	WRG-13	RARS, Warangal, Andhra Pradesh
12.	PRG-148	RARS, Palem, Andhra Pradesh
13.	LRG-41	RARS, Lam Farm, Guntur, Andhra Pradesh
14.	WRG-150	RARS, Warangal, Andhra Pradesh
15.	C-11	Karnataka
16.	ICPL-88027	ICRISAT, Hyderabad
17.	JKM-169	Madhya Pradesh
18.	GAUT-001	Gujarat
19.	WRG 51-R	RARS, Warangal, Andhra Pradesh
20.	WRP-266	Gulbarga, Karnataka
21.	WRG 51-Y	RARS, Warangal, Andhra Pradesh
22.	BSMR-853	Maharastra
23.	Amrapali-3	RARS, Lam Farm, Guntur, Andhra Pradesh
24.	SM-8	RARS, Lam Farm, Guntur, Andhra Pradesh
25.	SM-17	RARS, Lam Farm, Guntur, Andhra Pradesh
26.	SM-33	RARS, Lam Farm, Guntur, Andhra Pradesh
27.	SM-34	RARS, Lam Farm, Guntur, Andhra Pradesh
28.	SM-44	RARS, Lam Farm, Guntur, Andhra Pradesh
29.	SM-45	RARS, Lam Farm, Guntur, Andhra Pradesh
30.	SM-67	RARS, Lam Farm, Guntur, Andhra Pradesh
31.	WRG 27-E	RARS, Warangal, Andhra Pradesh
32.	SM-97	RARS, Lam Farm, Guntur, Andhra Pradesh
33.	SM-113	RARS, Lam Farm, Guntur, Andhra Pradesh
34.	PRG-171	RARS, Palem, Andhra Pradesh
35.	OGVK-1	Karnataka
36.	Local 2007-4	RARS, Lam Farm, Guntur, Andhra Pradesh
37.	ICP-7035	ICRISAT, Hyderabad
38.	ICP-7349	ICRISAT, Hyderabad
39.	ICP-8850	ICRISAT, Hyderabad
40.	RST-1	RARS, Lam Farm, Guntur, Andhra Pradesh
41.	TRG-7	RARS, Tirupati, Andhra Pradesh
42.	WRGE-65	RARS, Warangal, Andhra Pradesh
43.	RST-16	RARS, Lam Farm, Guntur, Andhra Pradesh
44.	WRGE-79	RARS, Warangal, Andhra Pradesh
45.	WRG-132	RARS, Warangal, Andhra Pradesh
46.	WRG-136	RARS, Warangal, Andhra Pradesh
47.	Chittoor local	Local Collection from Chittoor
48.	TRG-44	RARS, Tirupati, Andhra Pradesh
49.	TRG-31	RARS, Tirupati, Andhra Pradesh

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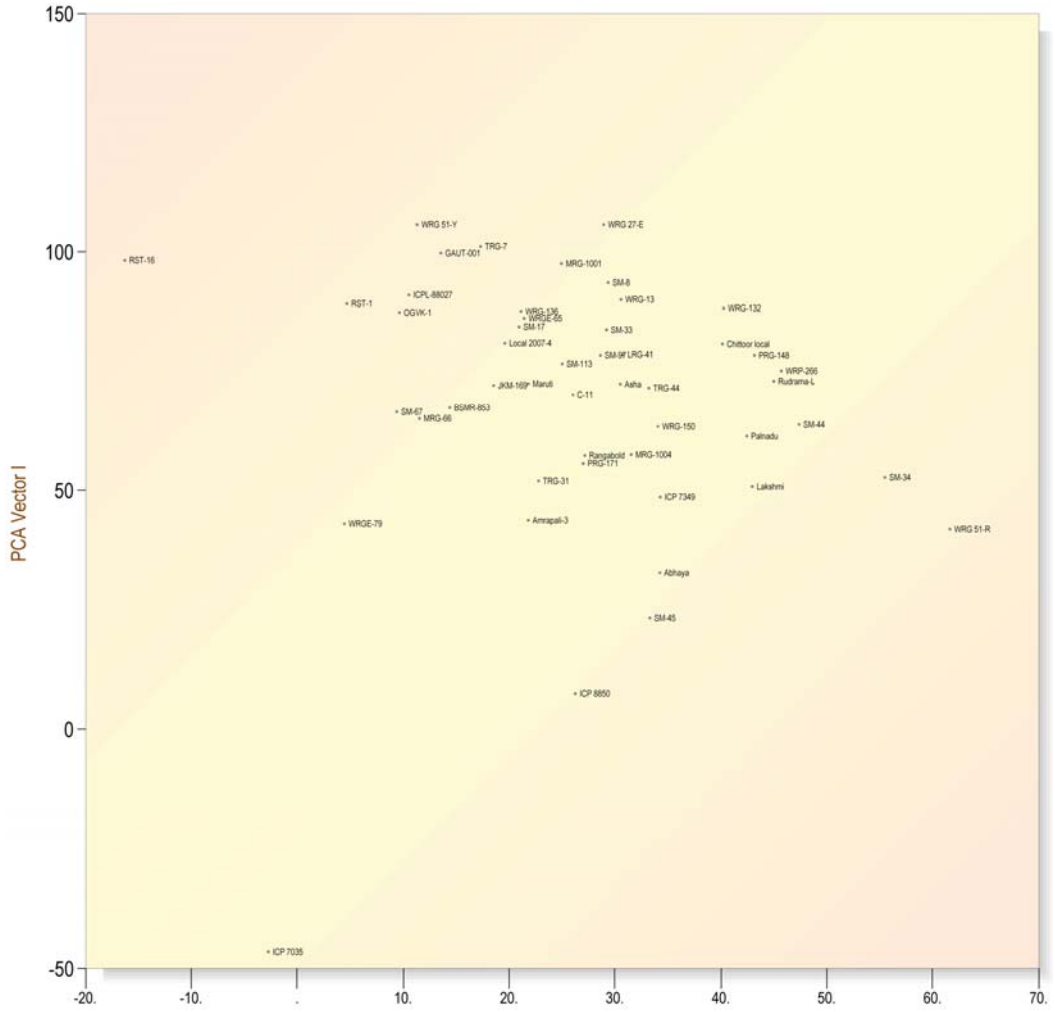

Figure. 1.Two dimensional graph showing relative position of 49 genotypes of pigeonpea based on PCA scores

Table 2:The eigen values, proportion of total variance, cumulative per cent variance and component loading of different characters for five principal components in pigeonpea.

	PC_1	PC_2	PC_3	PC_4	PC_5
Eigen Value (Root)	3.413	2.253	1.821	1.088	1.027
% Variance Explained	28.440	18.777	15.176	9.068	8.558
Cumulative Variance Explained	28.440	47.217	62.393	71.461	80.019
Days to 50% Flowering	0.282	0.287	0.435	0.030	0.009
Days to Maturity	0.345	0.336	0.284	0.040	-0.171
Plant Height (cm)	0.399	-0.179	-0.125	0.271	-0.215
No. of primary Branches/plant	-0.067	-0.519	-0.071	-0.280	0.319
No. of. secondary Branches /plant	0.445	-0.195	0.079	-0.049	0.116
No. of pods/ Plant	0.431	-0.277	-0.176	0.043	0.121
Pod Length (cm)	-0.291	-0.269	0.430	0.275	-0.085
No. of seeds /pod	-0.095	-0.214	-0.363	0.170	-0.603
Seed Yield/ Plant (gm)	0.144	-0.437	0.361	0.262	0.186
100 Seed Weight (gm)	-0.371	-0.033	0.255	0.307	0.109
Protien Content (%)	-0.024	0.259	-0.316	0.143	0.594
Phenol Content (%)	0.040	0.110	-0.245	0.744	0.153

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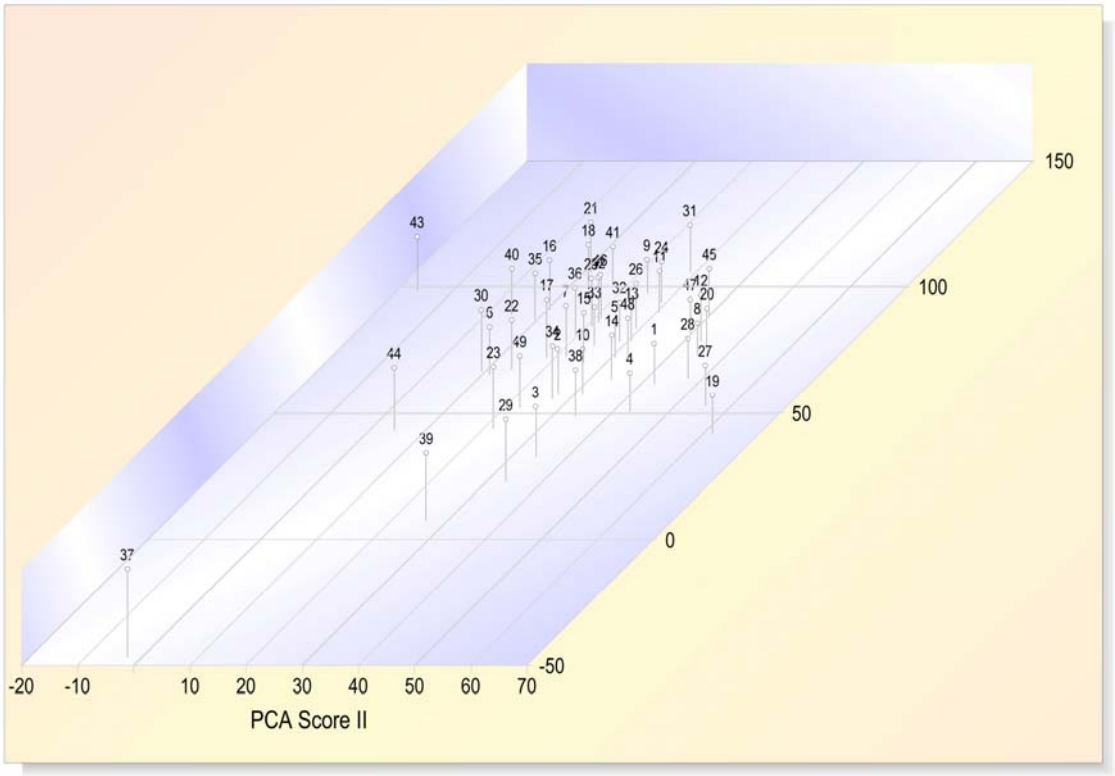

Figure. 2.Three dimensional graph showing relative position of 49 genotypes of pigeonpea based on PCA scores (Number of genotypes correspond to Table 1)

The plot of PC1, PC2 and PC3 showed clear differentiation of genotypes according to their cluster membership of each cluster. Genotypes belonging to a common cluster have fallen nearer to each other and vice versa. Thus the principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and to confirm the results of principal component analysis.

Hierarchical clustering (Wards minimum variance) method was followed to group the forty nine genotypes into 8 clusters (Fig. 3). The distribution of genotypes into various clusters was random, indicating lack of parallelism between genetic and geographic diversities. Cluster IV was the largest comprising of 10 genotypes followed by cluster I and III with 9 genotypes in each, cluster V and VI with 6 genotypes each. The maximum inter cluster distance was observed between cluster V and VIII (368.44) followed by cluster II and VIII (351.22) and cluster IV and VIII (349.06) as shown in Table.4. Cluster II recorded high mean values for phenol content (7.94), Cluster IV recorded high mean values for plant height (165.64), number of secondary branches per plant (37.56), number of pods per plant (493.24) and seed yield per plant (141.15). Where as cluster VIII recorded high mean values for days to 50% flowering (95.00), days to maturity (138.00) (early maturity), number of primary branches per plant (20.60), pod length (7.61), seeds per pod (4.9), 100 seed weight (20.98) as shown in Table 5. Based on these studies crosses may be effective between the genotypes of these clusters to obtain better and desirable segregants. Utilization of principal component analysis combined with hierarchical cluster analysis in genetic diversity studies was reported by earlier workers Altaher and Singh (2003) in cotton and Vasantha Rao *et al.* (2010) in pigeonpea. Genotypes LRG-41 and SM-97 (high in phenol content), MRG-1001 (high in protein content), WRG 51-Y, RST-16 and ICP 7035 which shows superior performance for seed yield and its contributing characters appear to be desirable for inclusion in crossing programme aimed for improvement of pigeonpea.

The present study depicted the relative divergence of yield and yield component traits. The clustering pattern could be utilised in identifying the best cross combinations for generating variability with respect to various characters under study. The genotypes clubbed in the different clusters if inter crossed may generate wide variability. Some combinations may also exhibit heterosis for seed yield i.e. transgressive segregants may also be expected.

Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence. There are forces other than geographical separation, which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variations as shown in Table. 1 (Murthy and Arunachalam, 1966). Similar results were derived by Virangama and Goyal (1994) and Katiyar et al. (2004).

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Table 3: The mean genotypic scores or PCA scores for 49 genotypes of pigeonpea

Genotype	PCA I	PCA II	PCA III
	X vector	Y vector	Z vector
Palnadu	61.472	42.456	93.939
Rangabold	57.354	27.151	105.158
Abhaya	32.845	34.241	114.467
Lakshmi	50.833	42.956	88.104
Asha	72.424	30.506	82.514
MRG-66	65.176	11.535	110.312
Maruti	72.519	21.814	115.961
Rudrama-L	73.027	44.999	73.851
MRG-1001	97.575	24.954	75.217
MRG-1004	57.543	31.531	103.886
WRG-13	90.060	30.578	92.625
PRG-148	78.477	43.158	105.345
LRG-41	78.650	30.781	75.641
WRG-150	63.483	34.056	101.663
C-11	70.231	26.032	113.235
ICPL-88027	91.037	10.546	111.655
JKM-169	72.167	18.546	131.549
GAUT-001	99.775	13.561	96.646
WRG 51-R	42.002	61.629	87.710
WRP-266	75.237	45.705	94.195
WRG 51-Y	105.728	11.315	113.297
BSMR-853	67.485	14.407	112.325
Amrapali-3	43.855	21.822	141.851
SM-8	93.619	29.369	93.758
SM-17	84.434	20.942	108.263
SM-33	83.812	29.203	100.442
SM-34	52.748	55.505	94.063
SM-44	63.893	47.384	91.334
SM-45	23.196	33.305	140.286
SM-67	66.574	9.403	140.546
WRG 27-E	105.730	28.939	107.318
SM-97	78.507	28.638	88.718
SM-113	76.694	25.030	88.859
PRG-171	55.679	27.004	121.846
OGVK-1	87.407	9.644	103.040
Local 2007-4	81.031	19.596	106.456
ICP 7035	-46.460	-2.735	200.247
ICP 7349	48.617	34.275	107.495
ICP 8850	7.357	26.247	154.237
RST-1	89.214	4.694	102.800
TRG-7	101.168	17.302	84.497
WRGE-65	86.213	21.429	100.665
RST-16	98.253	-16.269	123.697
WRGE-79	43.128	4.446	144.427
WRG-132	88.316	40.263	107.943
WRG-136	87.666	21.142	98.524
Chittoor local	80.872	40.162	81.758
TRG-44	71.631	33.213	92.751
TRG-31	52.002	22.793	120.131

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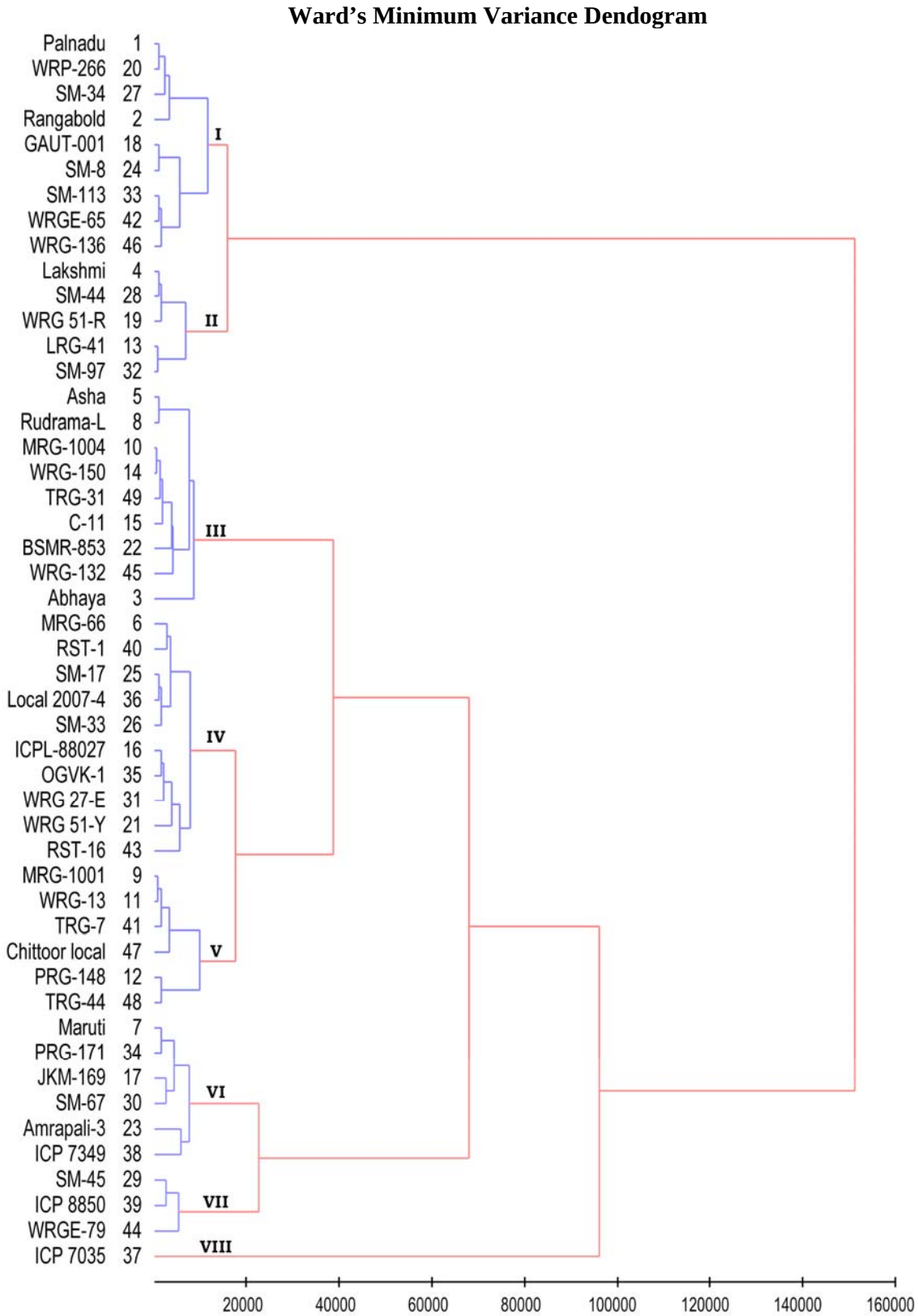

Figure. 3.Dendrogram showing relationship of 49, pigeonpea genotypes in eight clusters.

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Table 4: Intra cluster (diagonal) and inter cluster distances for eight clusters in pigeonpea (Ward's minimum variance method)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	83.63	100.59	110.86	123.53	140.49	189.88	185.29	344.68
Cluster II		72.52	146.42	178.24	193.82	244.86	220.22	351.22
Cluster III			85.08	118.74	117.70	151.01	141.40	304.27
Cluster IV				81.92	103.05	133.38	167.36	349.06
Cluster V					83.59	126.45	176.88	368.44
Cluster VI						93.33	132.81	318.40
Cluster VII							90.24	219.46
Cluster VIII								0.00

Table 5: Cluster means for twelve characters of pigeonpea

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches / plant	Number of secondary branches/ plant	Number of pods/ plant	Pod length (cm)	Number of Seeds/ pod	100-seed weight (g)	Protein content (%)	Phenol content (%)	Seed yield/ plant (g)
Cluster I	99.77	149.90	163.17	16.91	29.09	373.82	5.07	3.78	9.32	24.90	6.77	119.59
Cluster II	96.00	148.86	149.18	13.06	15.86	337.96	5.12	3.82	10.09	25.51	7.94	92.17
Cluster III	97.44	147.27	151.56	15.52	27.97	377.79	4.91	3.59	11.30	26.03	5.40	123.29
Cluster IV	98.60	150.09	165.64	17.43	37.56	493.24	5.33	3.79	8.51	24.40	5.11	141.15
Cluster V	96.25	148.84	163.73	18.62	32.23	434.65	4.47	3.57	8.38	25.65	4.73	111.33
Cluster VI	98.66	149.08	141.66	16.38	24.62	301.28	5.22	3.87	9.48	23.97	3.30	96.04
Cluster VII	97.16	146.33	127.75	13.00	14.40	201.20	5.83	4.06	13.16	23.66	3.87	84.44
Cluster VIII	95.00	138.00	125.33	20.60	5.20	73.33	7.61	4.90	20.98	24.61	3.39	76.33

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