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## STUDY ON GENETIC DIVERSITY OF POINTED GOURD USING MORPHOLOGICAL CHARACTERS

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### Abstract

The genetic diversity among 64 pointed gourd *genotypes* were assessed through multivariate analysis from an experiment conducted in Regional Agricultural Research Station, Ishurdi, Pabna during the growing season 2002-2003. The genotypes were grouped into twelve clusters. The cluster V consisted of highest number of genotypes and it was nine, the cluster VI and cluster VIII contained the lowest number of genotypes and it was two in each. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. The genotypes of Jessore were distributed in different clusters. The highest inter genotype distance as 366.3 observed between the genotypes P0022 and P0007 and the lowest 2.6 as observed between the genotypes P0043 and P0044. Cluster V had the highest cluster mean value for internode length, fruit weight per plant and yield the highest inter-cluster distance was noticed between cluster III and II (45.71) and the lowest between cluster VII and VI (3.33). The highest intra cluster distance was computed for cluster III and that was lowest for the cluster II. The first five axes accounted for 77.65% of the total variation among the 13 characters describing 64 pointed gourd genotypes. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence. The results obtained by D<sup>2</sup> analysis were confirmed by canonical analysis.

Key Words: Diversity pointed gourd, morphological characters.

### Introduction

As a dioecious crop, pointed gourd has high cross-pollination mechanism. Due to its out crossing characteristics, variability is always generating in this crop. Quantification of such variability from genetic point of view is very scanty that the first axis largely accounted for the variation among the genotype (28.66) followed by second axis (16.53). The first five axes for accounted 77.65 % of the total variation among the 13 characters describing 64 pointed gourd genotypes while the former two accounted for 45.19%. These results are in agreement with the findings of Ram (2001)

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**Table 1. Latent roots (Eigen values) and percent of variation in respect of 13 characters in pointed gourd.**

Principal component axis	Latent roots	% of total variation accounted for	Cumulative percent
I	3.725	28.66	28.66
II	2.149	16.53	45.19
III	1.705	13.12	50.31
IV	1.535	11.81	70.12
V	0.978	7.53	77.65
VI	0.817	6.28	83.93
VII	0.689	5.28	89.21
BIII	0.566	4.36	93.57
IX	0.269	2.07	95.64
X	0.243	1.88	97.52
XI	0.187	1.45	98.97
XII	0.088	0.68	99.65
XIII	0.045	0.35	100.00

**Construction of scatter diagram**

On the basis of principal axes I and II from the principal component analysis, a two way dimensional scatter diagram ( $Z_1Z_2$ ) using component score I as X-axis and component score 2 as Y-axis was constructed, which is presented in Figure 1. The distribution of genotypes in scattered diagram (Fig. 1 and Fig. 2) was apparently distributed into 12 groups, which revealed that there exists considerable diversity among the genotypes.

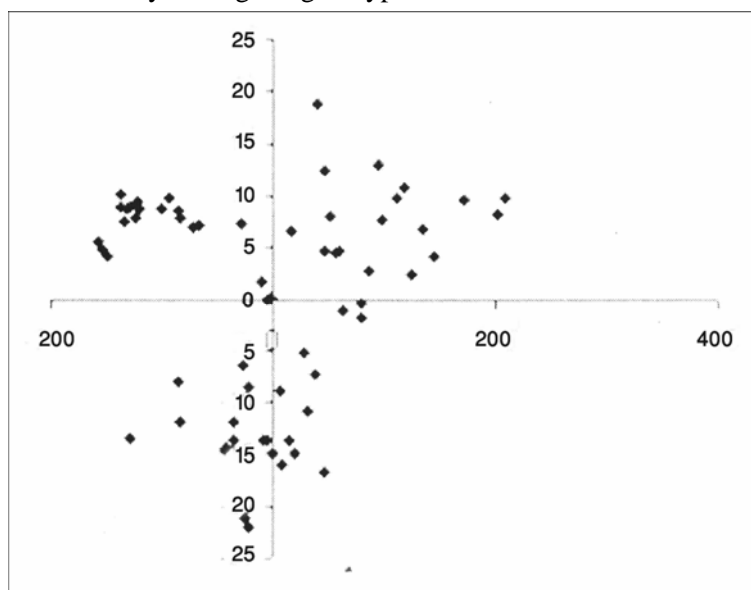


Fig 1. Scattered diagrams of 64 pointed gourd genotypes based on their principal Component scores

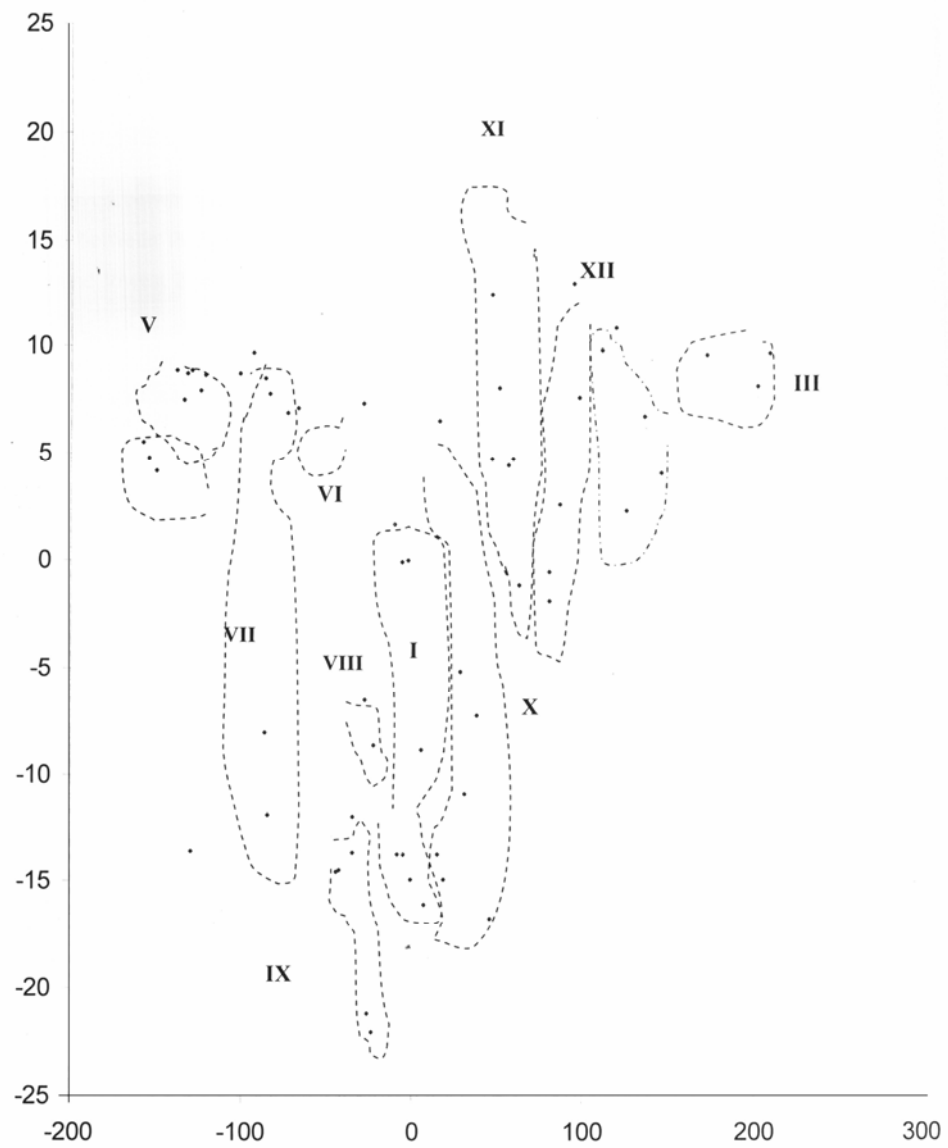


Fig 2. Scattered diagram of 64 pointed gourd genotypes based on their principal component scores superimposed with clustering.

### Principal Coordinate Analysis (PCO)

Inter genotypic distance  $D^2$  were obtained from principal coordinate analysis for all possible combinations between pairs of genotypes. The highest inter genotype distance was 366.3 observed between the genotypes PG022 and PG007 followed by the distance 362.9 observed between the genotypes PG022 and PG013. The lowest distance was 2.6. which was observed between the genotypes PG043 and PG044 followed by the distance 3.0 was observed between the genotypes PGI4 and PG0I5 (Table 2). The difference between the highest and lowest inter-genotype distance indicated the presence of variability among the 64 genotypes of pointed gourd.

**Table 2 Ten of each lower and higher Inter- genotypes distances between pairs of genotypes.**

10 lower $D^2$ values	Genotypes combination	10 higher $D^2$ values	Genotypes combination
2.6	43×44	366.3	22×7
3.0	14×15	362.9	22×12
3.1	27×31	359.7	27×18
3.2	25×31	359.0	22×12
3.5	40×42	352.5	12×18
3.7	28×33	347.0	22×30
3.9	57×61	343.2	22×27
4.1	7×13	341.2	22×31
4.2	30×37	340.7	18×30
4.3	10×6	338.3	25×2

The 1mm cluster distance was computed by using the values of inter accession distance from distance matrix according to Singh and Chaudhary (1985). The magnitudes of the intra cluster distances were not always proportional to the number of genotypes in the clusters (Table 4). In the study, it was observed that although the cluster composed of the highest number of genotypes nine (Tables 5) but its intra-cluster distance was not necessarily the highest. Statistical distances represent the index of genetic diversity among the clusters. The highest intra cluster distance was computed for cluster III (28.96) composed of three genotypes followed by cluster IV (24.69), cluster XII (21.0), cluster X (20.02), cluster XI (17.45), cluster I (15.83) and cluster VIII (15.0). The minimum intra cluster distance was found in cluster 11 (5.63). The intra cluster distance of cluster V, cluster VI, cluster VII, and cluster IX were 14.45, 14.0, 13.2 and 12.9 consisting of 9, 2, 6 and 6 genotypes, respectively.

### Canonical Variant Analysis (CVA)

Canonical variant analysis was performed to obtain the cluster distance (Mahalanohis's  $D^2$  value). The values of inter cluster distance ( $D^2$ ) are presented in Table 3. Statistical distances represent the index of genetic diversity among the clusters. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 3).

Based on the thirteen quantitative characters of pointed gourd genotypes, PCO was carried out to determine inter accession distance ( $D^2$ ). The intracluster distance, obtained by using the values of inter genotypes distance under each cluster as suggested by Singh and Chaudhuary (1985), and intra cluster distance was obtained from CVA are presented in Table 4.

**Table 3 Average inter and intra- cluster distance ( $D^2$ ) for 64 pointed gourd genotypes.**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	<b>15.83</b>											
II	19.96	<b>5.63</b>										
III	26.68	45.71	<b>28.96</b>									
IV	18.43	37.75	9.16	<b>24.69</b>								
V	17.13	6.81	43.02	34.69	<b>14.45</b>							
VI	6.73	12.73	34.42	25.99	9.18	<b>14.0</b>						
VII	10.93	9.81	34.92	28.62	6.97	3.33	<b>12.90</b>					
VIII	5.51	18.97	28.70	20.16	15.51	7.17	9.77	<b>15.0</b>				
IX	5.41	16.43	31.23	22.89	12.78	5.23	7.48	5.31	<b>13.2</b>			
X	5.90	23.42	23.01	14.89	20.50	12.07	14.46	7.43	8.60	<b>20.02</b>		
XI	8.18	27.18	19.31	11.05	24.17	15.77	18.18	10.38	12.69	4.90	<b>17.45</b>	
XII	12.48	32.09	14.87	6.83	29.04	20.34	22.93	14.74	17.04	8.50	5.86	<b>21.0</b>

The cluster III and II were more diverse as indicated by maximum inter cluster distances between them (45.71) followed by the distance between clusters V and III (43.02). IV and II (37.75), VII and III (36.92), V and IV (34.69), IV and III (34.72) XII and II (32.09) and between IX and III (31.23). The maximum values of inter cluster distance indicated that the genotypes belonging to cluster III were far away from those of cluster II. Similarly, the higher inter cluster values between cluster V and III. IV and II. VII and III. V and IV, IV and III, XII and II and IX and III indicated that the genotypes belonging to each pair of cluster were far diverse. The minimum inter cluster divergence was observed between cluster VII and VI (3.33) indicating that the genotype of these cluster were genetically

closed. Higher inter and intra-cluster distances indicate higher genetic variability among genotypes between and within clusters, respectively. The minimum inter and intra-cluster distance indicates closeness among the genotypes of two clusters and within the cluster also. These relationships were also reflected in the scatter diagram (Fig. 1). The cluster means of nine characters for 64 genotypes are given in Table 4. Difference in clusters means existed for almost all the characters.

### **Non-hierarchical clustering**

None hierarchical clustering using co-variance matrix grouped 64-pointed gourd genotypes into twelve different clusters (Table 5). It may be concluded that these results were confirmatory with the clustering pattern of the genotypes obtained through principal component analysis. Ram (2001) carried out component analysis and cluster analysis in (7) pointed gourd genotypes, and all genotypes got disbursed into 8 groups in the present study. Cluster V contained the highest number of genotypes (9) followed by cluster 1 (8), cluster X (7), cluster IX (7), cluster X (6), cluster VII (6) and cluster IV (5), respectively. While cluster II, III, and VIII and cluster VI having three and two genotypes, respectively. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location can also group into different clusters. The genotypes of Jessore were distributed in different clusters. The genotypes belonging to different locations were grouped in the same cluster (Table 5). This shows that geographic diversity was not related to genetic diversity of these materials. Masud *et al.* (1995) also reported similar results in sweet gourd.

### **Contribution of different characters towards divergence**

The contribution of the thirteen characters towards divergence is presented in Table 6. The results of CVA revealed that in vector I ( $Z_1$ ), the important characters responsible for genetic divergence in the major axis of differentiation were female flower length, node order, fruit weight, seeds per fruit, dry matter and fruits weight per plant (Table 6). In vector II ( $Z_2$ ), days to first flowering, node order, fruit weight, seeds per fruit, pulp seed ratio, and fruits weight per plant played a major role, while rest of the characters played a minor role in the second axis of differentiation. The role of single fruit weight, seeds per fruit and fruits weight per plant in both the vectors indicated the important component of genetic divergence among the 64 pointed gourd genotypes. Besides these, days to flowering, female flower length, node order, pulp seed ratio and dry matter percentage contributed considerably towards divergence. Negative values in both the vectors for internode length, fruit length and fruit width indicated that had the

**Table 4 Cluster mean values for yield and yield contributing characters of pointed gourd and number of genotypes in each cluster.**

Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
Days to 1 <sup>st</sup> flowering	81.87	81.23	85.75	96.86	92.00	94.00	88.83	86.33	81.17	80.39	87.14	84.62
Female flower length (cm)	5.91	6.36	5.39	5.2	6.30	6.45	6.30	6.41	5.80	6.11	6.06	6.40
Node order at 1 <sup>st</sup> flowering	10.41	10.33	8.90	9.29	8.70	10.00	10.33	7.67	8.50	7.13	8.147	9.50
Internode length (cm)	8.07	7.95	6.97	8.24	10.21	8.82	7.85	10.32	9.39	8.71	9.90	9.43
Fruit weight (g)	52.59	45.12	35.89	35.53	46.76	44.72	47.49	49.01	61.30	51.09	36.98	41.47
Fruit width (cm)	3.61	3.36	3.33	3.47	3.86	3.54	3.59	3.62	3.76	3.69	3.48	3.52
Fruit length (cm)	10.75	10.35	10.40	10.58	9.76	10.09	10.38	9.93	10.40	11.27	10.91	10.54
Seeds/ fruit	23.89	32.44	25.31	22.21	19.36	23.66	26.97	25.01	21.84	24.28	20.71	19.64
Pulp: Seed	15.32	9.37	13.88	12.49	13.88	12.82	13.64	11.98	18.03	14.62	13.76	14.89
Dry mater (%)	7.08	6.85	6.55	7.21	7.00	6.87	7.22	7.90	6.91	6.93	7.57	6.92
Fruits wt./ plant (kg)	9.47	11.00	1.72	5.14	12.51	11.67	11.31	11.49	12.42	8.70	6.04	6.68
Yield (t/ha)	28.47	33.08	11.24	15.56	37.45	32.32	33.86	31.48	36.13	26.37	18.19	19.98
Number of genotypes	8	3	3	5	9	2	6	3	6	7	7	5

**Table 5. Distribution of 64 pointed gourd genotypes in 12 clusters.**

Cluster no.	Total no. of genotypes in cluster	Genotypes included in different clusters	Place of collection
I	8	PG029	Meherpur
		PG048, PG050 PG052 and PG54	Gaibandha
		PG06, PG00 and PG011	Pabna
II	3	PG07, PG02, and PG013	Kushtia
III	3	PG08, PG01 and PG 02	Rangpur
IV	5	PG03	Natore
		PG016, PG053	Bogra
		PG03 and PG04	Rajshah
V	9	PG025, PG026, PG027, PG028, PG030, PG31, PG033, PG037, and PG042	Jessore
VI	2	PG03	Kushtia
		PG05	Jessore
VII	2	PG005, PG006, PG009, PG004 and PG015	Kushtia
VIII	3	PG034 and PG036	Pabna
		PG039	Jessore
IX	6	PG040, PG041, PG043, PG044, PG045 and PG046	Jessore
X	7	PG001	Rangpur
		PG04	Pabna
		PG07, PG049 and PG051	Gaibandha
		PG061	Rajshah
		PG06	Chuadanga
XI	7	PG02, PG038	Bogra
		PG05	Rangpur
		PG07	Chuadanga
XII	5	PG00, PG00 and PG017	Rangpur
		PG020 and PG058	Natore

lowest contribution to the total divergence. Hence, considerable emphasis should be given on single fruit weight, seeds per fruit and fruit weight per plant to increase fruit yield in pointed gourd. Mathex *et al.* (1986) reported that fruit weight per plant was the major contributor towards divergence in *Cucumis melo*. Masud *et al.* (1995) found that fruits weight was one of the important contributors to genetic divergence in sweet gourd.



**Table 6. Relative contribution of different characters towards divergence.**

Characters	Vector I	Vector II
Days to 1 <sup>st</sup> flowering	-0.0713	0.0068
Female flower length (cm)	- 1.2057	-0.5659
Node order at 1st flowering	0.1952	0.0394
Internode length (cm)	-0.2036	-0.5 172
Fruit weight (g)	0.0100	0.0353
Fruit length (cm)	-0.1525	-0.6790
Fruit width (cm)	-0.6464	-0.3479
Seeds/fruit	0.0419	0.0854
Pulp : Seed	-0.020	0.13182
Dry mater (%)	-0.0297	1.3182
Fruits/plant	-0.1172	-0.0294
Fruits wt./plant (kg)	0.1487	1.6650
Yield (t/ha)	-0.0957	-0.2561

### Selection of genotypes for future improvement

Considering the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance, the following genotypes were considered to perform better if used in hybridization programme. The genotypes PGOOI of cluster X could be selected for earliness and longer fruit. The genotypes PG023, PG029 and PG042 of the cluster V could he selected for lower seed, higher fruit weight per plant and yield. The genotypes PGOO7, PGOI2 and PCOI3 of the cluster II could be selected for higher number of fruits per plant. The genotypes PG043. PG044 PG045 and PG046 of the cluster IX could he selected for size and width of fruit.

**Table 7. Finally selected genotypes against important traits.**

Sl. No	Selection traits	Genotypes number	Clustered form	Mean value
1	Earliness (days)	PG001	X	80.39
2	Higher fruit length (cm)	PG001	X	11.27
3	Higher fruit width (cm)	PG043, PG044, PG045 and PG046	IX	3.76
4	Higher fruit weight per plant (Kg)	PG023, PG029 and PG042	V	12.51
5	Higher number of fruits per plant	PGOO7. PG 0 12 and PGOI3	II	40
6	Number of lower seed	PG023, PG029 and PG042	V	19.36
7	Yield (t/ha)	PG 023. PG029 and PG042	V	37.45

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