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# Study on Genetic Diversity of Pointed Gourd Using Morphological Traits

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**A B S T R A C T**

The genetic diversity among thirty six genotypes of pointed gourd was assessed from an experiment conducted at Vegetable Research Centre of G.B.P.U.A & T., Pantnagar during summer-rainy season, 2015. Thirty six genotypes of pointed gourd were grown in Augmented Block Design II with three checks (Kashi Alankar, Swarna Rekha and Rajendra Parwal-1). All the thirty nine genotypes of pointed gourd were classified into seven non-overlapping clusters on the basis of $D^2$ analysis and maximum inter-cluster distance were found between cluster VII and IV (72.42). This indicates that inter genotypic crosses between the members of cluster VII and IV would exhibit high heterosis and is also likely to produce new recombinants with desired traits. High cluster mean value for total soluble solid (4.13), number of primary branches (8.46), vine length (7.74) and nodes per vine (77.45) were presented in cluster III, however cluster I perceived genotypes with highest mean value for fruit length (9.35), fruit dry matter (7.24). Among the various traits studied, number of fruits per plant contributed the maximum (84.48%) towards divergence. A total of eight principal components were identified with principal component analysis which accounts 83.63 per cent of total variation.

## Introduction

The perennial pointed gourd (*Trichosanthes dioica* Roxb.), 2n=2x=22 is a highly nutritious cross pollinated cucurbit vegetable and highly coveted in markets of our country particularly during summer and rainy seasons. It is locally known as 'patal', `parval' or 'green potato' is an important summer cucurbit vegetable and it is extensively cultivated in eastern Uttar Pradesh, West Bengal, Bihar, Assam and lesser part in Odisha, Maharashtra and Gujarat (Nath and Subramanayam, 1972). *Trichosanthes*, a genus of family Cucurbitaceae, is an annual or perennial herb distributed in tropical Asia and Australia. De Candolle (1882) concluded that the species of *Trichosanthes* especially *Trichosanthes dioica* originated in old world most probably in India.

The productivity of pointed gourd is very low in our country. Several factors are considered responsible for this low yield of pointed gourd.

Lack of high yielding varieties and very less genetic information is available on improvement for yield. So, the objective of the present study was to use a diverse set of

pointed gourd genotypes to estimate the extent of genetic diversity with respect to yield and yield attributing components.

## Materials and Methods

The experiment was carried out during summer-rainy season 2015 at Vegetable Research Centre of G.B. Pant University of Agriculture & Technology, Pantnagar. Thirty nine genotypes of pointed gourd including three checks (Kashi Alankar, Rajendra Parwal-1 and Swarna Rekha) were maintained at experimental site.

All these genotypes were collected from different parts of India mainly from Uttar Pradesh and Bihar. The experiment was laid out in Augmented Block Design-II. Thirty six genotypes were maintained in six blocks and each block consists of six lines along with three checks.

The plants were planted on the row with spacing of 2.5m between the rows and 1m between the plants. The plant population includes both female and male plants in the ratio of 9:1. Twenty quantitative characters were taken for recording the observations from all the accessions.

The genetic diversity in thirty nine genotypes for twenty characters were analysed through Mahalanobis's $D^2$ statistic technique. The concept of principal component analysis, was developed by Hotelling (1933) after its original concept given by Pearson (1901).

## Results and Discussion

Genetic diversity is a pre-requisite for an effective plant breeding programme. It is an essential and useful tool for parent's choice in hybridization to develop high yield potential cultivars and to meet the diversified goals of plant breeding.

### Genetic divergence analysis

Genetic divergence is a method in which two or more populations of an ancestral species accumulate independent genetic changes with time to time, often after the populations have become reproductively isolated for some period of time.

The multivariate analysis using Mahalanobis's $D^2$ statistic by Mahalanobis (1936) has been proved to be a potential biometrical tool in quantifying the degree of divergence in germplasms collection.

It can be successfully used even in situations where overlapping of traits rendered the conventional methods of classification is ineffective. Mahalanobis's $D^2$ analysis was done to study divergence in thirty nine genotypes including three checks of various economic traits to initiate a breeding programme. The genotypes are grouped into seven distinct clusters are presented in Table 1.

Based on the distributing pattern, cluster V was the largest one comprising of thirteen genotypes followed by cluster III having eight genotypes, cluster VI having seven genotypes. Two genotypes were included both in cluster II and cluster IV each.

Some of the scientists assume that the genetic diversity is the reflection of geographical diversity. Sanchan and Sharma (1971) could not find any direct relationship between genetic diversity and geographical distribution. Under this study the clustering pattern revealed that, the geographical distribution was not associated with genetic diversity because the genotypes collected from same location were grouped into different cluster which shows no direct relationship between genetic and geographical diversity (Table 1).

## Intra and inter-cluster distances

A perusal of Table 2 revealed that the intra-cluster distance was maximum for cluster IV (40.68) and minimum for cluster II (21.098). The maximum inter-cluster distance was noted between cluster IV and VII (72.42) indicating highest genetic divergence existing among the genotypes of these clusters. The minimum inter-cluster distance was recorded between cluster V and VI (33.38) indicating close relationship and similarity for traits of the genotypes of these clusters.

Considering inter-cluster distances, the inter genotypic crosses between the members of cluster IV with cluster VII would give high heterosis and can produce new recombinants with desired characters. So more emphasis may be given on cluster IV and cluster VII in selecting inbreds for crossing in hybridising programmes of pointed gourd.

It was observed that, the inter-cluster distances were higher than the intra-cluster distances which shows that the existence of diversity among the parents and independent identity. The results presented here are in conformity with the reports of Devi and Mariappan (2014) in snake gourd, Singh *et al.*, (2013) in bitter gourd, Reddy *et al.*, (2012) in muskmelon.

## Cluster mean for various characters

The cluster mean for different characters are given in Table 3. The cluster I recorded the highest mean value for fruit length (9.350), fruit dry matter (7.241), fruit weight per plant (6.502). Cluster III recorded the highest mean value for total soluble solid (4.132), number of primary branches (8.457), vine length (7.749). In respect to minimum cluster mean value, cluster I had the lowest mean value for seeds per fruit (16.200), seed weight per fruit (1.372), 100 seed weight (9.633).

Considering the above cluster means for different characters, the genotypes belonging to the clusters I and III can be used in breeding programme to get better varieties as these two clusters having more cluster mean value towards desirable characters. Similar results were reported by Muralidhara *et al.*, (2014) who found Cluster V recorded highest mean values for weight of fruits per plant, number of seeds per fruit and by Singh *et al.*, (2013).

**Fig.1** Contribution percent of different characters towards genetic divergence

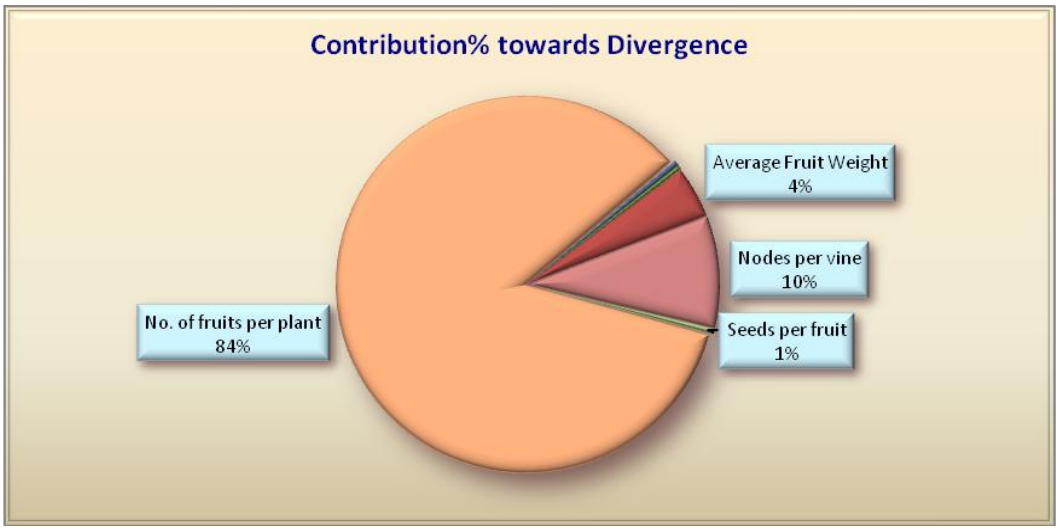

**Table.1** Distributing pattern of different genotypes of pointed gourd

| Cluster No. | No. of genotypes | Genotypes | Place of collection |
|---|---|---|---|
| I | 4 | PPG - 23 | Gaura, Varanasi, U.P. |
| | | PPG - 6 | Kumarganj, Faizabad, U.P. |
| | | PPG -34 | Gaura, Varanasi, U.P. |
| | | PPG - 33 | Gopalpur, Varanasi, U.P. |
| II | 2 | PPG - 1 | Jagdishpur, Faizabad, U.P. |
| | | PPG - 12 | Diara, Samastipur, Bihar |
| III | 8 | PPG - 17 | Fatehpurganjpurbi,Bareily, U.P. |
| | | PPG - 16 | Allahabad, U.P. |
| | | Kashi Alankar | IIVR, Varanasi, U.P. |
| | | PPG - 2 | Matethin Bujarg, Faizabad, U.P. |
| | | PPG - 9 | Gaura, Varanasi, U.P. |
| | | PPG - 26 | Ashapur, Varanasi, U.P. |
| | | Rajendra Parwal - 1 | Samastipur, Bihar |
| | | PPG - 18 | Fatehpurganjpurbi,Bareily, U.P. |
| IV | 2 | PPG - 5 | Kumarganj, Faizabad, U.P. |
| | | PPG - 14 | IIVR, Varanasi, U.P. |
| V | 13 | PPG - 32 and PPG - 31 | Gopalpur, Varanasi, U.P. |
| | | PPG - 30 | Fatehpurganjpurbi,Bareily, U.P. |
| | | PPG - 20 | Allahabad, U.P. |
| | | PPG - 29 | Fatehpurganjpurbi,Bareily, U.P. |
| | | PPG - 25 | Ashapur, Varanasi, U.P. |
| | | PPG - 4 | Bahadurganj, Faizabad, U.P. |
| | | PPG - 10 and PPG - 11 | Diara, Samastipur, Bihar |
| | | PPG - 7 | Diara, Samastipur, Bihar |
| | | PPG - 3 | Sarav, Baldiray, Sultanpur, U.P. |
| | | Swarna Rekha | HARP, Ranchi, Jharkhand |
| | | PPG - 15 | Gopalpur, Varanasi, U.P. |
| VI | 7 | PPG - 36 | Ashapur, Varanasi, U.P. |
| | | PPG - 35 | Allahabad, U.P. |
| | | PPG - 19 | Fatehpurganjpurbi,Bareily, U.P. |
| | | PPG - 28 | Gopalpur, Varanasi, U.P. |
| | | PPG - 22 and PPG - 24 | Gaura, Varanasi, U.P. |
| | | PPG - 8 | Kalyanpur, Samastipur, Bihar |
| VII | 3 | PPG - 13 and PPG - 21 | IIVR, Varanasi, U.P. |
| | | PPG - 27 | Ashapur, Varanasi, U.P. |

IIVR: Indian Institute of Vegetable Research (Varanasi, U.P.)
HARP: Horticulture and Agro-Forestry Research Programme (Ranchi, Jharkhand)
RAU: Rajendra Agricultural University (Samastipur, Bihar)

**Table.2** Average distance of intra and inter-cluster centroids

| | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| **I** | **22.402** | 38.998 | 34.817 | 49.768 | 34.05 | 34.041 | 46.442 |
| **II** | | **21.098** | 38.415 | 53.549 | 48.061 | 67.065 | 66.499 |
| **III** | | | **27.639** | 60.328 | 39.304 | 46.970 | 51.382 |
| **IV** | | | | **40.688** | 61.666 | 68.377 | 72.428 |
| **V** | | | | | **24.508** | 33.389 | 46.520 |
| **VI** | | | | | | **23.509** | 41.824 |
| **VII** | | | | | | | **33.472** |

**Table.3** Cluster mean for different economic traits in pointed gourd genotypes

| Sl. No. | Characters | Clusters | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | I | II | III | IV | V | VI | VII |
| 1 | Days to first female flowering | 55.711 | 50.194 | 51.576 | 55.044 | 58.822 | 55.028 | 52.564 |
| **2** | No. of nodes at first flowering | 8.396 | 6.756 | 7.713 | 7.339 | 7.178 | 7.156 | 7.162 |
| **3** | Days to first fruiting | 68.213 | 62.467 | 62.911 | 68.317 | 67.511 | 65.567 | 66.319 |
| **4** | Female flower length (cm) | 4.411 | 4.537 | 4.356 | 4.560 | 4.350 | 4.574 | 4.448 |
| **5** | Fruit length (cm) | 9.350 | 7.578 | 7.551 | 8.626 | 6.483 | 7.793 | 8.363 |
| **6** | Fruit diameter (cm) | 3.438 | 3.469 | 3.343 | 3.790 | 3.384 | 3.342 | 3.419 |
| **7** | Fruit circumference (cm) | 11.366 | 9.052 | 10.918 | 11.833 | 11.298 | 9.928 | 10.739 |
| **8** | Average fruit weight (g) | 39.709 | 33.183 | 36.072 | 42.234 | 34.484 | 32.786 | 35.931 |
| **9** | Fruit dry matter (%) | 7.241 | 6.357 | 6.896 | 6.692 | 7.073 | 7.079 | 6.842 |
| **10** | TSS ($^{\circ}$Brix) | 3.915 | 3.661 | 4.132 | 4.089 | 3.701 | 3.622 | 3.705 |
| **11** | No. of primary branches | 7.549 | 8.172 | 8.457 | 7.872 | 6.300 | 6.039 | 7.054 |
| **12** | Inter-nodal length (cm) | 10.489 | 10.565 | 9.753 | 11.757 | 13.378 | 11.108 | 10.883 |
| **13** | Vine length (m) | 6.617 | 7.245 | 7.749 | 6.417 | 7.629 | 6.034 | 7.177 |
| **14** | Nodes per vine | 68.036 | 65.572 | 77.452 | 57.939 | 57.356 | 56.181 | 71.402 |
| **15** | Seeds per fruit | 16.200 | 18.542 | 19.494 | 21.675 | 21.178 | 19.175 | 18.048 |
| **16** | Seed weight per fruit (g) | 1.372 | 2.008 | 1.993 | 2.007 | 2.150 | 1.862 | 1.823 |
| **17** | 100 seed weight (g) | 9.633 | 9.916 | 9.701 | 9.700 | 10.959 | 10.294 | 10.209 |
| **18** | No. of fruits per plant | 275.489 | 190.456 | 315.902 | 213.222 | 124.711 | 174.572 | 241.599 |
| **19** | Fruit weight per plant (kg) | 6.502 | 4.810 | 6.443 | 5.204 | 2.974 | 4.146 | 5.433 |
| **20** | Fruit yield per hectare (t) | 24.225 | 18.317 | 24.390 | 19.691 | 11.930 | 15.992 | 20.620 |

**Table.4** Eigen vector, Eigen root and associated variation for principal components in pointed gourd based on economic traits

| Sl. No. | Characters | PCA I | PCA II | PCA III | PCA IV | PCA V | PCA VI | PCA VII | PCA VIII |
|---|---|---|---|---|---|---|---|---|---|
| 1 | Days to first female flowering | 0.001 | 0.377 | 0.360 | 0.195 | 0.138 | 0.077 | 0.190 | 0.038 |
| 2 | No. of nodes at first flowering | 0.134 | 0.031 | 0.226 | 0.235 | -0.564 | 0.132 | 0.009 | 0.213 |
| 3 | Days to first fruiting | 0.047 | 0.342 | 0.347 | 0.286 | 0.198 | 0.015 | 0.207 | -0.036 |
| 4 | Female flower length (cm) | 0.148 | 0.283 | 0.043 | 0.023 | 0.035 | 0.321 | -0.463 | -0.289 |
| 5 | Fruit length (cm) | 0.298 | 0.241 | -0.094 | 0.041 | -0.176 | -0.332 | -0.109 | -0.070 |
| 6 | Fruit diameter (cm) | 0.211 | 0.130 | -0.083 | -0.522 | 0.069 | 0.013 | -0.020 | 0.339 |
| 7 | Fruit circumference (cm) | 0.263 | 0.181 | 0.052 | -0.304 | 0.131 | -0.027 | 0.171 | 0.303 |
| 8 | Average fruit weight (g) | 0.327 | 0.265 | 0.071 | -0.156 | -0.099 | -0.030 | -0.037 | 0.160 |
| 9 | Fruit dry matter (%) | -0.114 | -0.121 | -0.215 | 0.342 | -0.073 | -0.185 | -0.043 | 0.645 |
| 10 | TSS (ºBrix) | 0.024 | -0.134 | 0.281 | 0.221 | 0.391 | -0.082 | -0.170 | 0.173 |
| 11 | No. of primary branches | 0.172 | -0.299 | -0.098 | -0.109 | 0.096 | 0.379 | -0.178 | 0.003 |
| 12 | Inter-nodal length (cm) | -0.194 | 0.240 | -0.121 | 0.122 | 0.186 | -0.014 | -0.541 | 0.248 |
| 13 | Vine length (m) | 0.079 | -0.233 | 0.361 | -0.029 | 0.061 | 0.307 | -0.327 | 0.182 |
| 14 | Nodes per vine | 0.223 | -0.329 | 0.266 | -0.022 | -0.066 | 0.239 | 0.258 | 0.075 |
| 15 | Seeds per fruit | -0.165 | -0.116 | 0.372 | -0.253 | 0.170 | -0.268 | -0.029 | 0.137 |
| 16 | Seed weight per fruit (g) | -0.192 | -0.114 | 0.308 | -0.288 | -0.007 | -0.423 | -0.172 | -0.198 |
| 17 | 100 seed weight (g) | -0.121 | -0.040 | 0.298 | -0.057 | -0.536 | -0.126 | -0.253 | -0.003 |
| 18 | No. of fruits per plant | 0.283 | -0.310 | -0.008 | 0.264 | 0.179 | -0.227 | 0.017 | -0.126 |
| 19 | Fruit weight per plant (kg) | 0.419 | -0.096 | -0.021 | 0.105 | 0.024 | -0.239 | -0.141 | -0.072 |
| 20 | Fruit yield per hectare (t) | 0.421 | -0.083 | -0.007 | 0.096 | 0.022 | -0.224 | -0.142 | -0.074 |
| | **Eigen Value (Root)** | **4.561** | **2.769** | **2.665** | **1.804** | **1.425** | **1.356** | **1.223** | **0.924** |
| | **% Var. Exp.** | **22.806** | **13.846** | **13.324** | **9.019** | **7.125** | **6.779** | **6.116** | **4.618** |
| | **Cum. Var. Exp.** | **22.806** | **36.652** | **49.976** | **58.995** | **66.119** | **72.898** | **79.014** | **83.633** |

**Table.5** Finally selected genotypes against important traits

| Sl. No. | Selection traits | Genotypes | Clustered form | Mean value |
|---|---|---|---|---|
| **1** | Earliness (days) | PPG-12 and PPG-1 | II | 62.467 |
| **2** | Higher fruit length (cm) | PPG-34, PPG-33, PPG-6 and PPG-23 | I | 9.350 |
| **3** | Higher fruit diameter (cm) | PPG-5 and PPG-14 | IV | 3.790 |
| **4** | Less number of fruits per fruit | PPG-23, PPG-33, PPG-34 and PPG-6 | I | 16.200 |
| **5** | Higher number of fruits per plant | PPG-16, PPG-18 and PPG-17 | III | 315.902 |
| **6** | Higher fruit weight per plant (Kg) | PPG-34, PPG-23, PPG-6 and PPG-33 | I | 6.502 |
| **7** | Higher fruit yield per Hectare (t/ha) | PPG-16, PPG-9 and PPG-17 | III | 24.390 |

## Relative contribution of characters towards total divergence

From all the characters (Figure 1), number of fruits per plant contributed the maximum (84.48%) to the diversity by taking first rank with 626 times out of 741 combinations, followed by nodes per vine (9.58% with 71 times first rank), average fruit weight (4.45% with 33 times rank first), seeds per fruit (0.54% with 4 times rank first), while days to first female flowering and days to first fruiting had same level of contribution (0.40% with 3 times rank first each). The character fruit yield per hectare contributed 0.14% with single time ranked first towards diversity. The traits like number of fruits per plant, nodes per vine and average fruit weight collectively contributed 98.51% towards total divergence. Hence, these characters should be given more importance during breeding programme in segregating population. So, these characters should be given primary importance, which can give more yield per hectare.

Similar results of high contribution of characters towards total divergence were reported on individual fruit weight constituted a maximum per cent to the divergence, followed by length of fruit and fruits per vine (Sundaram, 2009), total soluble sugar followed by fruit yield per plant and total soluble solids (Tomar *et al.*, 2008), total soluble solid followed by fruit yield per plant (Rukam *et al.*, 2008).

## Principal component analysis

Principal component analysis (PCA) helps in identifying the most relevant characters that can be used as descriptors by explaining as much of total variation present in the origin set of variables with few components as possible and reducing the dimension of the problem. The higher the coefficients, regardless the sign, they are more effective in discriminating between genotypes thus they are important (Anand and Murthy, 1968).

The principal component analysis of thirty nine genotypes of pointed gourd clearly and concisely explained the genetic diversity. The linear transformation performed by this method generated a new set of eight independent variables, known as principal components, that expressed results in their Eigen roots (Eigen values) and Eigen vectors (Table 4). As per the calculation Eigen root

values calculated as 4.561 for the first principal component, 2.769, 2.665, 1.804, 1.425 and 1.356, 1.223, 0.924 for second, third, fourth, fifth, sixth, seventh and eighth principal component respectively.

The Eigen root of first principal component was accounted approximately 22.806 per cent variation of total variation followed by second to eighth components which accounted 13.846, 13.324, 9.019, 7.125, 6.779, 6.116 and 4.618 per cent of total variation presented among genotypes, respectively. About 83.633 per cent variation is formed by the eight principal components indicating that considerable diversity present among different characters and rest of the components are not much important.

The first principal component had high positive weight to fruit yield per hectare (0.421), fruit weight per plant (0.419), average fruit weight (0.327), fruit length (0.298) and number of fruits per plant (0.283). The second principal component exhibited high positive weight to days to first female flowering (0.377), high negative weight to nodes per vine (-0.329), number of fruits per plant (-0.310), number of primary branches (-0.299) and total soluble solid (-0.121). The eighth principal component showed high positive weight to fruit dry matter (0.645), fruit diameter (0.339), fruit circumference (0.303), inter-nodal length (0.248), and high negative weight to days to first fruiting (-0.036).

The principal component analysis revealed that first four components accounting for more than 58 cumulative percent and eight components accounting for more than 83 cumulative percent of total variation present in the population.

Similar earmarking approach have been emphasized by earlier workers like Nwofia *et al.*, (2015) who found that PC 1, PC 2 and PC 3 accounted for a total of cumulative variance of 70% in cucumber. Similar results were also reported by Gautam (2013) in ridge gourd, Trimech *et al.*, (2013) in muskmelon, Mladenovic *et al.*, (2012) in bottle gourd.

## 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 (Table 5) are considered to perform better if used in hybridization programme. The genotypes like PPG-6, PPG-23, PPG-33 and PPG-34 of cluster I could be selected for longer fruit, lower seed per fruit and higher fruit weight per plant. The genotypes PPG-12 and PPG-1 of cluster II could be selected for earliness. Similarly, the selection of genotypes in cluster III like PPG-16, PPG-18 and PPG-17 for more number of fruits per plant and PPG-16, PPG-9 and PPG-17 for higher fruit yield per hectare could be effective. The genotypes like PPG-5 and PPG-14 of cluster IV could be selected for higher fruit diameter, which can successfully use in hybridization programme.

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