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# STUDIES ON GENETIC DIVERGENCE IN PUMPKIN

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**ABSTRACT**
25 cultivars of Pumpkin are evaluated systematically during the research period. Analysis of variance studies indicates significant differences among all the genotypes for all the characters under study. Genetic diversity worked out using Mahalanobis $D^2$ statistic. Based on $D^2$analysis, the genotypes were grouped into 5 different clusters, where the cluster V possessed higher number (8) of genotypes followed by the cluster I (5) cluster IV (5), III (3), II (2) and VI (2). Clustering pattern revealed that geographical diversity was not associated with genetic diversity. The maximum inter-cluster distance was observed between the clusters III, VI and cluster II, III that of minimum in between the Clusters V and Cluster VI. The wider genetic diversity was observed in cluster II, III and VI which indicate the potentiality of this diverse genotype collection for providing basic material for future breeding programmes.

## INTRODUCTION

Pumpkin belongs to the family Cucurbitaceae having chromosome number 2n = 40. There are 27 species under the genus *Cucurbita,* five of which are in cultivation. These are *C. moschata*, *C. maxima*, *C. ficifolia*, *C. pepo* and *C. mixta,* commonly known as Pumpkin. *C. moschat*a is probably the most widely grown species of cucurbita and this species is cross compatible with C. maxima*, C.pepo* and *C.mixta* (Tindall, 1987). Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high carotenoid pigments and minerals (Bose and Som, 1998). It may contribute to improve the nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement (Satkar *et al*., 2013). In India, the area under cultivation of pumpkin is 0.36 million ha, with a total production of 3.50 million tonne/annum, productivity is about 9.72 tonnes/ha (NHB data, 2013). Though a fairly common crop, to-date there is no released variety of pumpkin with high yield potential and good quality in India.

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops and also important for crop improvement as well as variety development programme (Anand *et al*., 1975 and Gaur *et al*., 1978). Multivariate analysis by means of Mahalanobis $D^2$ statistics is useful tools in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Das and Gupta 1984). Many researchers have adopted this $D^2$ technique for measuring divergence among genotypes of pumpkin (Rashid *et al* 2000, kale *et al*., 2002 and blessing *et al*., 2012). An understanding of the nature and degree of variability among the germplasm is a prerequisite for its variety improvement. Therefore, the present study was undertaken to analyze the genetic divergence of a number of pumpkin genotypes for selecting parents of diverse group for further breeding programme.

## MATERIALS AND METHODS

The experiment was conducted at Experimental Research Field, Department of Horticulture, Allahabad School of Agriculture, SHIATS and Allahabad during *kharif season* 2013 with 25 genotypes of pumpkin. Which are evaluated systematically during the research period. The experiment is laid out in Randomized Block Design (RBD) with three replications. The seed are sowed at 8/8/2013, having plot size of $1 \times 2$m accommodating 10 plants per plot with row-to-row spacing of 2m and plant-to-plant spacing of 1m. Recommended doses and application methods of manure and fertilizers were applied in the experimental field (Chattopadhyay *et al.,* 2007). Bamboo stick support was given to the growing plants and allowed them to creep on a rope nets. Necessary intercultural operations and irrigation were done during the crop period to ensure normal growth and development of the plants. Control measures were taken against red pumpkin beetle at seedling stage and fruit fly at fruiting stage (Chattopadhyay *et al.,* 2007). Observations were recorded for node number of 1st male flower, node number of first female flower, days to first male flower, days to first female flower, fruit weight (g), fruit length (cm), fruit diameter (cm), seed cavity length (cm, ), seed cavity width (cm), flesh thickness (cm), placenta weight (g), days to first fruit harvest, number of

fruits per vine, vine length (cm), fruit yield (kg/vine). The data on fifteen quantitative characters are recorded on five competitive and randomly selected plants in each genotype and in each replication, except number of fruits per plant, fruit weight and fruit yield per plant which arc recorded on whole genotype basis.

All the statistical analysis was carried out using OPSTAT statistical software. The genetic divergence among genotypes was estimated by using $D^2$ statistics (Mahalanobis 1936). All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952). The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1985).

## RESULTS AND DISCUSSION

Based on $D^2$ values, the genotypes were grouped into six highly divergent clusters (Table 1) the magnitude of $D^2$ values confirmed that there was considerable amount of diversity in the experimental material evaluated. Cluster-V contained highest number of genotypes (8), while cluster-VI and cluster-II had lowest number of genotypes (2). The pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier findings of Sutariya *et al*. (2011) and Binod Kumar *et al.,* 2013.

### Cluster mean

A perusal of results of cluster mean (Table 2) revealed the cluster I with 5 genotypes exhibited highest fruit length (16.64), average fruit weight (1.55), seed cavity length (12.31) and lowest mean value for node number at first male flower appearance (5.23), days to first female flower appearance (39.70). Cluster II had two genotypes, which exhibited highest in node number of first male (5.73) and female flowers appearance (17.75) and lowest in fruit length (15.01). Cluster III was characterized by highest in placenta weight (410.74), lowest in flesh thickness (2.15) while the cluster IV had maximum in days to first fruit harvest (66.54) and lowest in fruit yield yield (4.36). Cluster V with eight genotypes exhibited highest in seed cavity width (6.34) and lowest in average fruit weight (1.23), placenta weight (203.67). Cluster VI with 2 genotypes exhibited highest in days to first female flower appearance (45.83) while lowest in fruit diameter (14.40), seed cavity width (5.15), vine length (230.76), number of fruits per vine (1.88). None of the cluster contained genotypes with all the desirable traits, which could be directly selected and utilized. Similar results were also reported by Khatun *et al.,* 2010 in snake gourd and Singh *et al*. 2013 in bitter gourd. All the minimum and maximum cluster mean value was distributed in relatively distant clusters. While studying the genetic divergence in Pumpkin genotypes thereby underlining the fact that the hybridization between genotypes of different cluster is necessary for the development of desirable genotypes (Fig.1). Based on the per se performance of the best genotypes within the clusters, there may be directly selected or may be used as potential parents in hybridization programme.

### Intra and inter cluster distances

The 25 lines were grouped into 6 clusters based on $D^2$ values (Table 3). The cluster-II displayed the least intra cluster distance, while the maximum intra cluster distance was recorded for cluster IV. The highest inter cluster generalized distance was

**Table 1: Clustering pattern of 25 genotypes of pumpkin by Ward's method**

| Cluster | No. of genotypes | Genotypes |
|---|---|---|
| I | 5 | VRP-6, HARP-10, VRPK-11-01, KPS-01, VRPK-11-02 |
| II | 2 | PUSA VIKASH, SWARNA AMIT |
| III | 3 | VRPK-02, VRPK-09-01, VRPK-15 |
| IV | 5 | VRPK-171, VRPK-113, PUNJAB SAMRAT, PPU-72, VRPK-38 |
| V | 8 | VRPK-51, VRPK-113-01, VR-14, VRPK-222-02, ARKA CHANDAN, VRPK-72-11-02, CO-02, KASHI HARIT |
| VI | 2 | CM-350, VRPK-207-02 |

**Table 2: Mean values of clusters for fifteen characters in for 25 Pumpkin genotypes**

| S.NO | Character | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|---|
| | No of genotypes | 5 | 2 | 3 | 5 | 8 | 2 |
| 1 | Node number of first male flower | 5.23 | 5.73 | 5.54 | 5.46 | 5.65 | 5.70 |
| 2 | Node number of first female flower | 17.18 | 17.75 | 16.46 | 17.34 | 17.30 | 17.75 |
| 3 | Days to first male flower | 28.33 | 28.43 | 29.25 | 28.36 | 28.71 | 30.35 |
| 4 | Days to first female flower | 39.70 | 42.25 | 39.10 | 42.35 | 41.09 | 45.83 |
| 5 | Average fruit weight (g) | 1.55 | 1.15 | 1.24 | 1.23 | 1.23 | 1.23 |
| 6 | Fruit length (cm) | 16.64 | 15.01 | 15.85 | 15.62 | 15.24 | 15.51 |
| 7 | Fruit diameter (cm) | 17.56 | 19.63 | 17.25 | 16.49 | 14.50 | 14.40 |
| 8 | Seed cavity length (cm) | 12.31 | 10.96 | 12.21 | 11.61 | 10.59 | 10.68 |
| 9 | Seed cavity width (cm) | 5.94 | 5.23 | 6.34 | 5.84 | 6.34 | 5.15 |
| 10 | Flesh thickness (cm) | 2.23 | 3.40 | 2.15 | 2.24 | 2.41 | 2.40 |
| 11 | Placenta weight (g) | 291.02 | 215.88 | 410.74 | 307.28 | 203.67 | 221.50 |
| 12 | Days to first fruit harvest | 60.95 | 60.68 | 60.34 | 66.54 | 62.01 | 74.30 |
| 13 | Number of fruits per vine | 2.23 | 2.10 | 2.36 | 2.08 | 2.23 | 1.88 |
| 14 | Vine length (cm) | 310.66 | 328.66 | 240.51 | 249.53 | 268.92 | 230.76 |
| 15 | Fruit yield (kg/vine) | 7.31 | 4.92 | 6.40 | 4.36 | 5.53 | 4.72 |

**Table 3: Average intra (bold) and inter-cluster $D^2$ values for six clusters among twenty five genotypes of Pumpkin**

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 79.202 | 124.279 | 158.027 | 138.478 | 152.533 | 232.057 |
| II | | 42.017 | 271.497 | 172.871 | 121.505 | 158.849 |
| III | | | 67.908 | 142.026 | 277.151 | 296.881 |
| IV | | | | 91.22 | 154.963 | 153.316 |
| V | | | | | 77.58 | 130.049 |
| VI | | | | | | 56.343 |

**Table 4: Percent contribution of different characters towards diversity in 25 genotypes of pumpkin**

| S. No. | Character | Times ranked 1st | Per cent contribution |
|---|---|---|---|
| 1 | Node number of first male flower | 0 | 0.00 |
| 2 | Node number of first female flower | 0 | 0.00 |
| 3 | Days to first male flower | 0 | 0.00 |
| 4 | Days to first female flower | 1 | 0.33 |
| 5 | Average fruit weight (g) | 2 | 0.67 |
| 6 | Fruit length (cm) | 2 | 0.67 |
| 7 | Fruit diameter (cm) | 17 | 5.67 |
| 8 | Seed cavity length (cm) | 0 | 0.00 |
| 9 | Seed cavity width (cm) | 3 | 1.00 |
| 10 | Flesh thickness (cm) | 0 | 0.00 |
| 11 | Placenta weight (g) | 110 | 36.67 |
| 12 | Days to first fruit harvest | 20 | 6.67 |
| 13 | Number of fruits per vine | 4 | 1.33 |
| 14 | Vine length (cm) | 61 | 20.33 |
| 15 | Fruit yield (kg/vine) | 20 | 6.67 |

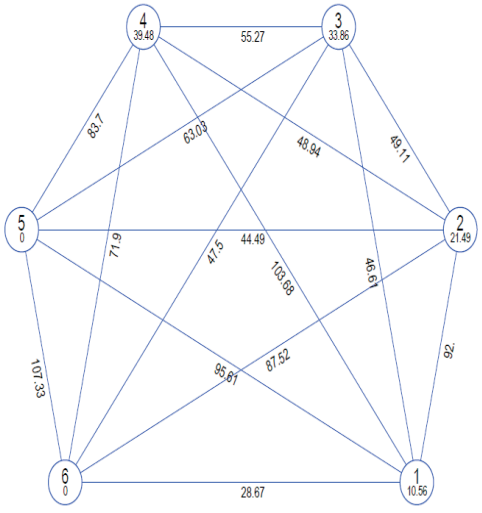


**Figure 1: Cluster diagram showing the average intra and inter cluster distances; (D = $D^2$) of pumpkin genotypes Inter and intra-cluster distance**

found between cluster-III and cluster-VI followed by clusters-II and III. The involvement of genotypes belonging to cluster III and VI, II and III and III and V in hybridization would help in achieving novel recombinants (Joshi *et al.*, 2008 in pointed gourd).

**Contribution of individual character towards total divergent**

The contribution of each trait to total divergence is presented in Table 4. Among the traits studied placenta weight contributed maximum divergence (36.67%) followed by vine length (20.33%), fruit yield (6.67%), fruit diameter (5.67%). The traits *viz*., placenta weight, vine length, fruit yield, fruit diameter contributed 69.34% towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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