

VARIABILITY AND DIVERGENCE IN PUMPKIN (*CUCURBITA MOSCHATA* POIR)

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Abstract: Fifty pumpkin genotypes evaluated during 1988-89 differed significantly in all characters except yield per plant. The coefficients of variation, heritability and genetic advance indicated that variation is mainly genetic. Genotypic coefficient of variation was maximum for seeds per fruit followed by average fruit weight and productive branches per plant. The carotene content in the genotypes ranged from 4.46 to 215 μg per 100 g, while iron content ranged from 0.51 to 2.74 mg per 100 g. The genotypes were classified into five clusters based on Mahalanobis D^2 statistics. The clusters I, II, III, IV and V contained 2, 7, 9, 12 and 20 genotypes respectively.

Key words: *Cucurbita moschata*, divergence, pumpkin, variability.

INTRODUCTION

Pumpkin (*Cucurbita moschata* Poir) is one of the popular cucurbits grown in India. Low cost of production, long keeping quality of fruits and comparatively high content of carotene in fruits have enhanced the usefulness of the crop. In spite of the popularity and importance, very little effort is made to upgrade the generic make up of pumpkin in India. In the present study, the genetic variability, heritability, genetic advance and genetic divergence of the population were studied to formulate future breeding strategy of the crop.

MATERIALS AND METHODS

Fifty pumpkin genotypes were grown in a randomized block design with two replications during June-October, 1988. There were three pits per genotype per replication with two plants per pit. The spacing adopted was 4. x 1.5 m. Cultural practices were done as per KAU (1986). The two plants in the central pit of each plot were used for taking observations namely nodes on main vine, main vine length, days to first male and female flower anthesis, node at which first flower is formed, female flowers per plant, male flowers per plant, node at which first fruit is retained, primary branches per plant, productive branches per plant, internodal length, average fruit weight, fruit length, fruit diameter, flesh thickness, seeds per fruit, 1 seed weight, fruits per plant and yield per plant. Carotene and iron contents of fruits were estimated as per AOAC (196) and Jackson (1973) respectively.

Variability existing in the population and heritability were assessed as per Burton (1952) and expected genetic advance by Lush (1949) and Johnson *et al.* (1955). The genetic divergence was calculated as per Mahalanobis (1928).

RESULTS AND DISCUSSION

Among the 2 quantitative characters studied, the 5 pumpkin genotypes exhibited significant difference for all characters except yield per plant. Wide ranges of variation was observed for all the characters studied. In CM 135, the first female flower appeared 45 days after sowing and was the earliest. (Table 1). Average fruit weight ranged from .9 to 6.7 kg. Longest fruit (32.7 cm) was born in CM 154. Yield per plant was maximum in CM 177 (13.4 kg) followed by CM 153 (9.7 kg). The carotene content in the genotypes ranged from 4.46 μg per 1 g in CM 18 to 215 g per 1 g in CM 111. Iron content in the fruits also exhibited a wide range (.51-2.74 mg per 1 g.)

Genotypic coefficient of variation was maximum for seeds per fruit (37.36%) closely followed by average fruit weight (35.25%) and productive branches per plant (34.72%). Lower values of gcv were observed for days to first male flower anthesis (12.27%), node at which first female flower was formed (12.77%) and days to first female flower anthesis. Mangal *et al.* (1981) also observed lower values of gcv for days to flower and node to first female

Table 1. Mean, range, coefficients of variation, heritability and genetic advance for 20 quantitative characters

| Characters | Mean + S E | Range | gcv | pcv | Herita- bility | G.A, % |
|--|-------------|-------------|-------|-------|-------------------|-----------|
| Days to first male flower anthesis | 56.20 +1.69 | 41.0-73.0 | 12.27 | 13.08 | 0.88 | 23.70 |
| Days to first female flower anthesis | 59.17 +1.80 | 41.0-84.50 | 15.01 | 15.61 | 0.92 | 29.73 |
| Node at which first female flower formed | 22.48 +0.59 | 15.50-29.0 | 12.77 | 13.29 | 0.92 | 25.25 |
| Female flowers per plant | 3.15 +0.30 | 2.25-5.00 | 16.82 | 21.66 | 0.60 | 26.91 |
| Male flowers per plant | 54.66 +5.15 | 32.50-92.50 | 22.53 | 26.17 | 0.74 | 39.94 |
| Sex ratio | 17.64 +1.67 | 11.93-28.19 | 17.12 | 23.37 | 0.64 | 28.94 |
| Node at which first fruit is retained | 36.60 +2.10 | 24.0-78.50 | 29.68 | 30.76 | 0.93 | 58.98 |
| Main vine length, m | 0.26 +1.05 | 6.69-13.99 | 18.09 | 24.21 | 0.56 | 27.83 |
| Nodes on main vine | 76.71 +7.53 | 45.0-117.0 | 19.64 | 24.05 | 0.67 | 33.02 |
| Primary branches per plant | 2.60 +0.61 | 1.00-5.00 | 21.28 | 39.62 | 0.29 | 23.54 |
| Productive branches per plant | 4.45 +1.17 | 1.00-10.50 | 34.72 | 50.89 | 0.47 | 48.81 |
| Internodal length, cm | 16.64 +1.84 | 10.5-21.50 | 13.93 | 20.94 | 0.44 | 19.10 |
| Mean fruit weight, kg | 2.80 +0.63 | 0.90-6.70 | 35.25 | 47.37 | 0.55 | 54.03 |
| Fruit length, cm | 19.26 +1.73 | 12.25-32.75 | 23.74 | 26.93 | 0.78 | 43.79 |
| Fruit diameter, cm | 17.53 +1.53 | 9.75-27.00 | 19.91 | 23.44 | 0.72 | 34.84 |
| Flesh thickness, cm | 2.95 + 0.33 | 1.45-4.65 | 22.87 | 27.87 | 0.67 | 38.67 |
| Seeds per fruit | 424.8+37.27 | 62.5-717.0 | 37.37 | 39.37 | 0.90 | 73.05 |
| 100 seeds weight, g | 10.94 +0.44 | 5.35-18.90 | 27.50 | 28.09 | 0.96 | 55.46 |
| Fruits per plant | 1.87 +0.47 | 1.00-4.00 | 20.44 | 40.80 | 0.25 | 21.05 |
| Yield per plant, kg | 5.10+1.84 | 0.90-13.4 | 27.71 | 58.17 | 0.23 | 27.20 |
| Carotene content, $\mu\text{g} / 100 \text{g}$ | 38.38 | 4.46-215.00 | - | - | - | - |
| Iron content, $\text{mg} / 100 \text{g}$ | 1.24 | 0.51-2.74 | - | - | - | - |

flower emergence. The highest heritability was observed for 1 seed weight (95.5%) as reported by Rajendran (1989) in watermelon. High heritability along with high generic advance was observed for 1 seed weight (95.5% and 55.46%) and seeds per fruit (9.1% and 73.5%) which indicates additive

gen action. Involvement of additive gene effects for the above, characters suggests improvement through selection (Burton, 1952). Though heritability was high for days to female flower anthesis and node at which first female flower was formed, the genetic gain was of low magnitude indicating non additive

Table 2. Details of pumpkin genotypes constituting different clusters

| Cluster no. | Cultivars included | Total no. |
|-------------|---|-----------|
| I | CM 136, CM 188 | 2 |
| II | CM 14C, CM 104, CM 106, CM 126, CM 147, CM 167, CM 171 | 7 |
| III | CM 88, CM 91, CM 153, CM 154, CM 157, CM 165, CM 175, CM 185, CM 201 | 9 |
| IV | CM 14, CM 14, CM 102, CM 103, CM 111, CM 135, CM 139, CM 149, CM 179, CM 183, CM 189, CM 192 | 12 |
| V | CM 89, CM 93, CM 95, CM 107, CM 108, CM 109, CM 113, CM 125, CM 131, CM 133, CM 148, CM 160, CM 162, CM 163, CM 176, CM 177, CM 180, CM 181, CM 193, CM 201 | 20 |

Table 3. Average intra and inter cluster D^2 values of five clusters of pumpkin considering 20 characters

| Cluster no. | I | II | III | IV | V |
|-------------|--------|--------|-------|-------|-------|
| I | 28.90 | - | - | - | - |
| II | 224.48 | 35.80 | - | - | - |
| III | 128.56 | 64.05 | 39.17 | - | - |
| IV | 48.85 | 141.77 | 75.37 | 30.04 | - |
| V | 95.85 | 75.50 | 45.28 | 48.63 | 34.28 |

gene action. This implies development of early varieties by utilizing transgressive segregants in the heterosis breeding programme.

Absence of inbreeding depression, presence of monoecious condition and colourful, large and showy flowers and more seeds per fruit point to the suitability of the crop for F_1 seed production. Selection of parents for hybridization programme is mainly based on genetic diversity. More divergent the parents, the more will be expression of heterosis. In the present study, the 5 genotypes were grouped into five clusters based on genetic distance (Table 2). Cluster V was the largest, containing twenty genotypes. Cluster IV contained twelve genotypes, cluster III nine genotypes, Cluster II and I containing seven and two genotypes respectively. Such

irregular pattern of distribution was reported by Kalloo *et al.*, (1982) in *Cucumis melo*.

Maximum genetic distance was exhibited between clusters I and II ($D^2 = 224.48$, Table 3). Clusters showing the largest genetic distance show the maximum divergence. In future programmes, selection of parents from clusters I and II for hybridization is likely to give heterotic hybrids. The inter cluster distance was also high between clusters I and III (128.56) and clusters II and IV (141.77). The maximum intra-cluster distance was shown by cluster III indicating high degree of variability within cluster which offer scope for improvement by various selection methods.

ACKNOWLEDGEMENT

This paper forms a part of M.Sc.(Hort) thesis of the senior author submitted to the Kerala Agricultural University in 1989. We are grateful to the Indian Council of Agricultural Research for the financial assistance by way of junior fellowship to the senior author.

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