DIVERGENCE STUDIES IN PUMPKIN

(Cucurbita moschata Poir*)*

BY

SURESH BABU, V

THESIS

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VELLANIKKARA TRICHUR

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DECLARATION

I hereby declare that this thesis entitled "DIVERGENCE STUDIES IN PUMPKIN (Cucurbita moschata Poir)" is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society

Vellanikkara,
21 12-1989

Suresh Babu V.

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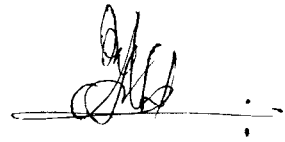
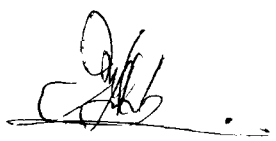


Dr. T. R. Gopalakrishnan
Chairman
Advisory Committee
Associate Professor
Department of Olericulture

Vellanikkara,
21-12-1989

CERTIFICATE

We, the undersigned members of the Advisory Committee of ***Mr. Suresh Babu V.****, a candidate for the degree of Master of Science in Horticulture, agree that the thesis entitled* ***"Divergence studies in pumpkin"*** *may be submitted by* ***Mr. Suresh Babu V.*** *in partial fulfilment of the requirement for the degree*



Dr. T. R. Gopalakrishnan
(Chairman)
Associate Professor
Department of Olericulture

Dr. K. V. Peter
Professor and Head
Department of Olericulture

Sri V.K.G. Unnithan
Associate Professor
Department of Agricultural Statistics

Dr. V.K. Venugopal
Associate Professor
Department of Soil Science
and Agricultural Chemistry

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Suresh Babu V.

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Introduction

INTRODUCTION

"One new variety raised by man will be a more important and interesting subject for study than one more species added to the infinitude of already recorded species"

Darwin (1859)

If Darwin is correct, it is our duty to study the widely grown underexploited crops where practically not much work has been done. Pumpkin (Cucurbita moschata Poir) is one of the widely grown underexploited vegetables in which sufficient attention has not been paid for genetic improvement. Introduced to our country from South America by foreign navigators and emissaries, pumpkin is grown throughout the length and breadth of India. The young leaves, flowers and fruits are rich in carotene, a precursor of Vitamin A. Importance of pumpkin as a potential supplier of carotene has not been exploited till date.

Yield in pumpkin remains low due to a conglomeration of factors, both genetic and environmental. Poor genetic stock, inadequate and improper management practices and incidence of diseases, particularly mosaic, are the main reasons for the low productivity. Development of high yielding, carotene rich, mosaic resistant varieties which

can entrap the abundantly available solar energy should be the ultimate aim of pumpkin improvement in the country.

Quantifying the available variability and divergence is the primary step of any crop improvement programme. High amount of cross pollination is the basic reason for the existing variability in pumpkin. The choice of breeding method either selection or hybridization depends primarily on the extent of heritability of the character under improvement. Selection of parental materials with maximum genetic divergence is of utmost importance in developing transgressive segregants. The extent of variability that would be available in the subsequent cycles of selection also depends on the extent of genetic divergence of parents involved in hybridization.

Absence of inbreeding depression, monoecious nature, showy and large flowers and a large number of seeds from a single act of pollination point to suitablity of the crop for exploitation of hybrid vigour. Selection of genetically divergent parents is very crucial in hybridization programmes. Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence.

Area under pumpkin in the country is fast being reduced day by day due to wide occurence of virus diseases particularly yellow vein mosaic and pumpkin mosaic. Development of high yielding varieties will be futile, if they do not have adequate resistance to these viruses. A single variety resistant to yellow vein mosaic and pumpkin mosaic will really make a boost in cultivation of pumpkin in Kerala.

Review of literature indicated that only a meagre attempt has been made in pumpkin in these directions. Hence the present work is highly necessary and was undertaken with the following objectives.

1. To estimate extent of available variability for imporotant characters in pumpkin.
2. To study extent of genetic divergence among the genotypes and to group them into clusters based on genetic distance.
3. To select high carotene lines in pumpkin
4. To screen pumpkin genotypes for resistance to yellow vein mosaic and pumpkin mosaic.

Review of Literature

REVIEW OF LITERATURE

Information available on genetic variability, divergence and resistance to mosaic diseases are very much limiting in pumpkin. Inorder to project the magnitude of the problem and to have a general guidance, information on other cucurbits are also reviewed and presented under the following heads:

A. Genetic variability, heritability and genetic advance

B. Genetic divergence and clustering of genotypes

C. Resistance to mosaic diseases

A. Genetic variability, heritability and genetic advance

1. Genetic variability

The knowledge of genetic variability of a breeding material helps a plant breeder in choosing desirable parents and to improve characters of economic importance. Burton (1952) introduced a convenient procedure for calculation of phenotypic and genotypic coefficient of variation. Johnson et al. (1955) introduced a methodology for partitioning the variability in a population into heritable and non-heritable components with the aid of genetic parameters such as coefficients of variation, heritability and genetic advance which could also serve as a basis for selection.

Kubiaki and Walezak (1976) reported large differences within and between varieties with respect to β carotene content in 19 varieties belonging to Cucurbita pepo, Cucurbita maxima and

Cucurbita moschata. The variety Golden Delicious (Cucurbita maxima) recorded the highest carotene content. Gopalakrishnan (1979) studied variability for 25 quantitative characters among 18 genotypes of Cucurbita moschata and found that the genotypes were significantly different for all the characters studied. Fruit yield/plant ranged from 5.45 kg in CM 18 to 16.10 kg in CM 17. Carotene content ranged from 0.152% to 0.527%. This study identified lines CM 17 and CM 14 (Ambili) as high yielders (16.10 kg and 15.38 kg/plant respectively) having desirable characters. The maximum value of genotypic coefficient of variation was for male flowers/plant (56.23) followed by fruits/plant (50.32). Rana (1982) while studying variability in 19 lines of pumpkin found that the lines grown in two environments differed significantly for the 10 characters studied. Dorjode (1983) reported ample variability for T.S.S. and carotene among 7 inbred lines of pumpkin. The T.S.S. content ranged from 4.7 to 8.1% and β carotene from 1.7 to 8.65 mg/100 g

Nath and Dutta (1970) reported that varieties of watermelon (Cucurbita lanatus (Thunb.) Mansf.) differed much for number of fruits (1.2 to 4.5), average fruit weight (1.0 to 7.5 kg), average T.S.S. (8 to 12%) and yield/acre (6.5 to 31.14 t). Variability in watermelon was reported by Thakur and Nandpuri (1974) for vine length which ranged from 2.64 to 4.84 m, branches/vine (5.34 to 7.65), sex ratio (15.7:1 to 2.5:1), days to first fruit picking (81.5 to 99.2), fruits/vine (0.64 to 1.85), average fruit weight (2.29 to 5.95 kg),

yield/vine (2.43 to 6.60 kg), number of seeds/kg of fruit weight (53.7 to 260.3), 100 seed weight (4.92 to 13.85 g) and T.S.S. (6.17 to 8.74%). Phenotypic coefficient of variation (pcv) was the maximum for seeds/kg of fruit weight (41.31) and it was the minimum for days to first picking (6.46). The coefficients of genotypic variation (gcv) also had the same trend. Vashista et al (1975) observed considerable variability in length, width, 100 seed weight and seed colour in watermelon. Vashista et al (1983) reported significant differences among varieties for all the characters except fruits/plant. Wide variations were observed in days required for appearance of first female flower, duration in picking of fruits, number of female flowers, number of fruits, total yield/vine, T.S.S. and flesh seed ratio in different varieties (Bhathal and Sandhu, 1984). Gill and Kumar (1986) recorded variability for different traits which ranged from 1.00 to 1.52 for fruit shape index, 7.76 to 9.51% for T.S.S., 5.66 to 9.69% for total sugars and 5.01 to 8.23 mg/100 g of fruit flesh for vitamin C content.

In a study involving 30 genotypes of watermelon, Rajendran (1989) observed that vine length ranged from 1.13 to 3.58m and the pcv and gcv were 35.45 and 21.86 respectively. Days to first female flower anthesis ranged from 37.17 to 61.72 and the pcv and gcv were 19.10 and 11.91 respectively. The sex ratio ranged from 12.83 to 131.47 with moderately high value of pcv (86.72)

and gcv (60.68). Fruits/vine ranged from 0.64 to 3.17 and pcv and gcv were 58.29 and 39.83% respectively. Fruit yield/vine ranged from 0.383 to 9.546 kg and pcv and gcv for yield were 88.34 and 67.60 respectively. Seeds/fruit had a wide range of 20.50 to 539.83 and pcv and gcv were 58.76 and 44.64 respectively.

Srivastava and Srivastava (1976) studied variability in 10 lines of bittergourd (Momordica charantia L.) and observed significant differences for all the characters except for male flowers/plant. The highest genotypic coefficient of variation was observed for fruits/plant (37.45) followed by yield/plant (32.13) and fruit weight (30.02). Male flowers/plant had the lowest genotypic coefficient of variation (11.47). Singh et al. (1977) evaluated 20 varieties of bittergourd and obtained maximum value of gcv for fruits/plant (39), followed by fruit yield/plant (35). Days to flower had the least genotypic coefficient of variation (4). Ramachandran (1978) observed significant variation for 13 quantitative characters in 25 diverse lines of bittergourd. He observed the highest phenotypic coefficient of variation (39.88), genotypic coefficient of variation (37.82) and genetic gain (81.9) for yield/plant. The lowest value of genotypic coefficient of variation (5.72) was observed for seeds/fruit.

Mangal et al. (1981) estimated genotypic and phenotypic coefficients of variation in 21 varieties of bittergourd. Highly significant variation was observed for all the characters. Yield/plant recorded the highest gcv while days to first female flower anthesis, the

minimum. Indiresh (1982) assessed 24 lines of bittergourd and found high gcv for fruit weight, yield/plant, fruit cavity length, leaf area and fruit length. Chaudhari (1987) observed the highest phenotypic and genotypic coefficient of variation for yield/plant, fruits/plant, vine length and fruit weight. The estimates of pcv and gcv were low for early female flower formation and early harvest.

Vahab (1989) evaluated 50 genotypes of bittergourd at College of Horticulture, Vellanikkara. Average fruit weight had the maximum value of pcv (48.77) followed by yield/plant (39.91) and fruits/plant (31.82). The lowest value of pcv was observed for node at which the first female flower is formed (8.18). The gcv resulting in high heritability was of high magnitude for fruit weight (99), yield/plant (99) and fruits/plant (99).

In a comparative yield trial of 24 varieties of cucumber (Cucumis sativus) Solanki and Seth (1980) observed considerable phenotypic variation for most of the characters studied. Minimum variation was found for internodal length and fruit yield. Joshi et al. (1981) reported the least variation for primary branches in twenty varieties of cucumber. They further found that the pcv and gcv did not show differences for different characters except vine length, number of primary branches and flesh/seed ratio. Rudragowda and Patel (1985) examined relative performance of 21 genotypes of cucumber in which 'Pusa Sanyog' had the longest vine with higher number of nodes on main shoot.

Kalyanasundaram (1976) evaluated three muskmelon (Cucumis melo L.) varieties - Annamalai, Hara Madhu and Arka Rajhans - and observed significant differences among the three varieties for economic characters. Chhonkar et al. (1979) while studying the genetic variability in 11 muskmelon varieties found that the phenotypic variation was quite large but genotypic variation was low. Vijay (1987) found that fruits/vine, flesh thickness and yield/vine had the maximum genotypic coefficient of variation in 95 cultivars studied.

Joseph (1978) studied variability in 25 snakegourd (Trichosanthes anguina L.) types with respect to 21 characters and found that the types differed significantly with respect to all the characters studied. Singh et al. (1985) reported maximum value of g.c.v. for seed volume (21.95) followed by seed weight (21.89) and fruit yield/plant (18.37) in 25 cultivars of pointed gourd (Trichosanthes dioica Roxb).

Arora et al. (1983) evaluated 13 varieties of sponge gourd (Luffa cylindrica Roem). Maximum range of variation and high genotypic and phenotypic coefficients of variation were for yield/plant followed by fruits/plant and sex ratio. Reddy and Rao (1984) found that in ridge gourd (L. acutangula Roxb.) p.c.v. ranged from 14.38 to 162.62% and the g.c.v. from 13.56 to 112.03% for days to first marketable fruits and yield/plant respectively. The p.c.v. and g.c.v. for yield/plant were the highest. The lowest values of p.c.v. and g.c.v. were realised for days to first picking and fruit diameter.

2. Heritability and genetic advance

Kubiaki and Walezak (1976) studied heritability of carotene content in a few Cucurbita spp. The carotene content and T.S.S. in Cucurbita spp. recorded high heritability estimates. The inbred lines developed through selfing and selection, recorded 70%, 50% and 20% more β carotene, where the parental populations were Melonowa Zolta, Golden Delicious and Nagydebos Sulolok respectively. Gopalakrishnan (1979) reported the highest heritability estimate of 99.14% for male flowers/plant followed by percentage of female flowers and female flowers/plant in Cucurbita moschata. The lowest heritability estimate of 76.96% was observed for fruitset (%). He also found that male flowers/plant had the highest value of genetic gain (52.32%). Rana (1982) observed high estimates of heritability and genetic advance for vine length and fruitset (%) in pumpkin. Hassan et al. (1984) found that broad sense heritability [$h^2(b)$] was high for average fruit weight but affected by environment. Broad sense heritability [$h^2(b)$] and narrow sense heritability [$h^2(n)$] values for fruit length were 80% and 51% respectively. The $h^2(b)$ was high but $h^2(n)$ was low for fruit width and fruit shape index. Doijode and Sulladmath (1985) reported that out of 6 quantitative fruit characters studied, all characters except total soluble solids showed high narrow sense heritability. Sirohi et al. (1986) reported high heritability and low genetic advance for days to first harvest, fruit weight, fruit shape index and flesh thickness.

Thakur and Nandpuri (1974) reported a heritability estimate of 92.92% for 100 seed weight and 84.97% for seeds/kg of fruit in watermelon The minimum heritability estimate of 25.95% was observed for branches/plant. The maximum genetic advance was observed for seeds/kg of fruit (83.75%). The lowest estimate of genetic advance was observed for days to first picking (5.78%). Brar and Nandpuri (1978) conducted genetic analysis of yield and fruit number in watermelon. The $h^2(b)$ was moderate (48.92%) and $h^2(n)$ low (23.64%) for yield/plant. The $h^2(b)$ was higher (72.29%) and $h^2(n)$ was moderate (66.90%) for fruit number. Vashista et al. (1983) reported high heritability estimates for all characters except yield/plant. Gill and Kumar (1986) reported high heritability for fruit shape index, T.S.S., total sugars and vitamin C content in watermelon. According to them, though T.S.S. showed high heritability (82.76%), the expected genetic advance was very low (10.42%) The geretic gain was high for vitamin C content of fruits. Rajendran (1989) studied heritability and genetic advance in watermelon and reported that heritability and genetic gain were 38.00 % and 27.76 % respectively for vine length. They also reported low heritability (25%) and moderate genetic advance (47.40%) for leaves/vine, moderate heritability (39%) and low genetic gain (15.3%) for days to first female flower anthesis, moderate heritability (49%) and comparatively high genetic gain (87.46%) for sex ratio, moderate heritability (47%) and moderate genetic gain (56.06%) for fruits/vine, low heritability (4.00%) and genetic gain (6.97%) for crop duration and medium heritability (58%) and genetic

gain (69.87%) for seeds/fruit.

Srivastava and Srivastava (1976) reported that fruits/plant had the highest estimate of genetic advance (71.73%) resulting from the highest estimate of variability (g.c.v. - 37.45%) and heritability (99.31%) in bittergourd). Male flowers/plant recorded the lowest estimate of genetic gain (16.78%) and heritability (49.98%). High heritability associated with moderate variability resulting in high genetic gain was observed for fruit weight, yield/plant and fruit length. Singh et al. (1977) observed high estimate of heritability and expected genetic advance for fruit yield, fruits/plant and fruit length in bittergourd. Ramachandran (1978) reported that heritability in broad sense was quite high for all the 21 characters he studied in bittergourd except for seeds/fruit. Fruits/plant had the highest heritability of 99.80% which was closely followed by yield/plant (99.74%) and vitamin C content (99.63%). The lowest heritability was for seeds/fruit (43.37%). Genetic gain was the highest for yield/plant (81.93%) followed by vitamin C content (70.72%) and fruits/plant (64.3%). Mangal et al. (1981) noted high heritability values for leaf length, plant height, average fruit weight, branches, fruits and yield/plant and seeds/fruit. Indiresh (1982) found that heritability estimates were high for all characters studied, except yield/plant and days to fruit development. Chaudhari (1987) reported that the genetic advance was very high for yield/plant (1114.39) and vine length (151.53) Vahab (1989) reported

high heritability along with genetic gain for fruit weight, yield/plant and fruits/plant. Though heritability was high for primary branches/ plant and days to opening of first female flower, the genetic gain was of low magnitude.

Miller and Quisenberry (1976) observed moderately high heritability for days to first female flower anthesis, in cucumber. Solanki and Seth (1980) reported association of high heritability with high genetic advance for plant height, leaves/plant, ~~Cucumis~~ male flowers/plant, female flowers/plant, internodal length, days to matutity and fruit yield in Cucumis sativus.

Chhonkar et al. (1979) reported that the value of heritabilities and genetic advance showed effectiveness in selection for pulp thickness, fruit weight and percentage of total soluble solids in muskmelon. Vijay (1987) noticed high heritability and high genetic advance for fruits/vine, T.S.S., flesh thickness, yield/vine, fruit weight and days to flowering.

Joseph (1978) studied heritability and expected genetic advance for 21 characters in snakegourd. Fruit length had the highest heritability of 99.19% followed by fruit girth (98.60%) and vitamin C content (97.59%). Yield/plant had comparatively a low estimate of heritability (45.90%). The lowest heritability estimate was recorded for fruits/plant (21.20%).

In spongegourd, Arora et al. (1983) found high heritability estimates for all the characters studied except vine and internodal length and fruit diameter which showed moderate values. The genetic gain was also the highest for yield/plant followed by sex ratio and fruits/plant. Reddy and Rao (1984) found maximum genetic gain for fruit yield (157.14) followed by average fruit weight (130.70), leaf area (108.77) and number of fruits (108.14) in ridgegourd. The highest heritability was for average fruit weight and the lowest for days to first harvest.

B. Genetic divergence and clustering of genotypes

Importance of genetic divergence in selection of parents for hybridization was stressed by many workers. According to Singh and Gupta (1968) the more diverse the parents, with in a reasonable range, the more would be the chance of improving the character in question. The major sources of the origin of genetic diversity in plants could be enumerated as mutations, recombinations and polyploidization, whether they are accomplished through the natural agencies or through artificially controlled conditions (Rai, 1979). Usually in most of the conventional heterosis breeding programmes, geographical diversity at times and phenotypic diversity in many times are taken as the criteria for choosing genetically divergent populations for isolation of inbred lines. Phenotypic divergence in a population has also been considered as an index and criteria of genetic diversity (Rai, 1979).

Generally ecogeographic diversity has been considered as an index of genetic variability in crop plants. However, this may not be true for every case, as many workers postulate that geographic diversity need not necessarily be related to genetic diversity. Varieties from widely seperated localities are usually included in hybridization programmes presuming genetic divergence and greater likelihood of yielding better segregants. Validity of the above presumption depends upon the association between geographic diversity and genetic diversity (Singh and Bain, 1968) Studies on genetic diversity by use of multivariate analysis is practically nil in pumpkin. Doijode et al. (1982) in a study involving seven parents indicated wide genetic diversity among them. Sukhija et al. (1982) studied the genetic divergence among 46 lines of watermelon. The D^2 values varied from 3.84 to 308.43 showing high divergence among lines selected for the study. The 46 lines were grouped into 12 clusters. The intra cluster divergence ranged from 0 to 19.40. They also reported that the lines usually did not cluster according to their geographical distribution. In some cases, geographic origin influenced clustering. While studying 7 diverse watermelon varieties and their hybrids, Sidhu and Brar (1985) found that the clustering pattern of hybrids was not influenced by their parentage and their geographical origin They observed highly significant differences among the genotypes. The average fruit weight contributed maximum towards genetic divergence (28.04%) followed by fruits/plant (23.28%) which together contributed 51.32% of the divergence. The

28 populations were grouped into 7 clusters. The inter cluster values ranged from 12.88 to 39.39. The low intra cluster and high inter cluster values suggested that the populations grouped were homogeneous within and heterogeneous between clusters. However results did not show any consistent relationship between divergence and heterosis for yield in watermelon.

In a study involving 45 diverse lines of Cucumis melo, Kalloo et al. (1982) observed high diversity as indicated by the range of D^2 values from 2.52 to 210.14 among the lines. Depending on the genetic divergence, the 45 strains were grouped into 14 clusters. The maximum distance at intercluster level was 14.50 followed by 13.79. The intra cluster divergence ranged from 9.36 to 19.86. They also found that the genotypes usually did not cluster according to the geographical distribution. But in some cases, geographical origin influenced clustering.

Mathew et al. (1986) studied the genetic distance among five botanical varieties of Cucumis melo. Cucumis melo var. conomon (oriental pickling melon), Cucumis melo var. inodorus (muskmelon), Cucumis melo var. flexuosus (snakemelon), Cucumis melo var. utilissimus (longmelon) and Cucumis melo var. momordica (snap/melon). The genetic distance was calculated considering four quantitative characters, nodes to first female flower, fruit weight, seeds/fruit and fruits/plant. Maximum genetic distance of 12.49 was observed between musk melon

and snakemelon. Longmelon and snapmelon were the closest (D^2 = 0.38). Muskmelon and longmelon were also placed distantly (D^2 = 9.16) followed by muskmelon and snapmelon (D^2 = 8.79) Fruits/plant contributed maximum to total divergence (80%). Seeds/fruit did not contribute to total divergence. They found that selection of botanical varieties based on fruits/plant would be logical in selection of divergent parents.

In bittergourd, genetic divergence studies were conducted by Ramachandran et al. (1981) using 25 diverse genotypes. Observations on eight quantitative characters viz. primary branches/plant, main vine length, days to first female flower anthesis, female flowers/plant, branches/plant, fruits/plant, average fruit weight, fruit length and yield/plant were recorded. The 25 types were grouped into 10 clusters based on their D^2 values. The lowest intra cluster D^2 value was in cluster I (102.43) and cluster IV had the highest intra cluster D^2 value (360.50). They further reported that the characters, yield/plant fruits/plant, female flowers/plant and fruit length had contributed predominantly to divergence and that selection of divergent parents based on these characters may be useful for heterosis breeding in bitter gourd. Vahab (1989) also studied the divergence in bitter gourd using 50 genotypes and found that the genotypes differed significantly for all the 18 characters studied. The 50 genotypes were grouped into 5 clusters. Lines of different sources/origin fell in the same group and different groups consisted of lines from the same source/origin. In ridgegourd (Luffa acutangula Roxb.) multivariate analysis

was conducted by Kadam and Kale (1985) considering 14 vegetative and reproductive characters in 30 cultivars. Analysis of variance revealed considerable divergence among the cultivars. The 30 cultivars were grouped into 20 clusters based on their D^2 values. The lowest intra cluster D^2 value was 8.22 and the highest 18.59. The highest inter cluster distance was 387.11 and the lowest 19.79. They further found that deformed fruits/vine, yield/vine, fruits/vine and fruit volume and chlorophyll 'a' content were the important factors contributing towards divergence.

C. Resistance to mosaic diseases

Mosaic is the most dreadful disease affecting pumpkin and was reported from many parts of the country. Martyn (1968) reported occurence of 17 viruses in cucurbits. The wide spread occurence of yellow vein mosaic virus and pumpkin mosaic virus threaten cultivation of pumpkin in Kerala (Jayasree, 1984; Umamahewaran, 1985). The characteristics of pumpkin mosaic viruses reported from different parts of India are not very similar. Studies on mosaic diseases are reviewed under two heads viz. (1) nature of the disease and (2) sources and nature of resistance.

1. Nature of the disease

(a) Pumpkin mosaic

Pumpkin mosaic was first reported in India by Hariharasubramanian

and Badami (1964). They observed that the disease was characterised by severe blistering, distortion and stunting of leaves. Jaganathan and Ramakrishnan (1971) observed that mottling and malformation of leaves by a virus isolated from pumpkin. They also reported that plants infected early in the season remained dwarf and flowered sparingly. A few leave exhibited dark green vein banding along the mid rib and lateral veins of affected plants. Shanker et al. (1972) observed that the symptoms of pumpkin mosaic virus disease first appeared a mosaic mottling of the leaves. Some times leaves showed chlorosis of veins and veinlets leaving interveinal areas green. The leaf lamina was very often distorted and reduced. The severely affected vines were extremely dwarf and some times did not bear leaves or flowers, as the whole vine was turned into a thread like structure.

Bhargava and Bhargava (1977) reported from Gorakhpur (U.P.) that seven cultivated cucurbits (Cucurbita moschata, Cucumis sativus, Lagenaria siceraria, Momordica charantia, Citrullus lanatus, Benincasa hispida and Trichosanthes dioica and 2 wild cucurbits were affected by pumpkin yellow vein mosaic virus, pumpkin mosaic virus, cucumis virus 3, 3 strains of cucumber mosaic virus and 7 strains of watermelon mosaic virus (WMV). Ghosh and Mukhopadhyay (1979) isolated nine different strains of viruses from Cucurbita moschata from West Bengal and among them the isolate, A-7 produced characteristic mottling with mild green blisters and green vein bonding in the leaves of infected plants. Singh (1982) studied the effect of pumpkin mosaic virus infection

on the Hill reaction and primary productivity of Cucurbita maxima and found that the production of dry matter was reduced and respiration rate increased in infected leaves compared with healthy ones. The rate of dye reduction (Hill reaction) was higher in healthy samples than in infected ones at comparable ages. Umamaheswaran (1985) observed that the leaves of Cucurbita moschata which were naturally infected with the virus showed severe mottling and disfiguration. A few leaves exhibited dark green vein banding. At times, irregular chlorotic spots appeared on the leaf lamina which later coalasced and became large yellow areas. Very often, the leaf lamina showed mottling with mild green blisters. The infected seedlings remained stunted and they flowered very sparingly and that also with less number of female flowers and reduced fruit setting. On mechanical inoculation of 10 days old test plants, he found that the flowering was delayed, the flower size was much reduced and they did not bear any fruits.

(b) Yellow vein mosaic

Verma 1955) reported for the first time the yellow vein mosaic of Cucurbita pepo from Pune. The infected plants showed yellow vein mosaic symptoms on leaves with no reduction in size of leaf lamina. He found that the virus could infect Cucurbita, Cucumis sativus and Luffa acutangula. Conen and Nitzany (1960) described a virus causing typical yellow vein mosaic in cucumber from Israel. Conspicuous vein clearing and chlorosis of cucumber were reported

and these were found apparently identical with the symptoms of bottlegourd mosaic. Harpaz and Cohen (1965) reported the vein yellowing virus of cucumber from Israel.

Capoor and Ahmad (1975) noted a yellow vein mosaic of Cucurbita pepo from Deccan. They observed that the symptoms appeared on young leaves as faint yellowing of finer veins which later became characteristic vein yellowing with chlorotic patches over larger areas of leaf lamina. They also found that the host range included Cucurbita moschata and Luffa acutangula.

Ghosh and Mukhopadhyay (1979) isolated a strain of virus from pumpkin (Cucurbita moschata) from West Bengal, which resembled yellow vein mosaic of cucumber reported from Israel by Harpaz and Cohen (1965). The symptoms appeared as irregular, chlorotic spots on the margin of the lamina which gradually coalasced and became yellow. The host range recorded includes Momordica charantia. Luffa acutangula, Citrullus lanatus etc.

Jayasree (1984) while studying yellow vein mosaic disease of pumpkin in Kerala, reported that the symptoms of disease appeared as faint yellowing of finer veins which later developed into characteristic vein yellowing. In advanced stages of infection, chlorotic areas were seen on the leaf lamina along with vein yellowing symptoms. The size of the leaves was reduced markedly and the overall growth of infected plants was severely retarded. The infected plants produced

less number of female flowers and when infected at a later stage produced undersized fruits. The host range included Cucurbita pepo Luffa acutangula, Trichosanthes anguina and Momordica charantia. Infection of plants at an early stage of growth caused reduction in number of leaves, leaf size, internodal length, number of branches, total vine length and number of flowers and also resulted in complete loss of yield. The yield loss of pumpkin due to yellow vein mosaic virus infection was 100% when the plants were inoculated at seedling stage (Jayasree, 1984; Balakrishnan, 1988).

Cucumber mosaic virus could cause wilt and dying-off in pumpkin and vegetable marrow (Schmelzer, 1967). He also found that plants infected early may develop mosaic, curling and stunting. The fruits had distorted shape and were spotted. Moskovets and Fegla (1972) while conducting studies with watermelon mosaic virus found that the virus caused the production of shorter runners, nodes and fewer side runners in cucurbits. Almeida and Borges (1983) reported that watermelon mosaic virus produced mosaic and severe distortion of leaves of pumpkin. Singh (1986) assessed loss caused by a strain of watermelon mosaic virus in Cucurbita and found that pumpkin plants inoculated at early stages of growth produced shorter runners and internodes, fewer side runners and fewer smaller leaves.

Lockhart et al. (1982) found that squash mosaic virus caused typical ring mosaic symptoms in Cucurbita album. Cohen et al. (1983)

described that squash leaf curl virus (SLCV) produced severe stunting and leaf curl in leaves of Cucurbita moschata, Cucurbita maxima and Cucurbita pepo.

Sharma and Sharma (1982) while studying the mosaic virus on bottlegourd found that the host range of the bottlegourd mosaic virus was restricted to the family cucurbitaceae and the common hosts were Cucurbita pepo, Citrullus lanatus, Cucumis sativus, Cucumis melo Lagenaria siceraria and Luffa acutangula and all of them developed mosaic symptoms.

Igwegbe (1983) observed that the Cucumeropsis virus systemically infected Cucurbita pepo 'Small Sugar' and Cucurbita maxima 'Emerald'. The symptoms included severe stunting, severe leaf deformation, faint light to dark green or yellow mosaic, leaf puckering and small distorted faints with chlorotic spots. Provvidenti et al. (1984) reported occurence of Zucchini yellow mosaic virus in cucurbits from Connecticut, Florida, New York and California. Two strains of the virus were recognized, ZYCT-CT and ZYMV-FL. Plants infected at an early stage of growth failed usually to set any fruit, but those that were infected during the flowering stage produced severely knobbed fruits. They also found that colour break occured on fruits of every species, but was noticeable on those of yellow summer squash.

Herrington (1987) reported that studied the yield and quality of Cucurbita maxima increased with delayed infection by papaya ring spot virus type W. When 4 weeks old 'Queensland Blue' pumpkin plants were inoculated

with the virus the average yield/plant, was only 3.4 kg, but when inoculated 5 weeks later, the yield was 9.5 kg/plant. He suggested that losses could be reduced by delaying infection by using reflective mulches or by promoting rapid early growth before active spread of the virus or by the use of resistant cultivars.

2 Sources and nature of resistance

Provvidenti et al. (1978) found that Cucurbita ecuadorensis was immune or resistant to four viruses infecting cucurbits and it was compatible with Cucurbita maxima which would be a good source of resistance in breeding programmes. They also found that Cucurbita foetidissima is a good source of resistance to three viruses infecting cucurbits and that Cucurbita martinezzi was resistant only to two viruses, but could be used to transfer resistance to CMV to Cucurbita moschata. Pitrat and Dumas de Vaulx (1979) during their search for sources of resistance to cucumber mosaic and watermelon mosaic virus among Cucurbita species found that Cucurbita lundelliana, Cucurbita martinezi and Cucurbita ecuadoriensis were resistant to CMV and WMV.

Provvidenti (1982) reported that a single plant selection (P 1234608-1) of Queensland Blue' (Cucurbita maxima) from South Africa appeared to possess adequate resistance to isolate of cucumber

mosaic virus (CMV) but during the late autumn and early winter, plants inoculated with CMV at the cotyledonary stage tended to develop severe mosaic and stunting. He further reported that a single plant selection from Uruguay showed good tolerance to isolates of watermelon mosaic virus from New York, Florida, Nigeria and Hawai. Sharma and Sharma (1982 b) tested 31 summer squash genotypes in field against natural infection of a strain of Cucumis virus-1 (CMV) and found that 12 were moderately resistant, but none was immune. Pink and Walkey (1984) inoculated the plants of Cucurbita pepo cultivars Cindrella, Cobham Bush Green and Goldrush with six strains of CMV from different geographical areas and found that cv. Cindrella showed high resistance to all strains cv. Cobham Bush Green was moderately resistant and cv. Goldrush was highly susceptible. Walkey and Pink (1984) identified resistants to two British strains of CMV in some types of Cucurbita pepo with the highest level in cv. Cindrella and reported that the resistance in Cindrella is heritable.

Walkey et al. (1985) studied the nature of resistance to CMV and found that the level of resistance in the cv. Cindrella increased significantly when the postinoculation temperature was raised from 15 - 25°C and that the resistance is inherited. Pink and Walkey (1985 a) studied the effect of temperature on the resistance in Cucurbita pepo and found that at 25°C, most plants were symptomless. In another study the same authors (1985 b) reported high frequency of resistant

plants in cv. Cindrella in a screening trial of 64 inoculated accessions of Cucurbita pepo for CMV resistance. They further stated that resistance in the cultivar appeared to be quantitative and has been incurred by selection and the resistance was effective in glass house against 8 strains of the virus.

Unamaheswaran (1985) screened nine varieties of Cucurbita moschata for resistance to pumpkin mosaic virus and reported that none of the varieties were resistant to pumpkin mosaic virus. But some varieties were more susceptible when compared to others. Varietal screening studies by Balakrishnan (1988) using nine varieties of pumpkin revealed that all the varieties were susceptible to PMV. But, Hybrid-1 and Coimbatore-1 with 100% infection and Thathamangalam selection and CO-2 with 95% infections were highly susceptible varieties whereas CM-67 and Arka Suryamukhi were less susceptible with 55% infection.

Jayasree (1984) listed four varieties of pumpkin namely, CM-14, King of the Mammottis, Large Red and a local variety against yellow vein mosaic virus and found that infection of plants at early stage of growth resulted in complete loss of yield among all the four varieties.

Provvidenti et al. (1984) screened several hundred cultivars and plant introductions for resistance of Zucchini yellow mosaic virus and found that most of the germplasm tested was very susceptible,

but resistance or tolerance was found in individual accessions of seven cucurbit species. They also reported that a Cucurbita sp. from Nigeria and a Cucurbita ecuadorensis from Ecuador were resistant.

Munger and Provvidenti (1987) studied inheritance of resistance to Zucchini yellow mosaic virus in Cucurbita moschata using Nigerian local and Butter Nut squash which is extremely susceptible to ZYMV. The studies indicated that a single gene when homozygous in Cucurbita moschata confers a high level of resistance to ZYVM. Provvidenti (1987) studied inheritance of resistance to a strain of Zucchini yellow mosaic virus in cucumber and found that the resistance was conferred by a single recessive gene (ZYM). Paris et al. (1988) reported that resistance to Zucchini Yellow Mosaic Virus in Cucurbita moschata was controlled by a single dominant gene designated ZYM.

Igwegbe (1983) reported that Cucurbita sp. 'Nigerian Local', Cucurbita colocynthes 'Nigerian Local', Luffa acutangula Cucumis melo and Telfaria occidentalis are immune to a virus infecting Ahu (Cucumeropsis edulis L.) in Nigeria.

Greber (1978) reported that watermelon mosaic virus-1 and 2 in Queensland infected all commercially available watermelon, vegetable marrow and pumpkin cultivars. Maluf et al. (1986) reported that a Cucurbita ecuadorensis, 4 Cucurbita moschata cultivars and 3 Cucurbita maxima were resistant to watermelon mosaic virus-1. When inoculated with the inoculum obtained from infected plants

of Cucurbita pepo at three leaf stage and again 4 days later.

Singh (1986) found that in Cucurbita maxima, the plants inoculated at 20, 30, 40, 50, 60 and 70 days after planting with watermelon mosaic virus yielded 2, 2, 3, 4, 4 and 5 fruits respectively with average total fruit weight of 0.6, 0.79, 1.0, 2.5, 3.1 and 4.8 kg/plant.

Materials and Methods

MATERIALS AND METHODS

The present studies were conducted at the Research Plots of the Department of Olericulture, College of Horticulture, Vellanikkara Trichur, Kerala during June 1988 - March 1989. This station is located at an altitude of 23 m above MSL and is situated between 10° 32" N latitude and 76° 16" E longitude. Geographically it falls in the humid tropical climatic zone. The meteorological data for the seasons under experimentation are presented in Appendix 1.

Experimental materials

The experimental materials consisted of 71 pumpkin genotypes. This involved genotypes maintained in the Department of Olericulture, College of Horticulture, Vellanikkara and genotypes collectged from all over India and exotic collection made through N.B.P.G.R, New Delhi The source and morphological description of the genotypes are presented in Table 1.

Methods

The experiment comprised of two parts

A. Assessment of variability and divergence and grouping of genotypes based on D^2 values.

B. Evaluation of genotypes for resistance/tolerance to mosaic diseases.

Table 1 Source and Morphological description of 71 pumpkin genotypes

Accession No	Place of collection	Local name	Fruit shape	Stem end fruit shape	Blossom end fruit shape	Fruit shape	Fruit size
CM 14A	Trichur	Local	Oval	Depressed	Rounded	Rounded	Medium
CM 14B	"		Flattened	"	Depressed		Big
CM 14C			Globular	Flattened	"		Big
CM 39	IARI		Pyriform	Depressed		Intermediate	Medium
CM 85	Shethala		Oval		"		Big
CM 88	Kakinada AP		Flattened	"	Rounded	Rounded	Medium
CM 8			a	Flat eve	Depressed	Nor bs	g
CM 0	Assam		Globular	Depressed			Medium
CM 9	Assam		va	Flattened	Flattened		Medium
CM 92			Globular	Depressed	Depressed		Medium
CM 93	Trichur		Flattened	"	"	Rounded	Sma
CM 94	"		Oval	Flattened	Rounded		Medium
CM 95			Oval	Flattened	Flattened	Rounded	"
CM 97	Ponnam Mahashtra		Flattened	Depressed	Depressed	Nor bs	Big
CM 0	TNAU	CO1	Globular	Flattened	"	"	Med m
CM 02	"	CO2	Oval	"	Rounded	Rounded	Medium
CM 03	Payyanur	Local	Globula	Depressed	Depressed	"	Medium
CM 04	Moovattupuzha		Heart shape	Flattened	Pointed	Nor bs	Big
CM	Ambalavayal			Depressed	Depressed	Rounded	
CM 06	Kasargod Pachu		Elongate	Flattened	Flattened	Nor bs	Medium
CM 07	Kolamgode Pachha		Oval	"	Depressed	Rounded	ma
CM 08	Muthalamada		Flattened	Depressed	"	"	Big
CM 39	Chavakkadam		Flattened	Depressed	"	"	Medium
CM	Jorhat Assam	C 4	Oval	Flattened	Flattened	Nor bs	Medium
CM 2		C 0		"		Rounded	
CM		C 7	y form		Rounded	Nor bs	
CM 25	Mudkode Trichur	Local	Flattened	Depressed	Depressed	Rounded	Big
CM 26			Globular	"	"	"	"
CM 30	Sreekrishnapuram		Oval	"	Rounded	"	Medium
CM 13	Trichur		Oblong	Flattened	"	Nor bs	Big
CM 32	Channyuva		Globular	Depressed	Depressed	Rounded	Big
CM 33			Flattened	Depressed	"	"	Medium
CM 135	Pattambi		Oval	Flattened	Flattened	"	Medium
CM 136	Cheruthuruthi		Globular	Depressed	Depressed	Nor ribs	"
CM 38	Thrissur Nagha	Local	"	"	"	Rounded	"
CM 39	Thrissur Pattambi		Globular	Depressed	Depressed	"	"
CM 47	Kakinada AP	Sugarpumpkin	Flattened	"	Rounded	Intermediate	Sma
CM 48	mbalam	Local	Heart shape		Depressed	"	Big
CM 49	Palayur		Oval	Rounded	Rounded	Rounded	"
CM 0	mbalam		Globular	Depressed		Intermediate	Big
CM	Chalakudy		obular		Depressed	ounded	Big
CM 4	Nilambur		Elongated	Flattened			
CM			Globular	Depressed	Depressed		
CM 57	Pattambi		Elongated	Rounded	Rounded	Nor bs	Sma
CM 58	Chittur		Oval	Flattened			Sma
CM 59	Pattambi					Rounded	Medium
CM 60	Palayur		Globular	Depressed	Depressed	Nor bs	"
CM 162	Cannanore		Oval	"	"	Rounded	"
CM 163	Cannanore	Local	Oval	Depressed	Flattened	Rounded	Big
CM 64	Malappuram			Flattened	Depressed	"	Medu
CM 65	Palakkad		Heart shaped	Depressed	Pointed	Intermediate	
CM 6	Cannanore		Globular	"	Depressed	Rounded	
CM 171	Irimbalam			"		"	
CM 75	Punnamannu		Flattened	Flattened			
CM 176	mbalam		Globular	Depressed			Big
CM 77	Palghat		Globular	"			
CM 79	Pochampalli			"			Medium
CM 80	Kuzhalmannam		Heart shaped	"	Pointed	Intermediate	Big
CM 82	Vayakunnu		Flat		Depressed	Rounded	Medium
CM 83	mbalam		Elongated	Depressed	Rounded	Nor b	Medium
CM 85			Globular	Flattened	Depressed		
CM 86	Kozhikodepuram		Oval	Flattened	Rounded	Rounded	
CM 88	Vayakurnu			"	"	"	
CM 89	Kozhakamchery		obular	Depressed	Depressed	"	Big
CM 92	Shimoga	Local Farm Assam		"	Flattened		Sma
CM 9			a	Flattened			
CM 9	Vandukkara	Local					Medium
CM 98							Big
CM 20	Pathanamthitta Cheria		Elongate		Depressed		Medium
CM 2 0	Trichur		Heart shape	Depressed	Flattened	Intermediate	Big
CM 2 4	NBPGR New Delhi	Niger Local EC 258 9	om				Medium

A. Assessment of variability and divergence and grouping of genotypes based on D_2 values

The 50 pumpkin genotypes were grown in a randomized block design with 2 replications during June - October 1988. There were 3 pits/genotype /replication. The sacing adopted was 4.0 m x 1.5 m.

Five seeds were sown in each pit and only two healthy plants were retained after thinning. During the cropping period, cultural operations and plant protection measures were adopted as per the package of Practices Recommendations of the Kerala Agricultural University (1986).

1. Plant characters studied

Only the plants in the central pit of each plot were considered for taking observations and for further analysis. The quantitative and quality characters studied were as follows :

(a) Earliness

(i) Days to first female flower anthesis

(ii) Days to first male flower anthesis

(iii) Node at which the first female flower is formed

(iv) Node at which the first fruit is retained

(b) Vegetative

(i) Main vine length (m)

(ii) Nodes on main vine

(iii) Primary branches/plant

(iv) Productive branches/plant

(v) Inter nodal length (cm). Length of 20th, 21st and 22nd internodes were measured and averaged

(c) Flower and fruit characters

(i) Male flowers/plant

(ii) Female flowers/plant

(iii) Sex ratio ($\delta/♀$)

(iv) Fruits/plant

(v) Average fruit weight (kg)

(vi) Fruit length (cm)

(vii) Fruit diameter (cm)

(viii) Flesh thickness (cm)

(ix) Seeds/fruit

(x) 100 seed weight (g)

(xi) Fruit yield/plant (kg)

(d) Quality characters of fruit

(i) Carotene content (μ g/100 g). Carotene content of fresh fruit flesh was estimated using spectronic 20 spectrophotometer after extracting the carotene with 1:1 mixture of Petroleum etherand Acetone (A.O.A.C. 1960)

(ii) Iron content (mg/100 g). Iron content of dired fruit was estimated by Ortho phenanthroline-red ferrous complex

method using spectronic 20 spectrophotometer (Jackson, 1973).

The fruit characters and quality characters were recorded from the first mature fruit.

2. Statistical analysis

Analysis of variance for randomized block design in respect of the various characters was done as per Panse and Sukhathme(1957). The break up of the total variance is given in Table 2.

(a) Estimation of variability, heritability and genetic advance

Variability existing in the population for various characters was estimated by the method suggested by Burton (1952).
The formulae used were

(i) Genotypic coefficient of variation (g.c.v) =

$$\frac{\text{Genotypic standard deviation}}{\text{Mean of the character under study}} \times 100$$

(ii) Phenotypic coefficient of variation (p.c.v) =

$$\frac{\text{Phenotypic standard deviation}}{\text{Mean of the character under study}} \times 100$$

(iii) Environmental coefficient of variation (e.c.v)=

$$\frac{\text{Environmental standard deviation}}{\text{Mean of the character under study}} \times 100$$

(iv) Standard error or mean =

Table 2. Analysis of variance of the design

Source of variation	df	Mean square observed	Expected
Total	99		
Between replications	1	M_1	
Between genotypes	49	M_2	Error variance + [number of replication x genotypic variance]
Error	49	M_3	Error variance

$$\frac{\text{Environmental standard deviation}}{\sqrt{\text{Number of replications}}}$$

The genotypic, phenotypic and environmental standard deviations were obtained by solving following equations from the respective analysis of variance table for different characters.

M_3 - Error variance

M_2 = Error variance + number of replications x genotypic variances

$$\text{Genotypic variance} = \frac{M_2 - M_3}{\text{Number of replications}}$$

Phenotypic Variance = Genotypic variance + Error variance

(v) Heritability

Heritability in broad sense was estimated by the formula suggested by Burton (1952).

$$h^2 (b) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}}$$

(vi) Expected gentic advance

The expected genetic advance of the available germplasm at 5% intensities of selection was calculated using the formula suggested by Lush (1949) and Johnson et al. (1955) using the constant 'i' as 2.06 as given by Allard (1960).

$GA = h^2 \times \sigma_p \times i$ where,

σ_p refers to phenotypic standard deviation and 'i' intensity of selection.

(b) Assessment of genetic divergence

The genetic distances among 50 genotypes of pumpkin were calculated considering 20 quantitative characters. The method suggested by Mahalanobis (1928) was used to estimate D^2, with x_1, x_2, x_3..... x_p as the multiple measurements available on each individual and d_1, d_2, d_3 ..... d_p as $x_1^{-1} - x_2^{-2} - x_2^{-2}$, ... $x_p^{-1} - x_p^{-2}$, respectively, being the difference in the means of two populations, where superscripts denotes genotypes and suffix denotes characters. Mahalanobis D^2 statistic is defined as

$$pD^2 = b_1 d_1 + b_2 d_2 + \ldots\ldots\ldots + b_p d_p$$

Here, the b value is to be estimated such that the ratio of variance between the population to the variance within the population is maximized. In terms of variances and covariances, the D^2 value is obtained as follows.

$$pD^2 = \sum W^{IJ} (x_I^{-1} - x_I^{-2})(x_J^{-1} - x_J^{-2})$$

Where, W^{IJ} is the I, Jth element of the inverse of the estimated variance covariance matrix.

The square root of D^2 value was calculated to obtain generalized statistical distance between two genotypes.

All the genotypes were grouped into a number of clusters, by the computer oriented interactive algorithm proposed by Suresh (1986) as follows.

(i) The two genotypes having maximum D^2 value between them were identified and they were termed the nuclei of two clusters.

(ii) Each genotype was considered in turn and allocated to the cluster for which its D^2 value with the nucleus genotype was minimum.

(iii) To increase the number of clusters by one, the maximum D^2 within the above two clusters was found and the genotypes having maximum D^2 was considered as the nuclei in addition to the nucleus genotype of the remaining clusters. The genotypes were re assigned as in (ii).

The initial clusters thus obtained was further optimised using the iterative algorithm as described below:

Numbered the genotypes from 1 to 50 where there are '50' genotypes.

Took out genotype No.1 from the cluster to which it was allocated and calculated the average D^2 values between this genotypes and each cluster. Allocated this genotype to the cluster for which the average D^2 value was minimum.

Repeated (b) for all genotypes numbered from 1 to 50 with the clustering obtained in step (c) a second iteration may be started if necessary.

The iterations were continued till two successive iterations ended up with the same configurations of clusters.

To decide on the optimum number of clusters, a graph was drawn with weighted arithematic mean of average intracluster D^2 values against the number of clusters. The point just beyond the maximum curvature was taken as the optimum number of clusters to be formed.

B. Evaluation for resistance/tolerance to mosaic disease

Screening for resistance/tolerance to pumpkin mosaic and yellow vein mosaic viruses was done under natural conditions and artificial inoculation.

1. Screening under natural conditions

Seventy one accessions, including 50 accessions grown for divergence studies were screened for pumpkin mosaic and yellow vein mosaic diseases during June-October 1988. There was severe incidence of mosaic diseases in the evaluation plots as well as in the pumpkin seed production fields of Department of Olericulture.

The trial was laid out in a randomized block design with 2 replications. There were 3 pits/accession/replication with 2 plants/pit. Number of plants affected by pumpkin mosaic and YVM were counted at 15 days internel and rating was done as resistant, tolerant, susceptible and highly susceptible based on the symptoms expressed.

2. Screening under artificial inoculation

Twenty six accessions, exhibited better performance for tolerance to mosaic and yield. They were further grown during December-March (1988-89) in a replicated trial. There were 4 plants/accession/

replication. Artificial induction of mosaic virus was done by sap inoculation in individual plants (Kado, 1972).

In artificial inoculation, the inoculum was prepared by crushing the infected leaf of known weight into a fine pulp by adding one ml. of sterile distilled water for every gram of diseased tissue. The standard sap was strained through cotton wool and was inoculated on cotyledonary leaves of 10 days old test plants, by rubbing gently with cotton and carborandum powder (Umamaheswaran, 1985). After the inoculation, the carborandum power was washed off from the cotyledons with distilled water using a wash bottle.

The plants were observed for symptoms of pumpkin mosaic and yellow vein mosaic.

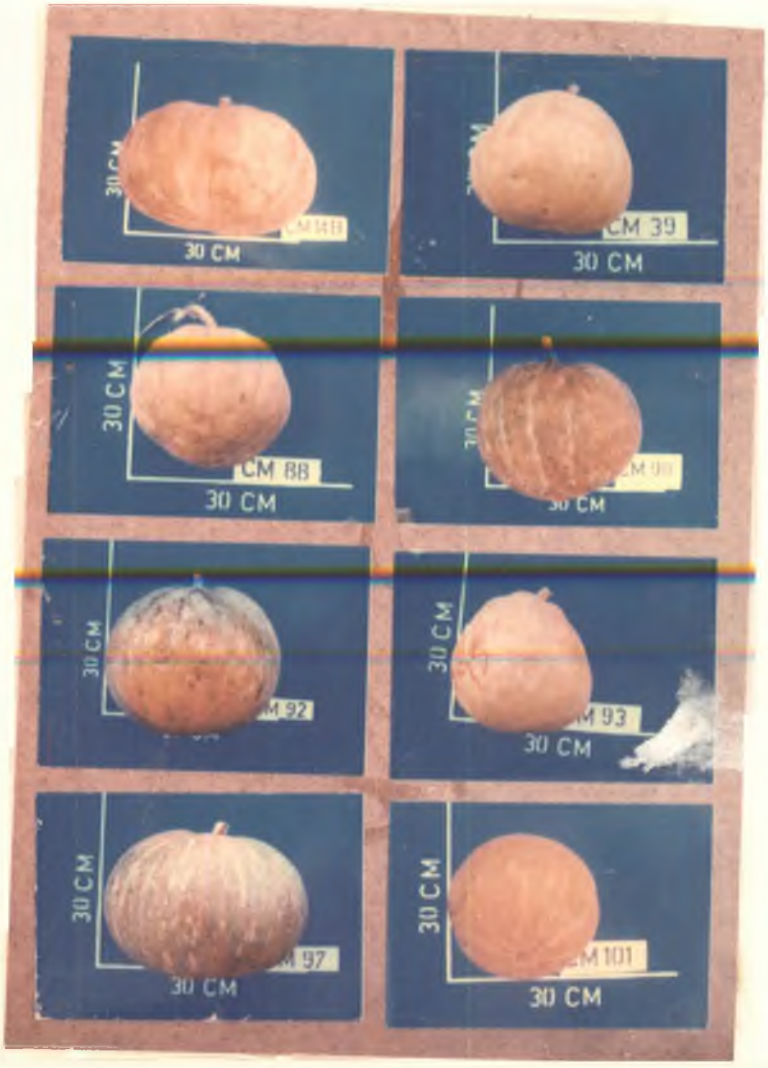


Plate 1. Fruit characters of pumpkin genotypes

Plate 2. Fruit characters of pumpkin genotypes

Plate 3. Fruit characters of pumpkin genotypes

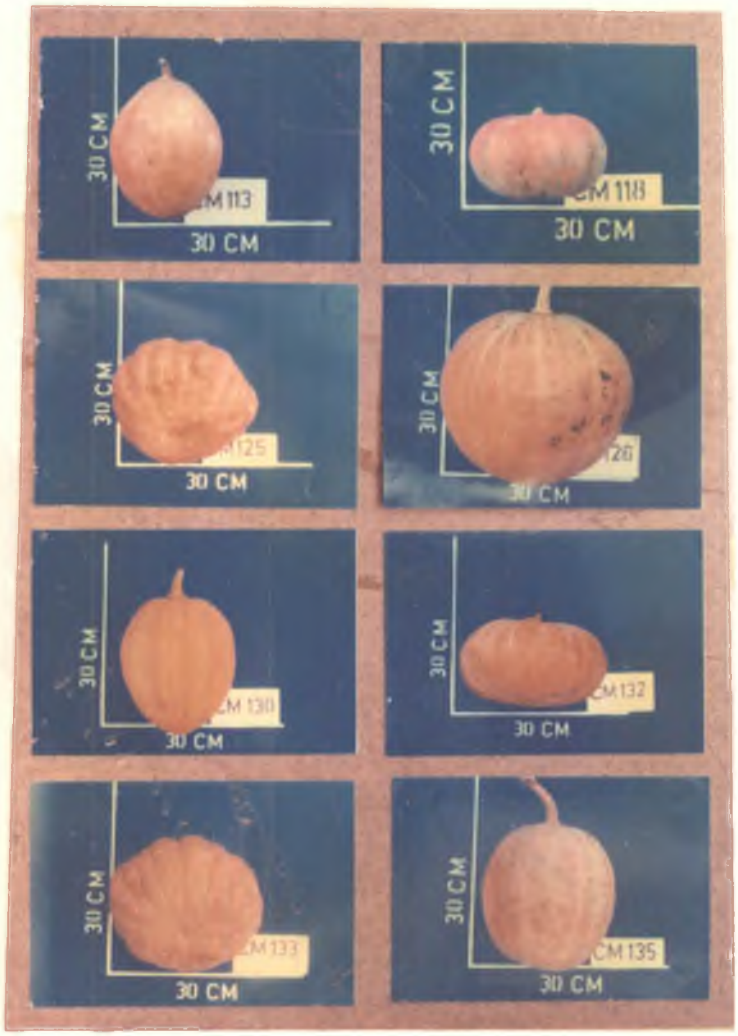


Plate 4. Fruit characters of pumpkin genotypes

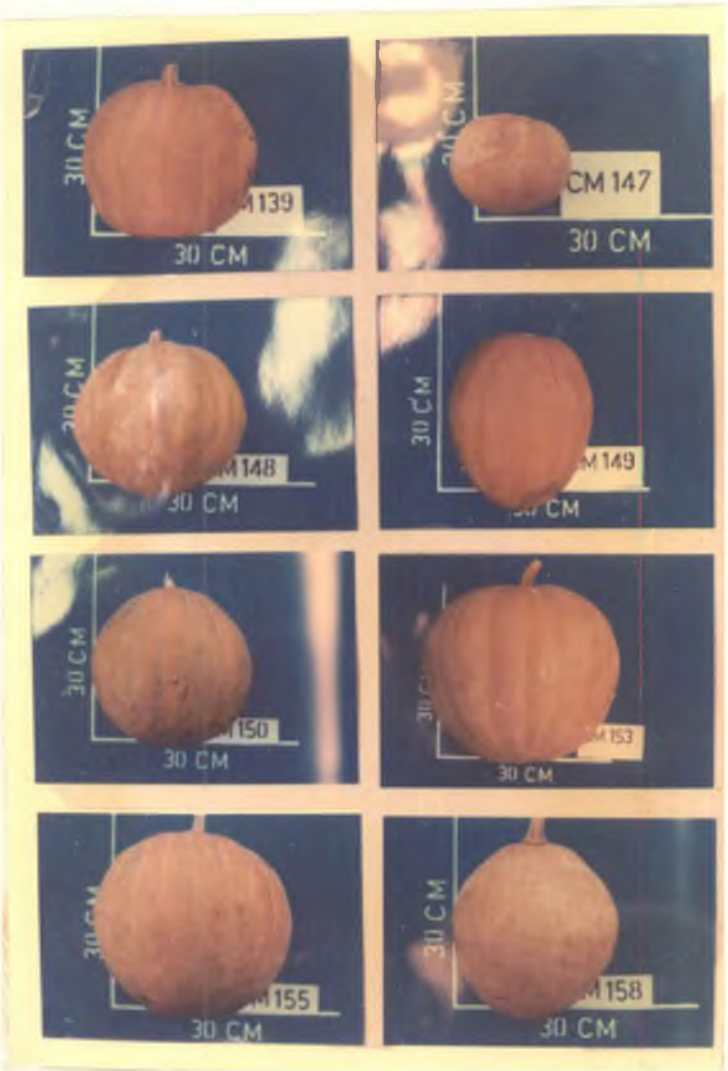


Plate 5. Fruit characters of pumpkin genotypes

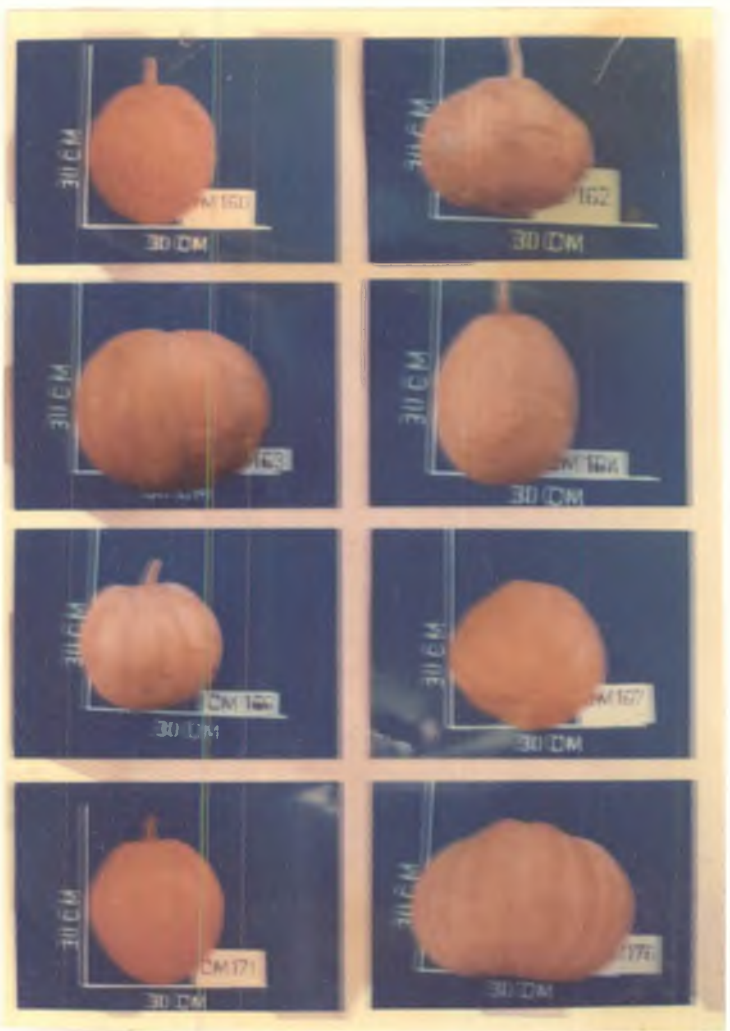


Plate 6. Fruit characters of pumpkin genotypes

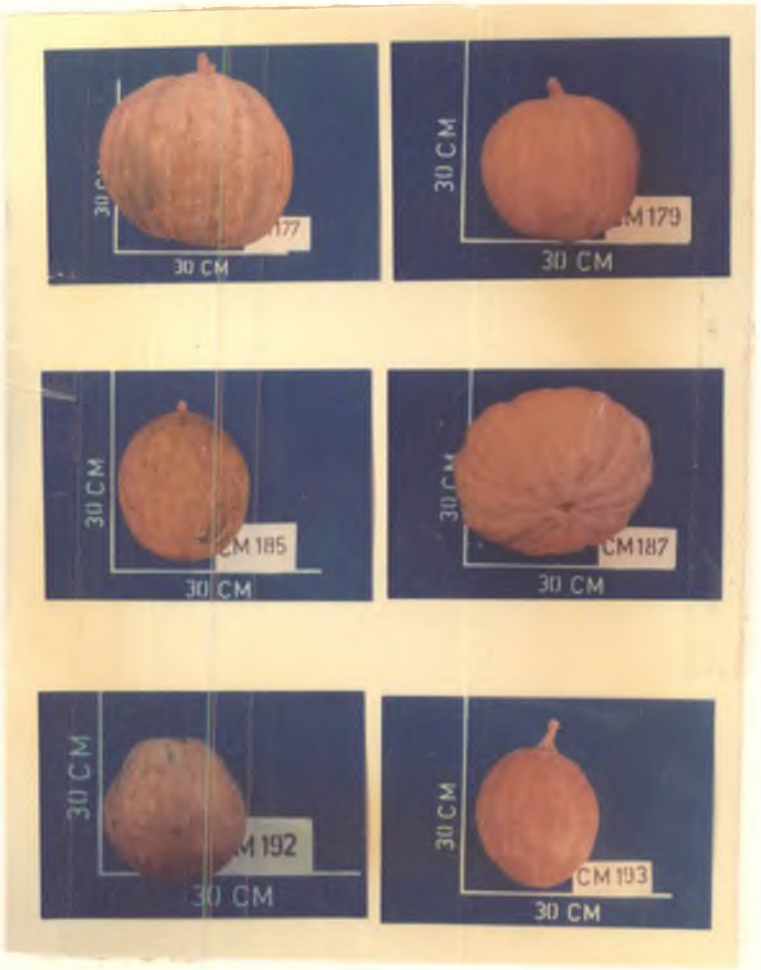


Plate 7. Fruit characters of pumpkin genotypes

Plate 8. Fruit characters of pumpkin genotypes

Results

RESULTS

Results of observations recorded from the present study are presented in the forecoming pages. The experiment comprised of two parts viz.

A. Assessment of variability and divergence and grouping of genotypes based on D^2 values.

B. Evaluation of genotypes for resistance/tolerance to mosaic diseases.

A. Assessment of variability and divergence and grouping of genotypes based on D^2 values.

1. Estimation of genetic variability, heritability and genetic advance.

The fifty pumpkin genotypes grown in a RBD with 2 replications were subjected to variability analysis with respect to 20 quantitative characters (Appendix 2). Partitioning of total variance into its three components viz. treatment, block and error indicated that the genotypes differed significantly for all the characters studied except for yield/plant (Table 3). The 50 genotypes exhibited wide range for most of the characters studied (Table 4). The coefficients of variation, heritability and genetic gain for the 20 characters indicated that the variability existing in the population is mainly genetic (Table 5). Results of individual observation are presented characterwise below.

Table 3. Abstract of analysis of variance for the different characters

Characters	Mean square values		
	Replications df = 1	Genotypes df = 49	Error df = 49
Days to first male flower anthesis	6.75	88.98**	5.70
Days to first female flower anthesis	15.25	164.22**	6.45
Node at which first female flower is formed	1.96	17.16**	0.70
Female flowers/plant	0.02	0.74**	0.18
Male flowers/plant	111.31	356.18**	53.01
Sex ratio (male/female)	15.52	24.90**	5.56
Node at which 1st fruit is retained	0.05	244.70**	8.80
Main vine length (m)	28935.99	78331.10**	22211.10
Nodes on main vine	86.56	567.28**	113.53
Primary branches/plant	4.00	1.37*	0.76
Internodal length (cm)	5.29	17.51**	6.76
Productive branches/plant	0.25	7.52**	2.74
Fruits/plant	0.01	0.73*	0.44
Average fruit weight (kg)	0.02	2.73**	0.78
Fruit length (cm)	3.42	47.78**	6.01
Fruit diameter (cm)	2.57	29.06**	4.70
Flesh thickness (cm)	0.32	1.13**	0.22
Seeds/fruit	1282.00	53174.94**	2777.84
100 seed weight (g)	1.46	18.48**	0.39
Yield/plant (kg)	0.02	10.79	6.80

* Significant at p = 0.05

** Significant at p = 0.01

Table 4. Range of variability for different characters among 50 pumpkin genotypes

Characters	Range				Mean ± SE
	Minimum	Accession No	Maximum	Accession No	
Days to first male flower anthesis	41	CM 192	73.00	CM 165	52.60 + 1.69
Days to first female flower anthesis	41	CM 135	84.50	CM 201	59.17 ± 1.80
Node at which first female flower is formed	15.50	CM 188	29.00	CM 177	22.48 ± 0.59
Female flowers/plant	2.25	14 C, 106 157	5.00	CM 165	3.15 + 0.30
Male flowers/plant	32.50	CM 14 C	92.50	CM 88	54.66 + 5.15
Sex ratio (male/female)	11.93	CM 111	28.19	CM 108	17.64 ± 1.67
Node at which first fruit is retained	24.00	CM 126, CM 189	78.50	CM 136	36.60 + 2.10
Main vine length (m)	6.69	CM 95	13.99	CM 136	926.25 + 105.38
Nodes on main vine	45.00	CM 180	117.00	CM 179	76.71 + 7.53
Primary branches/plant	1.00	CM 125	5.00	CM 193	2.60 + 0.614
Productive branches/plant	1.00	CM 183	10.50	CM 131	4.45 + 1.17
Internodal length (cm)	10.50	CM 108, CM 136	21.50	CM 148, CM 165, CM 185	16.64 + 1.84
Fruits/plant	1.00	CM 108, CM 113, CM 136, CM 157, CM 171, CM 182, CM 185, CM 188	4.0	CM 147	1.87 ± 0.47
Average fruit weight (kg)	0.90	CM 157	6.70	CM 177	2.80 + 0.63
Fruit length (cm)	12.25	CM 88	32.75	CM 154	19.26 ± 1.73
Fruit diameter (cm)	9.75	CM 147	27.00	CM 177	17.53 ± 1.53
Flesh thickness (cm)	1.45	CM 193	4.65	CM 188	2.95 + 0.33
Seeds/fruit	62.50	CM 185	717.00	CM 153	424.84 + 37.27
100 seed weight (g)	5.35	CM 107	18.90	CM 183	10.94 + 0.44
Yield/plant (kg)	0.90	CM 157	13.4	CM 177	5.10 + 1.84
Carotene content (ug/100 g)	4.46	CM 108	215.00	CM 111	38.38
Iron content (mg/100 g)	0.51	CM 135, CM 148	2.74	CM 183	1.24

Table 5. Genotypic (g.c.v.), phenotypic (p.c.v.) and environmental (e.c.v.) coefficient of variation heritability (B.S.), genetic advance and genetic gain (g.g.)

Characters	g.c.v.	p.c.v.	e.c.v.	Heritability (B.S.)	G.A.	G. Gain
Days to first male flower anthesis	12.27	13.08	4.54	.88	12.47	23.70
Days to first female flower anthesis	15.01	15.61	4.29	.92	17.59	29.73
Node at first female flower formed	12.77	13.29	3.71	.92	5.68	25.25
No. female flowers/plant	16.82	21.66	13.65	.60	.85	26.91
No. male flowers/plant	22.53	26.17	13.32	.74	21.83	39.94
Sex ratio	17.63	22.12	13.37	.64	5.11	28.9
Node at which first fruit is retained	29.68	30.76	8.10	.93	21.59	58.98
Main vine length	18.09	24.21	16.09	.56	257.81	27.83
Nodes on main vine	19.64	24.05	13.89	.67	25.33	33.02
Primary branches/plant	21.28	39.62	33.42	.29	6.12	23.54
Internodal length	13.93	20.94	15.62	.44	3.18	19.10
Productive branches/plant	34.72	50.89	37.20	.47	2.17	48.81
Fruits/plant	20.44	40.89	35.41	.25	.39	21.05
Average fruit weight	35.25	47.37	31.64	.55	1.51	54.03
Fruit length	23.74	26.93	12.73	.78	8.29	43.09
Fruit diameter	19.91	23.44	12.37	.72	6.11	34.84
Flesh thickness	22.87	27.87	15.92	.67	1.14	38.67
Seeds/fruit	37.37	39.37	12.41	.90	310.35	73.05
100 seed weight	27.50	28.09	5.71	.96	6.07	55.46
Yield/plant	27.71	58.17	51.15	.23	1.39	27.20

(a) Days to first male flower anthesis

Days to first male flower anthesis had a range of 41 to 73 days with a mean of 52.6. CM 192 was the earliest accession for days to first male flower anthesis (41 days), followed by CM 135 (41.5 days). CM 165 produced male flowers very late (73 days).

The genotypic coefficient of variation (g.c.v) and phenotypic coefficient of variation (p.c.v) of 12.27 and 13.08 respectively for days to first male flower anthesis were the lowest among the 20 characters studied. Though the percentage of broad sense heritability was high (88%), the genetic advance expressed as percentage of mean (genetic gain) was low (23.70%).

(b) Days to first female flower anthesis

Earliness as indicated by days to first female flower anthesis ranged from 41 days in CM 135 to 84.5 days in CM 201. Accession CM 14 B, a selection from CM 14 which has been released as 'Ambili', and CM 188 also flowered early (435 days). Mean value for days to flowering was 59.17 days.

The coefficients of variation was in general low as indicated by low g.c.v. and p.c.v. (15.01 and 15.61 respectively). This also recorded a high heritability of 92.4%. But the genetic advance expressed as percentage of mean was moderate (29.73%).

(c) Node at which the first female flower is formed

On an average the first female flower was born on the 22nd node among the 50 genotypes though the values ranged from 15.50 in CM 188 to 29.00 in CM 177. Genotypes CM 14B and CM 113 also recorded low values (17.5 and 18.5 respectively).

Node at which the first female flower is formed recorded the second lowest values of g.c.v. (12.77) and p.c.v. (13.29) among the 20 characters. It also recorded a high heritability of 92.2% and a genetic gain of 25.25%.

(d) Female flowers/plant

Mean number of female flowers was recorded as 3.15 with a range of 2.25 to 5.0. Minimum number of 2.25 was recorded by CM 14 C, CM 106 and CM 157 and the maximum of 5.0 by CM 165. CM 165 was closely followed by CM 147 and CM 177 (4.5 each).

G.c.v. and p.c.v. recorded were 16.82 and 21.66 respectively. Female flowers/plant had a medium heritability of 60.00% and a genetic gain of 26.91%.

(e) Male flowers/plant

Male flowers/plant had a wide range of 32.50 in CM 14 C to 92.50 in CM 88. The 50 genotypes studied gave a mean value of 54.66. Genotypes CM 106 and CM 180 also produced less number of female flowers (35.83 and 40.25 respectively).

The coefficients of variation were in general low (g.c.v.-22.52; p.c.v.-26.17). Male flowers/plant had a heritability of 74.1% and a medium value of genetic gain (39.94%).

(f) Sex ratio (Male/female)

Range for sex ratio was from 11.93 (CM 111) to 28.19 in CM 108 with a mean value of 17.64. Other genotypes with low values were CM 165 (12.41) and CM 102 (12.92).

Sex ratio recorded low values of coefficients of variation (g.c.v. 17.63, p.c.v. 22.12), a medium heritability of 63.5% and a low genetic gain of 28.94%.

(g) Node at which first fruit is retained

Node at which first fruit is retained ranged from 24.0 (CM 126 and CM 189) to 78.5 in CM 136. On an average the first fruit was retained on 36th node in the 50 genotypes studied.

Node at which the first fruit is retained estimated g.c.v. of 29.68 and p.c.v. of 30.76. It recorded the second highest heritability (93.1%) and a high genetic gain (58.98%).

(h) Main vine length (m)

Length of main vine ranged from 6.78 m (CM 95) to 13.98 m (CM 136). Mean was recorded as 9.26 m. Genotypes CM 201 and CM 93 had a vine length of 13.6[illegible] and 12.35 m respectively.

Coefficients of variation estimated were low (g.c.v. = 18.09; p.c.v. 24.21). It also recorded a moderate heritability (55.8%) and genetic gain (27.83%).

(i) Nodes on main vine

The number of nodes on main vine had a wide range from 45 in CM 180 to 117 in CM 179 with a mean value of 76.71. Genotypes CM 185 and CM 106 had low number of nodes on main vine (48.0 and 52.0 respectively).

G.c.v. and p.c.v. for nodes on main vine were 19.64 and 24.05 respectively. It also recorded a medium heritability (66.6%) and a genetic gain of 33.02%.

(j) Primary branches/plant

Average number of primary branches/plant for the 50 accessions was 2.6 and the values ranged from 1.0 in CM 125 to 5.0 in CM 193. The genotypes CM 106, 157, 177 and 176 produced four primary branches each.

The coefficients of variation were 21.28 (g.c.v) and 89.62 (p.c.v). The third lowest heritability value of 28.8% was recorded for this trait.

(k) Internodal length (cm)

Internodal length ranged from 10.5 cm to 21.5 cm. The genotypes CM 108 and CM 136 recorded 10.5 cm each. The highest value was for genotypes CM 148, CM 165 and CM 185. The mean length was 16.64 cm among the 50 genotypes studied.

The g.c.v. and p.c.v. were found to be low (13.93 and 20.94 respectively). Heritability was also low (44.8%). It also recorded the lowest genetic gain (19.10%).

(l) Productive branches/plant

Productive branches/plant ranged from 1.0 in CM 183 to 10.5 in CM 131 and the mean was 4.45 among the 50 genotypes. The next highest value was recorded by CM 107 and CM 176 (9.5 and 9.0 respectively).

The coefficients of variation recorded were 34.72 (g.c.v) and 50.89 (p.c.v). It also recorded a low heritability of 46.60% and a high genetic gain (48.81%).

(m) Fruits/plant

Fruits/plant showed a mean value of 1.87 with a range from 1.0 to 4.0. The genotypes CM 108, CM 113, CM 136, CM 157, CM 171, CM 182, CM 185 and CM 188 produced only one fruit each. The genotypes CM 147 produced 4.0 fruits/plant. CM 95 and CM 135 recorded the next highest value of 3.0.

G.c.v. and p.c.v. for fruits/plant were recorded as 20.44 and 40.89 respectively. It recorded the second lowest heritability (25%) among the characters studied. It also recorded a genetic gain of 21.05%.

(n) Average fruit weight (kg)

Average fruit weight ranged from 0.9 kg (CM 157) to 6.7 kg (CM 177) with a mean of 2.80 kg. The average fruit weight was also high in CM 153 (5.9 kg) and CM 171 (5.1 kg).

Coefficients of variation for average fruit weight were 35.25 and 47.37 respectively for g.c.v. and p.c.v. It recorded a medium heritability (55.4%) and a high genetic gain of 54.03%.

(o) Fruit length (cm)

Length of the fruit varied from 12.25 cm in CM 188 to 32.75 cm in CM 154, the mean value was only 19.26 cm among the genotypes considered. Next longest fruit was observed in CM 183 (23 cm). CM 183 had a fruit length of 23 cm.

G.c.v. and p.c.v. for fruit length were 23.74 and 26.93 respectively. Though this trait had only a medium heritability (77.7%), the genetic gain recorded was high (43.09%).

(p) Fruit diameter (cm)

Mean for fruit diameter was 17.53 cm, with a range of 9.75 cm (CM 147) to 27.0 cm (CM 177). Genotypes CM 153 (25 cm) and CM 14 B (24.5) also recorded high values.

Coefficients of variation for diameter of fruit were low (g.c.v. 19.91; p.c.v. 23.44). It also recorded a moderate value of heritability (72.1%) and genetic gain (34.84%).

(q) Flesh thickness (cm)

The fifty genotypes had a mean flesh thickness of 2.95 cm and it ranged from 1.45 to 4.65 cm. Flesh thickness was maximum in CM 188 (4.65 cm), followed by CM 175 (4.5 cm) and CM 109 (4.18 cm) and was minimum in CM 193 (1.45 cm).

The genotypic and phenotypic coefficients of variation were 22.87 and 27.87 respectively. Flesh thickness had moderate values of heritability (67.4%) and genetic gain (38.67%).

(r) Seeds/fruit

Though the mean number for seeds/fruit was 424.84, the number ranged from 62.5 in CM 185 to 717 in CM 153 among the 50 genotypes studied.

Seeds/fruit recorded the maximum value of g.c.v. (37.37). It also recorded a high value of heritability (90.1%) and the highest genetic gain of 73.05%.

(s) Hundred seed weight (g)

Hundred seed weight ranged from 5.35 g in CM 107 to 18.9 g CM 183 and the mean was 10.94 g. The genotypes CM 89 and CM 160 also recorded high values (16.8 g and 15.13 g respectively).

The g.c.v. for 100 seed weight was found to be comparatively high (27.50) and the p.c.v. was 28.09. It also recorded the highest

value of heritability (95.9%) along with a high genetic gain (55.46%).

(t) Yield/plant (kg)

Yield/plant ranged from 0.9 kg in CM 157 to 13.4 kg in CM 177 with a mean of 5.10 kg. The genotypes CM 153 and CM 189 also recorded high values (9.7 and 9.0 kg respectively).

Yield/plant recorded maximum value of p.c.v. (58.17) and but the g.c.v. was only 27.71. Heritability for yield/plant recorded the lowest value (22.7%), among the characters studied. It also recorded low genetic gain of 27.20%.

(u) Carotene content (µg/100 g)

Among the 50 genotypes studied the carotene content ranged from 4.46 µg/100 g in CM 108 to 215 µg/100 g in CM 111. It had a mean value of 38.38 µg/100 g. The genotypes CM 192 and CM 91 also recorded high values of 123.92 µg and 120.4 µg respectively.

(v) Iron content (mg/100 g)

Iron content ranged from 0.51 to 2.74 mg with a mean value of 1.24 mg/100 g. Lowest iron content was recorded by CM 135 and CM 148 (1.24 mg). The high values were recorded by CM 183, CM 162 and CM 104 (2.74 mg, 2.61 mg and 2.36 mg respectively).

2. Assessment of genetic divergence and grouping of genotypes

The fifty pumpkin genotypes included in the study were grouped into 5 clusters. Clusters I, II, III, IV and V comprised of 2, 7, 9, 12 and 20 pumpkin genotypes respectively (Table 6).

The intra and intercluster D^2 and D values of the 5 clusters worked out have been presented in Tables 7 and 8 respectively. From the tables it could be observed that the intracluster D^2 values were lower than the intercluster D^2 values.

The intracluster distances in the 5 clusters ranged from 28.90 in cluster 1 to 39.17 in cluster III. The remaining intracluster D^2 values were in the order of 30.04, 35.29 and 35.80 in clusters IV, V and II respectively. Cluster I was found to show the maximum average intercluster distances with any other clusters and it was the cluster having maximum distance in 3 out of the 4 combinations it could make (D^2 values 224.48 with cluster II, 128.56 with cluster III and 95.85 with cluster V). Cluster 5 which comprised of 20 genotypes showed the lowest intercluster distance with other clusters (D^2 values 45.28 with cluster III and 48.63 with cluster IV).

Results pertaining to the extremes in means of genotypes and overall mean for different characters of clusters I, II, III, IV and V are presented in Tables 9, 10, 11, 12 and 13 respectively.

The results of means and extremes of means in each cluster are furnished characterwise below :

Table 6. Details of pumpkin genotypes constituting different clusters

Cluster No.	Cultivars included	Total Number
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 14A, CM 14B, 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 7. 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

Table 8. Average intra and inter cluster D values of five clusters of pumpkin considering 20 characters

Cluster No.	I	II	III	IV	V
I	5.38				
II	14.92	5.98			
III	11.34	8.00	6.26		
IV	6.99	11.90	8.68	5.48	
V	9.79	8.69	6.73	6.97	5.86

Table 9. Extremes and mean of genotypes in Cluster I

Characters	Maximum	Accession No.	Minimum	Accession No.	Mean
Days to first male folower anthesis	53.00	CM 136	42.50	CM 188	47.75
Days to first female flower anthesis	58.00	CM 136	43.50	CM 188	51.00
Node at first female flower is formed	23.00	CM 136	15.50	CM 188	19.25
Female flowers/plant	3.75	CM 136	3.0	CM 188	3.38
Male flowers/plant	89.00	CM 136	46.50	CM 188	67.75
Sex ratio (male/female)	23.79	CM 136	15.50	CM 188	19.65
Node at which first fruit is retained	78.50	CM 136	56.00	CM 188	67.25
Main vine length (m)	13.99	CM 136	8.39	CM 188	11.19
Nodes on main vine	116.00	CM 136	75.50	CM 188	95.75
Primary branches/ plant	8.0	CM 136	3.0	CM 136	3.0
		CM 188		CM 188	
Internodal length (cm)	12.25	CM 188	10.50	CM 136	11.38
Productive branches/ plant	4.0	CM 136	2.50	CM 188	3.25
Fruits/plant	1.0	CM 136	1.00	CM 136	1.00
		CM 188		CM 188	
Average fruit weight (kg)	3.3	CM 188	1.3	CM 136	2.30
Fruit length (cm)	20.25	CM 188	16.5	CM 136	18.38
Fruit diameter (cm)	16.25	CM 188	13.25	CM 136	14.75
Flesh thickness (cm)	4.65	CM 188	1.8	CM 136	3.28
Seeds/fruit	379.00	CM 136	186.5	CM 188	282.75
100 seed weight (g)	11.2	CM 136	8.2	CM 188	9.70
Yield/ plant (kg)	3.3	CM 188	1.3	CM 136	2.30

Table 10. Extremes and mean of genotypes in Cluster II

Characters	Maximum	Acce-ssion No.	Minimum	Acce-ssion No.	Mean
Days to first male flower anthesis	61.5	CM 106	43.0	CM 14C	51.21
Days to first female flower anthesis	74	CM 147	45 5	CM 14C	62.14
Node at first female flower is formed	26.0	CM 147	20.5	CM 14C	20.07
Female flowers/plant	4.5	CM 147	2.25	CM 14C	3.07
				CM 106	
Male flowers/ plant	65.00	CM 147	32.5	CM 14C	50.30
Sex ratio (Male/ female)	20.65	CM 147	14.46	CM 14C	14.41
Node at which first fruit is retained	55.00	CM 147	26.50	CM 14C	33.21
Main vine length (m)	10.49	CM 171	5.33	CM 14C	7.91
Nodes on main vine	103.00	CM 147	52.00	CM 106	70.43
Primary branches/ plant	4.0	CM 106	1.50	CM 104	2.57
Internodal length (cm)	17.5	CM 147	12.75	CM 106	15.57
Productive branches/ plant	5.0	CM 147	2.5	CM 106	3.79
Fruits/plant	4.0	CM 147	1.0	CM 171	1.80
Average fruit weight (kg)	4.8	CM 126	1.2	CM 147	3.17
Fruit length (cm)	26.65	CM 106	13.50	CM 147	19.75
Fruit diameter (cm)	21.75	CM 14C	9.75	CM 147	17.52
Flesh thickness (cm)	3.80	CM 171	2.05	CM 106	2.74
Seeds/fruit	661.5	CM 126	313.5	CM 147	545.7
100 seed weight (g)	12.2	CM 126	5.4	CM 147	9.04
Yield/plant (kg)	7.3	CM 126	2.4	CM 106	4.77

Table 11. Extremes and mean of genotypes in Cluster III

Characters	Maximum	Accession No.	Minimum	Accession No.	Mean
Days to first male flower anthesis	73.0	CM 165	45	CM 185	57.16
Days to 1st female flower anthesis	84.5	CM 201	50.00	CM 175	65.66
Node at first female flowe is formed	26.0	CM 201	20.00	CM 153 CM 185	22.17
Fema e flower/plant	5.0	CM 165	2.25	CM 154	3.29
Male flowers/plant	92.50	CM 88	42.17	CM 157	59.94
Sex ratio (Male/female)	21.83	CM 201	12.42	CM 165	17 16
Node at which first fruit s retained	57.50	CM 201	30.00	CM 185	42.16
Main vine length (m)	13.65	CM 165	7.74	CM 157	10.18
Nodes on main vine	110.00	CM 201	48.00	CM 185	80 83
Primary branches/plant	4.00	CM 157	1.50	CM 153	2.66
Internodal length (cm)	21.50	CM 165 CM 183	14.50	CM 157	17.58
Productive branches/plant	6.50	CM 201	2.00	CM 175	4.05
Fruits/plant	2.50	CM 154	1.00	CM 157	1.82
Average fruit weight (kg)	5.90	CM 153	0.90	CM 157	2.84
Fruit length (cm)	32.75	CM 154	12.25	CM 88	20.80
Fruit diameter (cm)	25.00	CM 153	10.35	CM 157	16.84
Flesh thickness (cm)	4.00	CM 153	1.90	CM 157	3.14
Seeds/fruit	717.50	CM 153	102.50	CM 201	345.50
100 seed weight (kg)	13.10	CM 153	6.45	CM 88	9.76
Yield/plant (kg)	9.70	CM 153	0.90	CM 157	5.10

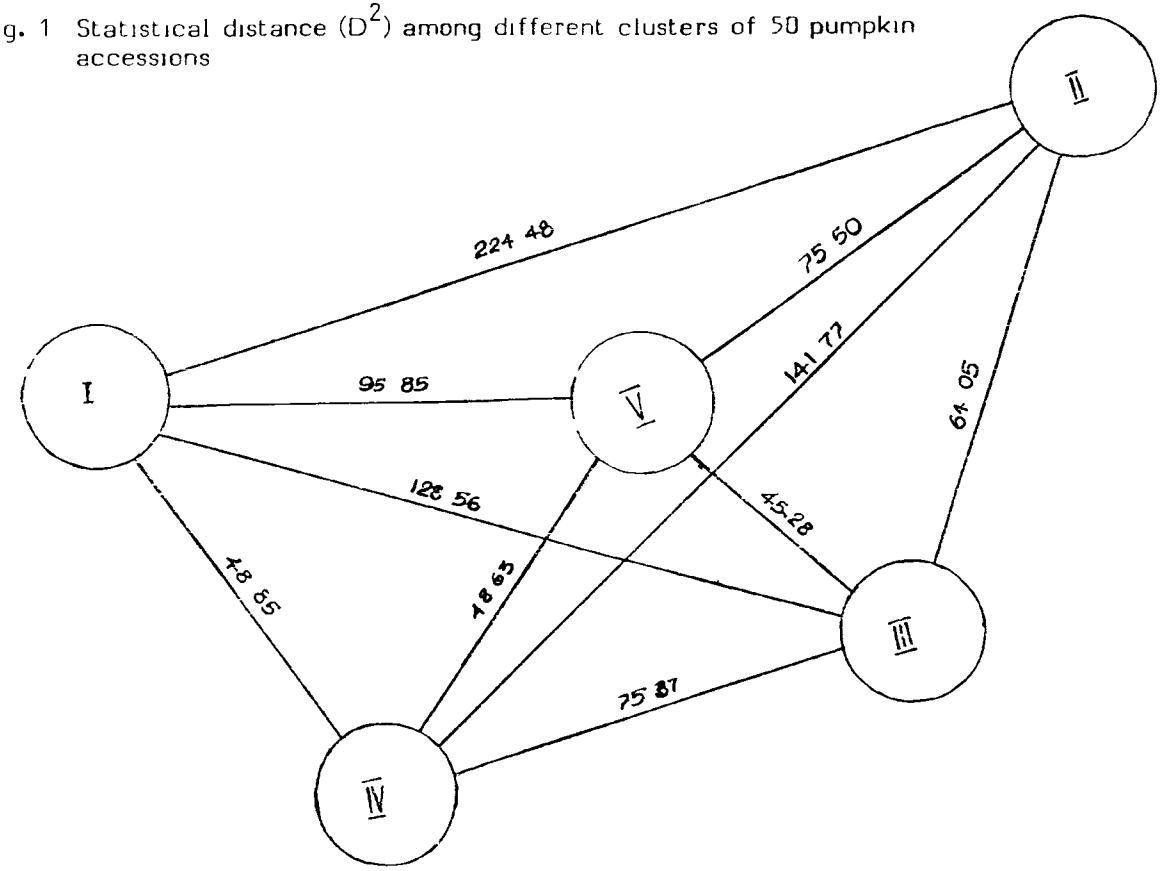
Table 12. Extremes and mean of genotypes in Cluster IV

Characters	Maximum	Accession No.	Minimum	Accession No.	Mean
Days to first male flower anthesis	57.0	CM 183	41.00	CM 192	48.38
Days to first female flower anthesis	63.5	CM 183	41.00	CM 135	52.00
Node at first female flower is formed	28.00	CM 103	17.50	CM 14B	21.83
Female flowers/plant	4.5	CM 103	2.50	CM 14B	3 20
Male flowers/plant	63.25	CM 183	41.75	CM 111	48.31
Sex ratio (male/female)	23.13	CM 103	11.93	CM 111	16.55
Node at which first fruit is retained	44.0	CM 183	24.00	CM 189	33.50
Main vine length (m)	11.79	CM 179	7.17	CM 14A	9.26
Nodes on main vine	117.0	CM 179	57.0	CM 189	73.50
Primary branches/plant	3.0	CM 111 CM 149	2.0	CM14A,CM14B, CM102,CM135, CM179,CM183, CM 192	2.30
Internodal length (cm)	21.0	CM 103	11.50	CM 192	16.90
Productive branches/plant	7.0	CM 139	1.00	CM 183	4.07
Fruits/plant	4.0	CM 149	1.50	CM179,CM183, CM 192	2.16
Average fruit weight (kg)	4.50	CM 189	1.55	CM 135	2.66
Fruit length (cm)	26.5	CM 183	11.50	CM 179	20.00
Fruit diameter (cm)	24.5	CM 14B	11.75	CM 111	17.27
Flesh thickness (cm)	4.0	CM 103	2.15	CM 135, CM 139	2.81
Seeds/fruit	573.0	CM 14B	106.00	CM 183	332.00
100 seed weight (g)	18.90	CM 189	10.90	CM 135	11.84
Yield/plant (kg)	9.0	CM 189	2.50	CM 192	5.33

Table 13. Extremes and mean of genotypes in Cluster V

Characters	Maximum	Accession No.	Minimum	Accession No.	Mean
Days to first male flower anthesis	62.5	CM 133	45.5	CM 180	54.05
Days to first female flower anthesis	68.5	CM 107	40.5	CM 193	60.33
Node at first female flower is formed	29.0	CM 163	18.5	CM 113	23.60
Female flowers/plant	4.50	CM 163	2.42	CM 93	3.14
Male flowers/plant	84.00	CM 162	39.00	CM 182	57.01
Sex ratio (male/female)	29.19	CM 108	14.27	CM 193	18.38
Node at which first fruit is retained	44.50	CM 176	27.00	CM 108	34.94
Main vine length (m)	12.35	CM 93	6.69	CM 95	865.30
Node on main vine	87.00	CM 125	45.00	CM 180	72.00
Primary branches/plant	4.00	CM 177	1.00	CM 125	2.70
Internodal length (cm)	21.50	CM 148	10.50	CM 108	16.96
Productive branches/plant	10.50	CM 131	2.00	CM 95	5.23
Fruit /plant	3.00	CM 95	1.00	CM 108, CM 113, CM 182	1.90
Average fruit weight (kg)	6.70	CM 177	1.50	CM 193	2.87
Fruit length (cm)	26.25	CM 131	13.25	CM 133	18.71
Fruit diameter (cm)	27.00	CM 177	12.30	CM 107	18.26
Flesh thickness (cm)	4.18	CM 109	1.45	CM 193	2.99
Seeds/fruit	678.00	CM 177	285.00	CM 193	469.83
100 seed weight (g)	16.80	CM 89	5.35	CM 107	11.31
Yield/plant (kg)	13.40	CM 177	2.60	CM 193	5.18

Fig. 1 Statistical distance (D^2) among different clusters of 50 pumpkin accessions



(a) Days to first male flower anthesis

The two genotypes CM 136 and CM 188 in cluster I produced first male flower 53 and 42.5 days after sowing with a cluster mean of 47.75.

The maximum and minimum values for the trait in cluster II were 51.5 (CM 106) and 43.0 (CM 14-C) with a cluster mean of 51.21. The corresponding values in cluster III were 73.0 (CM 165), 45.0 (CM 185) and 57.16 and that in cluster IV were 57.0 (CM 183), 41.0 (CM 192) and 48.38 respectively.

Days to first male flower anthesis for the 20 genotypes included in cluster V ranged from 62.5 (CM 133) to 45.5 (CM 180) with a cluster mean of 54.05.

Maximum mean value for days to first male flower anthesis was shown by cluster III and minimum by cluster I.

(b) Days to first female flower anthesis

Mean value for the two genotypes included in cluster I was 51.0. CM 14-C produced female flowers very early (45.5 days) and CM 147 was very late (74 days) among the 7 genotypes in cluster II and the cluster mean was 62.14.

CM 201 recorded the maximum value (84.5) and CM 175 showed minimum value of 50 in cluster III which had a cluster mean of 65.66. The corresponding values in cluster IV were 63.5 (CM 183), 41.0 (CM 13)

and 52 and that in cluster V were 68.5 in CM 107, 45.5 in CM 193 and 60.33 respectively.

Minimum mean value for days to first female flower anthesis was exhibited in cluster I and maximum in cluster III.

(c) Node at which first female flower is formed

Mean value for the trait ranged from 15.5 to 23.0 in cluster I, 20.5 to 26.0 in cluster II, 20.0 to 26.0 in cluster III, 17.5 to 28.0 in cluster IV and 18.5 to 29 in cluster V.

Maximum mean value for node at which the first female flower is formed was shown by cluster V (23.6) and minimum by cluster I (19.25).

(d) Female flowers/plant

In cluster I number of female flowers produced by the two genotypes were more or less equal. In cluster II maximum female flowers were born in CM 147 (4.5) and minimum in CM 14 C and CM 106 (2.25) and the corresponding values were 5.0 (CM 165) and 2.25 (CM 154) respectively. In cluster IV and V the maximum value for number of female flowers was same (4.5).

Out of the 5 clusters, cluster I had the maximum female flowers and cluster II, the minimum

(e) Male flowers/plant

Cluster I showed the maximum mean value (67.75) followed by cluster III (59.94) and cluster V (57.01) and cluster IV had the minimum mean value (48.31).

(f) Sex ratio (male/female)

The highest cluster mean of 19.65 was observed in cluster I which was closely followed by cluster V (18.38). The mean of male to female ratio was minimum in cluster II (14.41).

(g) Node at which first fruit is retained

The first fruit was retained at the lowest node in cluster II (33.21) which was on par with cluster IV. In cluster II the maximum mean value of 55.00 was observed in the genotype CM 147 and minimum in CM 14-C (14.46). In cluster IV the mean values ranged from 24.0 in CM 189 to 44.0 in CM 183.

(h) Main vine (m)

The mean values for length of main vine for the two genotypes in cluster I were 13.99 m (CM 136) and 8.39 m (CM 188). A range from 5.33 (CM 14 C) to 10.49 m (CM 171) was noticed in cluster II.

The corresponding values were 7.74 and 13.65 m in cluster III and 7.17 and 11.79 m in cluster IV.

Among the five clusters maximum mean value for length of main vine was for cluster I (11.19 m) and the minimum was for cluster II (7.91 m).

(i) Nodes on main vine

The highest cluster mean of 95.75 was recorded by cluster I (95.75) and lowest by cluster II (70.43). The remaining clusters viz. cluster III, IV and V had cluster means of 80.83, 73.50 and 72.0 respectively.

(j) Primary branches/plant

Primary branches/plant had its maximum mean value in cluster I (3.0) and cluster IV had the minimum mean (2.30). The cluster mean in the remaining 3 clusters were in between these extremes.

(k) Internodal length (cm)

Cluster III had the highest cluster mean value of 17.58 m which was closely followed by cluster V (16.96 m) and cluster IV (16.90 m) The cluster mean was minimum in cluster I (11.38 m).

(l) Productive branches/plant

Cluster V had the maximum mean values (5.23) for productive branches/plant and the minimum value was shown by cluster I (3.25) The means of genotypes included in clusters III and IV were on par.

The productive branches/plant of the 20 pumpkin genotypes had a very wide range (2.0 - 10.5). The maximum productive branches were born in the genotype C M 131.

(m) Fruits/plant

Both the genotypes in cluster I produced only a single fruit/plant. In cluster II the trait ranged from 1.0 in CM 171 to 4.0 in CM 147. Among the 9 genotypes in cluster III maximum fruits/plant was only 2.5. In cluster IV the maximum number of fruits (4.0) was borne in CM 149 and minimum of 1.5 in three genotypes viz. CM 179, CM 183 and CM 192. In cluster V maximum fruits were produced by CM 95.

The cluster mean for fruits/plant was maximum in cluster IV (2.16) and minimum in cluster I (1.0). The remaining three clusters had more or less equal cluster means.

(n) Average fruit weight

The two genotypes included in cluster I had an average fruit weight of 3.3 kg (CM 188) and 1.3 kg (CM 186). The average fruit

weight for the 7 genotypes included in cluster II had a wide range of 1.2 to 4.8 kg. In cluster III also a wide range of 0.9 to 5.90 kg was observed. In cluster III the fruit weight was maximum in CM 153. The maximum and minimum values were 4.5 (CM 189) and 1.55 kg (CM 135) in cluster IV and 6.70 (CM 177) and 1.50 kg (CM 193) in cluster V

Among the five clusters, cluster II showed maximum mean value (3.17 kg) and cluster I had minimum mean value (2.3 kg).

(o) Fruit length (cm)

Among the five clusters, cluster III had the maximum mean value (20.80 cm) and cluster I had the minimum mean value (18.38 cm) In cluster III the genotype CM 154 had the longest fruit (32.75 cm) and the fruit length was minimum in CM 88 (12.25 cm). Length of fruit in cluster IV ranged from 11.50 cm in CM 179 to 26.50 cm in CM 183 with a cluster mean of 20.00 cm which ranked second in length of fruit.

(p) Fruit diameter (cm)

Among the five clusters maximum cluster mean of 18.26 cm was shown by cluster V and minimum of 14.75 cm by cluster I. Cluster V was followed by cluster II (17.52 cm) and cluster IV (17.27 cm).

A range from 12.30 (CM 107) to 27.00 cm (CM 177) was noticed in cluster V and that in cluster II was from 9.75 (CM 147) to 21.75 cm (CM 14-C).

(q) Flesh thickness (cm)

The highest cluster mean of 3.28 cm was recorded in cluster I and was lowest in cluster II (2.74 cm). Cluster III had a mean flesh thickness of 3.14 cm.

The two genotypes comprised in cluster I, CM 188 and CM 138 had 4.65 cm and 1.8 cm respectively. The maximum and minimum values were 3.80 (CM 171) and 2.05 cm in cluster II, 4.0 (CM 153) and 1.90 cm in cluster III, 4.0 (CM 103) and 2.15 cm in cluster IV and 4.18 (CM 109) and 1.45 cm in cluster V respectively.

(r) Seeds/fruit

Among the five clusters, cluster II recorded the maximum mean value 545.7 followed by cluster V (469.83) and cluster III (345.9). The lowest mean was for cluster I (282.75).

(s) 100 seed weight (g)

Cluster IV showed the highest cluster mean (11.84 g) and cluster II the lowest (9.04 g). The 12 pumpkin genotypes included in cluster IV

had a range of 10.90 (CM 135) - 18.90 g (CM 189). In cluster V the maximum value of 16.8 gm was recorded for CM 89 and the minimum value of 5.35 g in CM 107.

(t) Yield/plant (kg)

The two pumpkin genotypes, CM 188 and CM 136 constituting cluster I showed wide variation in yield - 3.3 and 1.3 kg respectively. In cluster II maximum yield was obtained in CM 126 (7.3 kg) and minimum in CM 106 (2.4 kg). The range for the trait in cluster III was from 6.45 in CM 88 to 13.10 kg in CM 153. The highest and lowest yield was in CM 189 (9.0 kg) and CM 192 (2.5 kg) in cluster IV and CM 177 (13.4 kg) and CM 193 (2.60 kg) in cluster V respectively.

Out of the five clusters maximum cluster mean was for cluster IV (5.33 kg) and minimum was for cluster I (203 kg). Clusters V and III had mean values 5.18 and 5.10 respectively.

B. Evaluation of genotypes for resistance/tolerance to mosaic diseases

The seventy one pumpkin accessions were screened for resistance/ tolerance to pumpkin mosaic and yellow vein mosaic during June - October 1988 under natural field conditions. The genotypic differences for the expression of mosaic diseases were evidenced by the wide

variation in the intensity of mosaic symptoms and stage of the plant for the appearance of the disease.

Out of the seventy one accessions evaluated fifty were susceptible to both pumpkin mosaic and yellow vein mosaic viruses (Table 14). Based on the intensity of disease the genotypes were classified into highly susceptible, susceptible, tolerant and resistant. CM 214, a collection from Nigeria was found to be completely free of diseases and was resistant. Fifteen accessions, CM 97, CM 106, CM 130, CM 131, CM 132, CM 153, CM 154, CM 160, CM 164, CM 171, CM 176, CM 177, CM 186, CM 197 and CM 198 were less affected by yellow vein mosaic virus and were treated as tolerant. All the remaining sixty eight genotypes were either susceptible or highly susceptible to yellow vein mosaic virus. Typical vein clearing appeared at very early stage in twenty nine pumpkin accessions and resulted in poor growth of the crop.

All the pumpkin accessions were affected by yellow vein mosaic earlier than pumpkin mosaic. Out of seventy one genotypes twenty two were affected by yellow vein mosaic virus within fifteen days of sowing. In CM 154 and CM 197 vein clearing was noticed in the 60th day after sowing. In all the remaining genotypes yellow vein mosaic disease was expressed either at the vegetative phase or the early flowering phase.

Based on the intensity of light green banding, blistering and distortion of leaves, mottled yellow patches and other symptoms the

Table 14. Incidence of pumpkin mosaic and yellow vein mosaic disease in different varieties of pumpkin during June - October 1988 under natural condition

Accession Number	Pumpkin mosaic	Yellow vein mosaic	Accession Number	Pumpkin mosaic	Yellow vein mosaic
CM 14A	H.S.	S	CM 147	H.S.	H.S.
CM 14B	H.S.	S	CM 148	H.S.	H.S.
CM 14C	H.S.	S	CM 149	S	S
CM 39	H.S.	S	CM 150	S	S
CM 85	H.S.	S	CM 153	S	T
CM 88	T	H.S.	CM 154	S	T
CM 89	H.S.	S	CM 155	H.S.	H.S.
CM 90	H.S.	S	CM 157	H.S.	H.S.
CM 91	H.S.	S	CM 158	H.S.	H.S.
CM 92	H.S.	T	CM 159	H.S.	H.S
CM 93	H.S.	T	CM 160	S	T
CM 94	H.S.	S	CM 162	H.S.	H.S.
CM 95	H.S.	H.S.	CM 163	H.S.	S
CM 97	T	S	CM 164	S	T
CM 101	S	H.S.	CM 165	S	S
CM 102	S	S	CM 167	H.S.	H.S.
CM 103	H.S.	H.S.	CM 171	S	T
CM 104	H.S.	H.S.	CM 175	H.S.	H.S.
CM 105	S	S	CM 176	S	T
CM 106	T	S	CM 177	S	T
CM 107	H.S.	H.S.	CM 179	S	S
CM 108	H.S.	H.S.	CM 180	S	S
CM 109	H.S.	S	CM 182	H.S.	H.S.
CM 111	H.S.	H.S.	CM 183	H.S.	S
CM 112	H.S.	H.S.	CM 185	H.S.	S
CM 113	H.S.	T	CM 186	S	T
CM 125	H.S.	H.S.	CM 188	S	S
CM 126	H.S.	H.S.	CM 189	S	S
CM 130	S	T	CM 192	H.S.	H.S.
CM 131	S	T	CM 193	H.S.	H.S.
CM 132	H.S.	T	CM 197	S	T
CM 133	T	H.S.	CM 198	S	T
CM 135	S	H.S.	CM 201	H.S.	H.S.
CM 136	S	H.S.	CM 210	H.S.	S
CM 138	H.S.	H.S.	CM 214	R	R
CM 139	H.S.	H.S.			

H.S. Highly susceptible T - Tolerant

S - Susceptible R - Resistant

accessions were classified into highly susceptible, susceptible, tolerant and resistant as in case of yellow vein mosaic virus. The only accession resistant to both pumpkin mosaic and yellow vein mosaic was CM 214. But this Nigerian local failed to produce mature seeds. The fruits were knobed and did not reach the maturity stage. In accessions CM 97, CM 106 and CM 133 only a light green banding was noticed on the leaf lamina and the symptoms were not conspicuous and were treated as tolerant. All the remaining sixty seven accessions including CM 14-A, CM 14 B, CM 14-C, selections from CM 14, were highly susceptible or susceptible to pumpkin mosaic virus and the typical green and yellow mottling was much pronounced.

None of the pumpkin accessions were affected by pumpkin mosaic virus during the early vegetative phase, that is within fifteen days after sowing. Mosaic symptoms appeared only on the 45th day after sowing and its occurrence was noticed upto 75 days after sowing. In CM 97, CM 130, CM 131, CM 132, CM 153 and CM 154 the expression of pumpkin mosaic virus was observed only very late 75 days after sowing.

Based on the yield and tolerance to yellow vein mosaic and pumpkin mosaic twenty six superior accessions were selected and were further grown during December - January 1988-89. To confirm resistance or tolerance, these lines were grown when there was very high incidence of mosaic in the adjacent fields. Artificial inoculation

was also carried out. When the artificial inoculation was done at the three leaf stage symptoms of pumpkin mosaic appeared 15th day onwards in the newly emerged leaves. All the accessions except CM 214 was found to be susceptible to yellow vein mosaic and pumpkin mosaic (Table 15). CM 97, CM 106 and CM 133 which were found to be tolerant to pumpkin mosaic during the first season was severely infected with the virus under artificial inoculation.

Similarly tolerant accessions CM 92, CM 130, CM 131, CM 132, CM 153, CM 154, CM 160, CM 164, CM 171, CM 176, CM 177, CM 186, CM 197 and CM 198 during the first season became highly susceptible to yellow vein mosaic under artificial inoculation. During this season also, the resistant genotype CM 214 failed to produce mature fruits and seeds.

Table 15. Incidence of mosaic diseases in selected varieties of pumpkin under artificial inoculation during December - January 1988-89

Accession Number	Pumpkin mosaic	Yellow vein mosaic	Accession Number	Pumpkin mosaic	Yellow vein mosaic
CM 14B	H.S.	H.S.	CM 133	H.S.	H.S.
CM 85	H.S	H.S.	CM 148	H.S.	H.S.
CM 88	H.S.	H.S.	CM 154	H.S.	H.S.
CM 92	H.S.	H.S.	CM 160	H.S.	H.S.
CM 93	H.S.	H.S.	CM 164	H.S.	H.S.
CM 95	H.S.	H.S.	CM 171	H.S.	H.S
CM 97	H.S.	S	CM 176	H.S	H.S.
CM 106	H.S.	H.S.	CM 177	H.S.	H.S.
CM 113	H.S.	H.S.	CM 186	H.S.	H.S.
CM 126	H.S.	H.S.	CM 197	H.S.	H.S.
CM 130	H.S.	H.S.	CM 198	H.S.	H.S.
CM 131	H.S.	H.S.	CM 214	R	R
CM 132	H.S.	H.S.	CM 153	H.S.	H.S.

H.S. Highly susceptible S - Susceptible
T - Tolerant R - Resistant

Plate 9. Pumpkin mosaic disease

Plate 10. Yellow vein mosaic disease

Discussion

DISCUSSION

Pumpkin (Cucurbita moschata Poir) is one of the popular cucurbitaceous vegetables grown in India. Low cost of production, long keeping quality of fruit and comparatively high content of carotene, a precursor of vitamin A in fruits, point to the potentiality of the crop. Irrespective of the popularity and importance of the crop, very little effort is made to upgrade the genetic make up of pumpkin in India.

In any plant improvement programme, the main objective is the development of elite varieties through production breeding. The basic information a breeder usually requires as a pre-requisite to any breeding programme is the extent of variability in the available germplasm and gene action of the characters to be improved. Basic information on genetic variability, heritability and genetic advance that could be achieved in the next cycle of selection are of vital importance to the breeder for formulating appropriate breeding strategy.

Large showy flowers, monoecious and cross pollinated nature and more seeds/fruit offer greater potentiality for exploitation of hybrid vigour in pumpkin. Importance of genetic diversity of parents in hybridization programme was emphasised by many workers. The more diverse the parents, with in a reasonable range, the more would be chance of improving characters in question. Mahalanobis D^2 statistic is a powerful tool in the hands of plant breeders to assess degree

of relationship among the genotypes and to group them based on their phenotypic expression.

In India, breeding of vegetable crops as a conscious effort is hardly of three decades old and that too for resistance to diseases is still of recent origin (Swarup and Seshadhri, 1986). In a crop like pumpkin, production breeding and resistance breeding should go side by side. Due to heavy incidence of mosaic diseases, particularly pumpkin mosaic and yellow vein mosaic, the area under pumpkin in the state is getting reduced day by day (Balakrishnan,1988). None of the pumpkin varieties or improved lines in the country have tolerance to mosaic diseases.

The present investigation deals with collection of basic information, as a pre-requisite to production and resistance breeding programmes, in pumpkin and the results obtained during the entire study are discussed in the following pages.

Success of any breeding programme depends primarily on the extent of variability in the base population. Evaluation and estimation of genetic variability, heritability, expected genetic advance etc. are primary pre-requisites for all the crop improvement programmes (Johnson et al. 1955). In the present investigation, the genetic contribution in the phenotypic expression was studied to realize the performance of pumpkin genotypes. Among the 20 quantitative characters studied, the 50 pumpkin accessions exhibited significant

difference for all characters except for yield/plant. Solanki and Seth (1980) also observed the least variation for fruit yield in cucumber. The accessions showed significant variation for days to first female flower anthesis, days to first male flowers anthesis, node at which first female flower is formed, node at which first fruit is retained, main vine length, nodes on main vine, primary branches/plant, productive branches/plant, internodal length, male flowers/plant, female flowers/plant, sex ratio, fruits/plant, average fruit weight, fruit length, fruit diameter, flesh thickness, seeds/fruit and 100 seed weight. In pumpkin, Gopalakrishnan (1979), Rana (1982) and Doijode (1982) also observed wide variation for all the characters studied. Studies by Thakur and Nandpuri (1974) and Rajendran (1989) in watermelon, Srivastava and Srivastava (1976), Ramachandran (1978) and Vahab (1989) in bittergourd also found significant variation for all the quantitative characters studied.

Mean, range and variation around the mean are the various estimates of quantitative variability. In the present investigation, wide range of variation was observed for all the characters studied. In CM 135 the first female flower opened 45 days after sowing and was the earliest accession. CM 201 took 84.5 days for the anthesis of first female flower and was very late. Node at which the first female flower is formed ranged from 15.5 in CM 188 to 29.0 in CM 177. Female flowers/plant had a narrow range of 2.25 - 5.0. The ratio of male and female flowers was as low as 11.93 in CM 111 and as

high as 28.19 in CM 108. Though the mean number of nodes for the emergen e of first female flower was 22, the first fruit was retained only on 36th node, on an average. CM 147 produced a maximum of 4 fruits/plant. Average fruit weight ranged from 0.9 kg in CM 157 to 6.70 kg in CM 177. The longest fruit (32.7 cm) was born on CM 154. Fruit diameter in CM 177 (27 cm) was three times as that of CM 147. Flesh thickness was more in CM 182 (4.65 cm). Yield/plant was maximum in CM 177 (13.4 kg) followed by CM 153 (9.7 kg) and CM 189 (9 kg) and was minimum in CM 157 (0.9 kg).

Importance of pumpkin as a possible supplier of carotene has not been much emphasized. The present study brought out considerable variability in pumpkin genotypes with respect to carotene content. Kubiaki and Walezak (1976), Gopalakrishnan (1979) and Doijode (1983) also reported considerable variability with respect to carotene content in Cucurbita spp. Iron content in fruit also exhibited a wide range of variation (0.51-2.74 mg/100 g).

Estimates of quantitative variations like range, standard error around the mean etc. do not indicate the relative amount of variability for which coefficients of variation appear to be a better index, when the characters with different units of measurement are to be compared. Phenotypic coefficient of variation was maximum for yield/plant (58.17) followed by productive branches/plant (50.89), average fruit weight (47.37) and fruits/plant (40.89). Ramachandran (1978) and Vahab

(1989) observed high values of pcv for yield/plant in bittergourd. Chaudhari (1987) also reported higher pcv value for yield/plant, fruits/plant and fruit weight in bittergourd. Days to first male flower anthesis, node at which first female flower was formed and days to first female flower anthesis had only low values of pcv (13.08, 13.29 and 15.61 respectively). Mangal et al (1981), Chaudhari (1987) and Vahab (1989) also observed lower pcv estimates for node at first female flower was formed and days to first female flower anthesis in bittergourd. Phenotypic coefficient of variation was between 20% and 40% for the remaining characters. The higher magnitude of phenotypic coefficient of variation than the genotypic values indicated considerable influence of environment on the expression of characters.

The plant improvement programmes like selection and hybridization cannot be undertaken based on the phenotypic performance alone since it is the sum total of genotypic effect and environmental influence. Genotypic coefficient of variation was maximum for seeds/fruit (37.37), closely followed by average fruit weight (35.25) and productive branches/plant (34.72). As in case of pcv, 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. Thakur and Nandpuri (1974) in watermelon and Singh et al. (1985) in pointedgourd also reported maximum value of gcv for seed volume. Srivastava and Srivastava (1976), Mangal et al (1981) and Chaudhari (1987) also observed lower values of gcv for days to flowering and node at which first female flower was formed in bittergourd.

A character can be improved only if it is highly heritable. The magnitude of heritability indicates the effectiveness with which the selection of genotypes can be made based on phenotypic performance (Johnson et al., 1955). The highest heritability estimate in the study was observed for 100 seed weight (95.5%). Similar results were recorded by Thakur (1970), Thakur and Nandpuri (1974) and Rajendran (1989) in watermelon. High heritability resulting from high gcv and low ecv were also observed for node at which first fruit is retained (93.1%), days to first female flower anthesis (92.4%), node at which the first female flower is formed (92.2%) and seeds/fruit (90.1%). This indicates low impact of environment on expression of these characters. The impact of environment was evidenced by low values of heritability for yield/plant (22.7%), fruits/plant (25.0%) and primary branches/plant (28.8%). Vashista et al. (1983) reported low heritability estimate for yield/plant in watermelon. Indiresh (1982) in bittergourd and Joseph (1978) in snakegourd also got the same result.

Eventhough heritability values give an indication of effectiveness of selection based on the phenotypic performance, it does not necessarily mean a high genetic advance for a particular character. Heritability along with estimates of expected genetic advance should be considered while making selections.

In the present investigation genetic advance was estimated in absolute values and also in percentage of mean (genetic gain) for

comparing the different characters. High heritability along with high genetic gain was observed for 100 seed weight (95.9% and 55.46%, seeds/fruit (90.1% and 73.05%) and node at which first fruit is retained (93.1% and 58.98%). High heritability coupled with high genetic gain indicates additive gene action while high heritability with low genetic gain indicates non addictive gene effects which includes dominance and epistasis (Panse, 1957). The involvement of additive gene effects for the above three characters suggests improvement through selection (Burton, 1952).

Though heritability was high for days to first female flower anthesis and node at which first female flower is formed, the gentic gain was of low magnitude. Non-additive gene action for days to first female flower anthesis was reported by Srivastava and Srivastava (1976), Ramachandran (1978) and Vahab (1989) in bittergourd. This implies great scope for development of early varieties by utilizing transgressive segregants in the heterosis breeding programme. Pumpkin, though a highly cross pollinated crop, because of the hermaphrodite origin does not exhibit inbreeding depression and the production of inbreds is thus a practicable task. In pumpkin, the monoecious nature and large flowers make the emasculation process simple. Large number of seeds/fruit and the availability of successful selective gametocides are added advantages for the exploitation of hybrid vigour and F_1 seed production on a systematic, effective and commercial scale.

Though the potentiality of heterosis was realized as early as in 1763, its commercial utilization is yet to be tested in India. Inbreeding depression and laborious process of hand emasculation due to hermaphrodite nature are the major bottle necks in the massive F_1 seed production programmes. Absence of inbreeding depression, presence of monoecious condition and coleurful, long and showy flowers in pumpkin point to the suitability of this crop for F_1 production. More over standardisation of selective gametocides like 2,4-D, MH etc. makes the commercial F_1 seed production more easier. As many as 500 seeds with a single act of pollination in pumpkin makes the F_1 seed production, even by hand pollination, profitable.

Selection of parents for hybridization programme is mainly based on genetic diversity. More divergent the parents, the more will be the expression of heterosis. Mahalanobis D^2 statistics is a powerful tool for measuring genetic distance in plant breeding experiments. It permits precise comparison of all the genotypes by considering large number of characters simultaneously.

Main objective of the present study is to assess genetic diversity among 50 pumpkin genotypes and to group them into clusters based on genetic distance. On the basis of genetic distances compared with reference to 20 quantitative characters, the 50 genotypes were grouped into 5 clusters. The distribution of genotypes into clusters showed no regularity. Cluster V was the largest containing 20 genotypes. Cluster IV containted 12 genotypes, cluster III contained 9 genotypes

cluster II and I contained 7 and 2 genotypes respectively. Such an irregular pattern of distribution was reported by Sukhija et al. (1982), Sidhu and Brar (1985) in watermelon and Kalloo et al. (1982) in Cucumis melo.

Out of five clusters, cluster I which comprised of only two genotypes, showed high mean values for 8 characters - female flowers/plant, male flowers/plant, sex ratio, node at which the first fruit is retained, main vine length, nodes on main vine, primary branches/plant and flesh thickness (Table 16). Cluster I had the lowest mean values for rest of the characters viz. days to first male flower anthesis, days to first female flower anthesis, node at which the first female flower is formed, internodal length, productive branches/plant, fruits/plant, average fruit weight, fruit length, fruit diameter, seeds/fruit, 100 seed weight and yield/plant. Involvement of either maximum or minimum cluster means in this cluster may be due to the inclusion of only two genotypes which showed wide range of variation for all the characters.

Cluster II showed superiority for only two characters viz. average fruit weight and seeds/fruit. At the same time it was inferior to the rest of the clusters for female flowers/plant, sex ratio, node at which the first fruit is retained, main vine length, nodes on main vine and flesh thickness. Cluster III exhibited highest cluster means for days to first male as well as female flower anthesis and fruit length.

Increase in fruit yield is the primary objective of any breeding programme. Among the 5 clusters, cluster IV had maximum mean values for fruits/plant, yield/plant and 100 seed weight. This indicates the importance of cluster IV for further improvement.

Cluster V which contained maximum genotypes of 20 was intermediary for most of the characters except node at which first female flower is formed, productive branches/plant and fruit diameter for which it had maximum cluster mean.

Crossing among divergent parents is likely to yield heterotic hybrids. In the present study, maximum genetic distance was exhibited between clusters I and II (D^2 = 224.48, Table 16). Clusters showing the largest genetic distance show the maximum divergence. Cluster I is constituted by CM 136, a collection from Cheruthuruthi (Trichur Dist.) and CM 188, a collection from Valiyakunnu. CM 136 is characterised by more female flowers/plant and vegetative growth. CM 188 bears fruits having high flesh thickness. Cluster II is comprised of 7 genotypes having medium or large fruits. In future programmes, selection of parents from Clusters I and II for hybridization is likely to give heterotic hybrids.

The intercluster distance (D^2) was also high between Clusters I and III (128.56) and Clusters II and IV (141.77). The minimum inter cluster distance was observed between Clusters IV and V. This indicates the unsuitability of selecting male and female parents for hybridization from these two clusters.

Table 16. Cluster means of 20 quantitative characters

Characters	Mean values of clusters				
	I	II	III	IV	V
Days to first male flower anthesis	47.75	51.21	57.16	48.88	50 05
Days to first female flower anthes s	51.00	62.14	65.66	52.00	60.33
Node at first female flower is formed	19.25	20.07	22.17	21.83	23.60
Female flowers/plant	3.38	3.07	3.29	3.20	3.14
Male flowers/plant	67.75	50.30	59.94	48.31	57.01
Sex ratio (male/female)	19.65	14.41	17.16	16.55	18.38
Node at which first fruit is retained	67.25	33.21	42.16	33.50	34 94
Main vine length (m)	11.19	7.91	10.18	9.26	8.65
Nodes on main vine	95.75	70.43	80.83	73.50	72.00
Primary branches/plant	3.00	2.57	2.66	2.30	2.70
Internodal length (cm)	11.38	15.57	17.58	16.90	16.96
Productive branches/plant	3.25	3.79	4.05	4.07	5.23
Fruits/plant	1.00	1.80	1.82	2.16	1.90
Average fruit weight (kg)	2.30	3.17	2.84	2.66	2.87
Fruit length (cm)	18.38	19.75	20.80	20.00	18.71
Fruit diameter (cm)	14.75	17.52	16.84	17.27	18.26
Flesh thickness (cm)	3.28	2.74	3.14	2.81	2.99
Seeds/fruit	282.75	545.70	345.50	332.00	469.83
100 seed weight (g)	9.70	9.04	9.76	11.84	11.81
Yield/plant (kg)	2.30	4.77	5.10	5.33	5.18

The maximum intracluster distance was shown by cluster III (39.17) followed by cluster II (35.80) and cluster V (34.29). High intracluster distance in the clusters indicated high degree of variability within the clusters offering scope for improvement by various selection methods.

Evaluation for resistance to mosaic disease

Vegetables are facing serious problems due to outbreak of newer strains of virus. Existence of a host-host-parasite interaction makes the breeding programmes for virus resistance all the more complicated and the development of virus resistant varieties is still in infancy except in okra.

Due to severe incidence of mosaic diseases, pumpkin cultivation has faced a serious set back during the last 10 years in Kerala. Normally, the local cultivars are highly susceptible to the disease and yield loss upto 100% has been noticed. Development and cultivation of mosaic resistant pumpkin is the one and only way of combating this disease. As a preliminary step, the available lines were evaluated under natural field condition as well as under artificial inoculation.

In the screening of accessions carried out during June-October 1988, it was found that 70 out of 71 varieties were susceptible to pumpkin mosaic and yellow vein mosaic. There was variation in the intensity of the disease. Moskovets and Fegla (1972) while working with watermelon mosaic virus arrived at similar conclusion and reported

that none of the watermelon and pumpkin varieties tested were immune to the virus. Varietal screening studies by Umamaheswaran (1985) and Balakrishnan (1988) against pumpkin mosaic also revealed that all the varieties tested were susceptible to PMV.

When the tolerant and high yielding genotypes were artificially inoculated with the virus, none of the accessions except CM 214 was free from virus infection. It is probable that these lines might have escaped virus infection in the field evaluation. Symptoms of PMV and yellow vein mosaic disease appeared 15 days after inoculation. The same were also observed by Umamaheswaran (1985). In all the susceptible pumpkin accessions, the incidence of YVM was earlier than pumpkin mosaic.

The accessions CM 214 (Nigerian Local) which did not exhibit mosaic symptoms under artificial inoculation could be rated as resistant. In the screening for resistance conducted by Provvidenti et al. (1984) Nigerian Local was found resistant to cucumber mosaic virus, papaya ring spot virus (formerly known as watermelon mosaic 1), watermelon mosaic virus-1, and zucchini yellow mosaic virus. Nigerian Local was also resistant to viral infections occuring in Australlia, Taiwan, China, Japan, France, Italy, Egypt, Israel and Turkey. Munger and Provvidenti (1987) obtained some success in transfering resistance from 'Nigerian Local' to Cucurbita pepo. Seed germination, fruit setting and fruit development of Nigerian Local is quiet erratic and fruits are warty and knobbed. This necessitates the need for improving this variety by crossing with the locally adapted and high yielding varieties available in the country.

Summary

SUMMARY

The present studies were conducted at the Department of Olericulture, College of Horticulture, Vellanikkara during June 1988 January 1989. The experimental material consisted of 71 pumpkin genotypes collected from different parts of India as well as some exotic accessions. Of this, 50 selected pumpkin genotypes were grown in a randomized block design to assess the extent of variability and divergence among the genotypes and to group them accordingly based on D^2 values. The carotene and iron contents present in the 50 geno types were also estimated to find out the extent of variability. Studies were also made to screen the 71 genotypes for resistance/ tolerance to pumpkin mosaic and yellow vein mosaic diseases.

The findings of the study are summarized as follows:

The 50 genotypes differed significantly for all the characters except yield/plant which clearly indicates existence of abundant variability among the genotypes selected for the study.

The coefficients of variation, heritability and genetic gain for the 20 characters indicated that the variation existing is mainly genetic.

Genotypic coefficient of variation was maximum for seeds/ fruit (37.37), followed by average fruit weight (35.25) and productive branches/plant (34.72) and it was minimum for days to first male flower anthesis (12.27) and node at which first female flower is formed (12 77).

The highest heritability estimate in the study was for 100 seed weight (0.96) followed by node at which first fruit is retained (0.93), days to first female flower anthesis (0.92), node at which the first female flower is formed and seeds/fruit.

High heritability coupled with high genetic gain was observed for 100 seed weight, seeds/fruit and node at which first fruit is retained.

The carotene content in 50 pumpkin genotypes ranged from 4.46 µg in CM 108 to 215 µg/100 g in CM 111. Iron content in the genotypes showed a wide range (0.51-2.74 mg/100 g).

The genotypes were grouped into 5 clusters based on Mahalanobis D^2 statistic and the clusters I, II, III, IV and V contained 2, 7, 9, 12 and 20 genotypes respectively.

The intracluster distance (D^2) was maximum in cluster III and minimum in cluster I.

Cluster I showed the maximum average intercluster distance with any other cluster. Intercluster distance (D^2) was maximum between clusters I and II (128.50) and was minimum between clusters III and V (45.28).

Out of five clusters, cluster I showed high mean value for 8 characters out of 20 characters studied. It had the lowest mean value for 12 characters.

Cluster IV had the maximum mean value for fruits/plant, yield/ plant and 100 seed weight.

Screening studies carried out with 71 genotypes revealed that all the genotypes except CM 214 were susceptible to Pumpkin mosaic and yellow vein mosaic diseases.

Artificial inoculation studies confirmed the immunity of CM 214 (Nigerian Local) to pumpkin mosaic virus and yellow vein mosaic virus.

Plate 11. CM 214 immune to pumpkin mosaic and yellow vein mosaic

References

REFERENCES

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley & Sons, Inc., pp. 89 - 98.

*Almeida, M.M. and Borges, M. 1983. Watermelon mosaic virus in Portugal. Characteristics, serology, ultrastructural aspects of the host. Revista de Phytopathologie. 8:347 - 353.

A.O.A.C. 1960. Official Methods of Analysis of Association of Official Agricultural Chemists, 9th ed. Washington pp. 215 - 226.

Arora, S.K., Pandita, P.S., Partap, P.S. and Sidhu, A.S. 1983. Variability and correlation studies in sponge gourd (Luffa cylindrica Roem.). Haryana agric. Univ. J. Res. 13:146 - 149.

Balakrishnan, S. 1988. Mosaic diseases of pumpkin in Kerala. Research High lights on Vegetables. Kerala Agric. Univ., Trichur, Kerala. pp 44 46.

Bhargava, B. and Bhargava, K.S. 1977. Cucurbit mosaic virus in Gorakpur. Indian J. agric. Sci. 47:1 - 5.

Bhathal, G.S. and Sandhu, J.S. 1984. Evaluation of hybrids in watermelon [Citrullus lanatus Thunb. Mansf.]. The Punjab Veg. Grower 19:11 17.

Brar, J.S. and Nandpuri 1978. Genetic analysis of yield and fruit number in watermelon. Indian J. Hort. 35:225 - 228.

* Burton, G.W. 1952. Quantitative inheritance in grasses 6th Int. Grassld. Cong. Proc. 1:277 - 283.

Capoor, S.R. and Ahmad, R.U. 1975. Yellow vein mosaic disease of field pumpkin and its relationship with the vector, Bemisia tabaci. Indian Phytopath. 28:241 - 246.

Chaudari, S.M. 1987. Studies on heterosis, combining ability and correlation in bitter gourd (Momordica charantia L.). Ph.D. thesis, Mahathma Phule Agric. Univ., Rahuri, Maharashtra.

Chhonkar, V.S., Singh, D.N. and Singh, R.L. 1979. Genetic variability and correlation studies in musk melon. Indian J. agric. Sci. 49:361-363.

*Cohen, S., Duffus, J.E. Larsen, R.C., Liu, H.Y. and Flock, R.A. 1983. Purification, serology and vector relationships of squash leaf curl virus, a whitefly transmitted geminivirus. Phytopathology 73:1669 - 1673.

*Cohen, S. and Nitzany, F.E. 1960. A whitefly transmitted virus of cucurbits in Israel. Phytopath. Medit. 1:44 - 46.

*Darwin, C.R. 1859. On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life, Modern Library (Giants Series), New York, N.Y.

Doijode, S.D. 1983. Heterotic performance for TSS and carotene in pumpkin (Cucurbita moschata Poir). Genetica Agraria 37:233 - 238.

Doijode, S.D. and Sulladmath, U.V. 1985. Genetics of certain fruit characters in pumpkin (Cucurbita moschata Poir). Egyptian. J. Genet. Cytol. 14:35 - 40.

Doijode, S.D. Sulladmath, U.V. and Kulkarni, R.S. 1982. Graphic analysis and genetic diversity for vegetative and reproductive traits in pumpkin (Cucurbita moschata Poir). Mysore J. agric. Sci. 16:439 - 442.

Ghosh, S.K. and Mukhopadhyay. 1979. Viruses of pumpkin Cucurbita moschata in West Bengal. Phytopath. Z. 94:172 - 184.

Gill, B.S. and Kumar, J.C. 1986. Variability in genetic stock and heritable components in watermelon. J. Res., Punjab agric. Univ. 23:583 - 588.

Gopalakrishnan, T.R. 1979. Genetic variability and correlation studies in pumpkin (Cucurbita moschata Poir). M.Sc. (Hort.) thesis, Kerala Agric. Univ., Trichur, Kerala.

*Greber, R.S. 1978. Watermelon mosaic virus 1 and 2 in Queensland cucurbit crops. Australian J. agric Res. 29.1235 - 1245.

Hariharasubramanian, V. and Badami, R.S. 1964. A virus disease of cucurbits from India. Phytopath. Z. 51:274 - 279.

Harpaz, I. and Cohen, S. 1965. Semi persistent relationship between cucumber vein yellowing virus (CUYV) and its vector, the whitefly (Bemisia tabaci). Phytopath. Z. 54:240 - 248.

*Hassan, A.M. Sherif, H.S., Nazeem, H.R. and Abdul Magid, A.A. 1984. Genetic behaviour of some economic characters in squashes (Cucurbita sp). Annals of Agric. Sci. Moshtehor. 22:175 187.

*Herrington, M.E. 1987. Yield and quality of Cucurbita maxima increase with delayed infection by papaya ring spot virus type W. Queensland J. Agric. and Animal Sci. 44:117 - 121.

Iqwegbe, E.C.K. 1983. Properties of a virus causing severe mosaic of Cucumeropsis edulis in Nigeria. Plant Diseases. 65:315 - 317.

Indiresh, B.T. 1982. Studies on genotypic and phenotypic variability in better gourd (Momordica charantia L.) (Abstr). Thesis Abstr 8 p 52.

Jackson, M.L. 1973. Soil Chemical Analysis. Prentice Hall of India, Private Ltd, New Delhi. pp 389 - 391.

Jaganathan T. and Ramakrishnan, K. 1971. Studies on Virus diseases of cucurbits. Madras agric. J. 58:331 - 337.

Jayasree, P.K. 1984. Yellow vein mosaic disease of pumpkin in Kerala. M.Sc. thesis Kerala Agric. Univ., Trichur, Kerala.

*Johnson, H.W., Robinson, H.D. and Comstock, R.E. 1955. Estimates of genetical and environmental variability in soybeans. Agron. J. 47:314 - 318.

Joseph, S. 1978. Genetic variability and correlation studies in snake gourd (Trichosanthes anguina L.). M.Sc. thesis, Kerala Agric. Univ., Trichur, Kerala.

Joshi, S., Joshi, M.C., Singh, G. and Vishnoi, A.K. 1981. Genotypic and phenotypic variability in cucumber (Cucumis sativus L.). Veg. Sci. 8:114-119.

Kadam, P.Y and Kale, P.N. 1985. Genetic divergence in ridge gourd (Luffa acutangula L. Roxb.). Veg. Sci. 12:96 - 104.

*Kado, C.I. 1972. Mechanical and biological inoculation principles. (In) Principles and techniques in Plant virology. Kado, C.I. and Agarwal, H.O. (Ed.) Van Nostrand Reinhold Company, New York pp 12 - 16.

Kalloo, Dixit, J. and Sidhu, A.S. 1982. Genetic divergence in muskmelon (Cucumis melo L.). Genetica Agraria 36:1 - 8.

Kalyanasundaram, P. 1976. Evaluation of three muskmelon cultivars (Cucumis melo L.). South Indian Hort. 24:18 - 23.

Kerala Agricultural University, 1986. Package of Practices Recommendations. Directorate of Extension, Kerala Agric. Univ., Trichur, Kerala pp 199 - 201.

*Kubiaki, B. and Walezak, B. 1976. Variation and heritability of carotene content in some cultivars of Cucurbita spp. Genetica botanica 17:531 - 544.

Lockhart, B.E.L., Ferji, Z. and Hafidi, B. 1982. Squash mosaic virus in Morocco. Plant Diseases 66:1191 - 1193.

*Lush, J.L. 1949. Animal Breeding Plans. Iowa State Univ. Press, Ames, Iowa pp 473.

*Mahalanobis, P.C. 1928. A statistical study at Chinese head measurements. J. Asiatic Soc. Bengal 25:301 - 377.

* Maluf, W.R., Moura, W.DE.M , Silva, I.S.D.A. and Castelo - Branco, M. 1986. Screening of Cucurbita spp. accessions for resistance to watermelon mosaic virus - 1. Revista Brasileiva de Genetica 9:161 - 167.

Mangal, J.L., Dixit, J., Pandita, M.L. and Sindhu, A.S. 1981. Genetic variability and correlation studies in bitter gourd (Momordica charantia L.). Indian J. Hort. 38:94 - 99.

*Martyn, E.B. 1968. Plant Virus names. Commonwealth Mycol. Inst. Survey, England.

Mathew, S.M., Gopalakrishnan, P.K. and Peter, K.V. 1986. Genetic distance among five botanical varieties of Cucumis melo. Agric. Res. J. Kerala. 24:195 - 196.

Miller, J.C. and Quisenberry, J.E. 1976. Inheritance of time to flowering and its relationship to crop maturity in cucumber. J. Amer. Soc. Hort. Sci. 101:497 - 500.

*Moskovets, S.M. and Fegla, G.I. 1972. Effect of watermelon mosaic virus on the growth of cucurbits. Mikrobiologichuyi Z. 34:240 - 244.

Munger, H.M. and Provvidenti, R. 1987. Inheritance of Resistance to zucchini yellow mosaic virus in Cucurbita moschata. Rept. Cucurbit Genet Co-operative. 10:80 - 81.

Nath, P. and Dutta, O.P. 1970. A note on heterosis in watermelon. Indian J Hort. 27:176 - 177.

Panse, V.G. 1957. Genetics of quantative characters in relation to plant breeding. Indian J. Genet. 17:318 - 329.

Panse, V.G. and Sukhatme, P.V. 1957. Statistical methods for Agricultural Research Workers, ICAR, New Delhi. pp 63 - 69.

Paris, H.S., Cohen, S., Burger, V. and Joseph, R. 1988. Single-gene resistance to zucchini yellow mosaic virus in Cucurbita moschata. Euphytica 37:27 - 29.

Pink, D.A.C. and Walkey, D.G.A. 1984. Resistance in marrow (Cucurbita pepo L.) to different strains of cucumber mosaic virus. J. agric. Sci. 103:519 - 521.

Pink, D.A.C. and Walkey, D.G.A. 1985a. Effect of temperature and light intensity on resistance in marrow (Cucurbita pepo) to cucumber mosaic virus. J. agric. Sci. 104.325 - 329.

Pink, D.A.C. and Walkey, D.G.A. 1985b. Breeding for resistance to cucumber mosaic virus in courgette and vegetable marrow. Rept. Cucurbita Genet. Co-operative. USA. (8):74 - 75.

*Pitrat, M. and Dumas de Vaulx, R. 1979. Search for sources of resistance to powdery mildew and cucumber mosaic and watermelon mosaic virus in cantaloupe. Phytopathology 60:1466 - 1469.

Provvidenti, R. 1982. Sources of resistance or tolerance to viruses in accessions of Cucurbita maxima. Rept. Cucurbit Genet. Co-operative. (5):46 - 47.

Provvidenti, R. 1987. Inheritance of resistance to a strain of zucchini yellow mosaic virus in cucumber. Hort. Sci. 22:102 - 103.

Provvidenti, R. Gonsalves, D. and Humaydan, H.S. 1984. Occurence of zucchini yellow mosaic virus in cucurbits from Connecticut, New York, Florida and California. Plant Diseases 68:443 - 446.

*Provvidenti, R., Robinson, R.W. and Mungai, H.M. 1978. Multiple virus resistance in Cucurbita species. Cucurbit Genet. Co-operative (1):26 - 27

Rai, B. 1979. Heterosis Breeding, Agro. Biol. Publications, East Azad Nagar, Delhi pp 45 - 53.

Rajendran, P.C. Crop Improvement in watermelon (Citrullus lunatus Thumb. Mnsf) 1989. Ph.D. thesis, Tamil Nadu Agric. Univ Coimbatore, Tamil Nadu.

Ramachandran, C. 1978. Genetic variability, correlation and path coefficient analysis in bitter gourd (Momordica charantia L.). M.Sc. thesis, Kerala Agric. Univ., Trichur, Kerala.

Ramachandran, C., Gopalakrishnan, P.K. and Peter, K.V. 1981. Genetic divergence in bitter gourd. Veg. Sci. 7:100 - 104.

Rana, T.K. 1982. Variability and correlation studies in pumpkin (Cucurbita moschata Poir). (Abst). Thesis Abst. 8:90 - 91.

Reddy, K.S.S. and Rao, M.R. 1984. Studies on heritability, genetic advance and characters association in ribbed gourd. South Indian Hort. 32:97 - 100.

Rudragowda, M. Patil and Patel, A.A. 1985 Studies on relative performance of different genotypes of cucumber (Cucumis sativus L.). The Mysore J. agric. Sci. XXII:226.

Schmelzer, K. 1967. Symptoms of cucumber mosaic virus on cucurbits. Nachr. Bl. dt. Pfl. Schutz. dienst. Berl. NF. 21:109 110.

Shankar, G. Nariani, T.K. and Prakash, N. 1972. Studies on pumpkin mosaic virus (PMV) with particular reference to purification, electron microscopy and serology. Indian J. Microbiol. 12:154 - 165.

Sharma, O.P. and Sharma, B.R. 1982a. Studies on mosaic virus on bottle gourd. Veg. Sci. 9:51 - 54.

Sharma O.P. and Sharma, B.R. 1982b. Note on field evaluation of different genotypes of summer squash against vegetable marrow mosaic virus. Indian J. agric. Sci. 52:192 - 193.

Sidhu, A.S. and Brar, J.S. 1985. Genetic divergence and hybrid performance in watermelon. Indian J. agric. Sci. 55:459 - 461.

Singh, H.N., Srivastava, J.P. and Prasad, R. 1977. Genetic variability and correlation studies in bitter gourd. Indian J. agric. Sci. 47:604-607.

Singh, R.B. and Bain, S.S. 1968. Genetic divergence for ginning out turn and its components in upland cotton. Indian J. Genet. 28:262 - 268.

Singh, R.B. and Gupta, M.P. 1968. Multivariate analysis of divergence in upland cotton. Indian J. Genet. 28:151 - 157.

Singh S.J. 1982. Studies on the transmission of pumpkin mosaic virus by aphid (Aphis craccivora Koch.). Zetschrift fur Pflanzenkvankheiten und Pflanzenschutz. 89:79 - 87.

Singh, S.J. 1986. Assessment of losses caused by a strain of watermelon mosaic virus in pumpkin (Cucurbita maxima Duch.). Indian J. Plant Path. 4:165 167.

Singh, P. R., Mishra, G. M. and Jha, R. N. 1985. Studies on variability and scope for improvement in poin ed gourd (Trichosanthus dioica Roxb). South Indian Hort. 33: 257 260.

Sirohi, P. S., Kumar, T S. and Choudhury, B. 1986. Diallel analysis for variability in Cucurbita moschata Poir. Indian J. agric. Sci. 56: 171 173.

Solanki, S. S. and Seth, J. N. 1980. Studies on Genetic variability in Cucumber (Cucumis sativus L.. Progressive Hort 12: 43 49.

Srivastava, V.K. and Srivastava, L.C. 1976. Genetic parameter, correlation coefficients and p th analysis in bitter gourd (Momordica charantia L.). Indian J. Hort. 33:66 - 70.

Sukhija, B.S., Brar, J.S. and Sidhu, A S. 1982. Genetic divergence in watermelon. J. Res. Punjab Agric. Univ. 19:334 - 338.

Suresh, K.M. 1986. Standardisation of technique of clustering genotypes using Mahalanobis D^2 and Wilks Lambda Criterion. M.Sc. Thesis, Kerala Agric. Univ., Trichur, Kerala.

Swarup, V. and Seshadri, V.S. 1986. Breeding for disease resistance in vege table crops. Problems and Prospects. Veg. Sci. 13:101 - 106.

*Thakur, J.C. 1970. Genetic variability and correlation studies in watermelon. M.Sc. thesis, Punjab Agric. Univ , Ludhiana.

Thakur, J.C. and Nandapuri, K.S. 1974. Studies on variability and heritability of some important quantitative characters in watermelon (Citrullus lanatus Thunb. Mansf.). Veg. Sci., 1:1 - 8.

Umamaheswaran, K. 1985. Transmission, physical properties and host range of pumpkin mosaic virus. M.Sc. thesis, Kerala Agric. Univ., Trichur, Kerala.

Vahab, M.A. 1989. Homeostatic analysis of components of genetic variance and inheritance of fruit colour, fruit shape and bitterness in bitter gourd (Momordica charantia L.). Ph.D. thesis, Kerala Agric. Univ , Trichur, Kerala.

Verma, P.M. 1985. Ability of the whitefly to carry more than one virus simul taneously. Curr. Sci. 24:217 - 318.

Vashista, B.B., Sharma, J.C. and Seshadri, V.S. 1975. A note on variability in seed characters in watermelon (Citrullus lanatus Thunb Mansf.). South Indian Hort. 23:130 - 144.

Vashista, R N., Pratap, P.S. and Pandita, M.L. 1983. Studies on variability and heritability in watermelon (Citrullus lanatus Thunb Mansf.) Haryana agric. Univ. J. Res. 13:319 - 324.

Vijay, O.P. 1987. Genetic variability, correlation and path analysis in musk melon (Cucumis melo L.). Indian J. Hort. 44:233 - 238.

Walkey, D.G.A. and Pink, D.A.C. 1984. Resistance in vegetatble marrow and other Cucurbita spp. to two British strains of cucumber mosaic virus. J. agric. Sci. 102:197 - 205.

*Walkey, D.G.A., Pink, D.A.C., Zitter, T A., Bolland, C.J. and Miller, A. 1985. Virus diseases of marrow. (In) 35th Ann. Rept. 1984, Nati. Veg. Res. Stn , Welesbourne, Warwick, UK p. 91.

* Original not seen

Appendix - 1. Meteorological data during the cropping period (month-wise)

Months	Temperature (°C)		Mean relative humidity (%)	Total rainfall (mm)	No. of rainy days	Mean sunshine hours
	Maximum	Minimum				
1988						
June	30.0	23.7	86	632.1	25	4.2
July	29.0	23.2	88	545.0	26	3.0
August	29.2	24.3	86	507.8	25	3.7
September	29.9	23.2	85	700.0	24	5.1
October	31.7	23.3	78	116.6	9	7.1
November	32.6	22.9	68	11.0	1	7.9
December	32.6	22.3	57	14.9	2	9.0
1989						
January	33.4	22.2	54	-	-	8.1
February	36.3	21.2	45	-	-	9.8
March	36.5	23.3	58	31.3	2	9.5

Appendix 2 Mean performance of 50 pumpkin genotypes with respect to 20 characters

Accession No (CM)	Days to first male flowering anthesis	Days to first female flowering anthesis	Node of first female flower formed	Female flowers/ plant	Male flowers/ plant	Sex ratio (male/ female)	Number of fruits harvested	Length of main vine (m)	Number of fruits harvested	Fruit yield/ plant	Internode length (cm)
CM 14 A	43 50	44 00	21 00	3 15	45 50	14 45	27 50	7 17	7 50	2 0	15 00
CM 14B	42 00	43 50	1 50	2 0	46.25	18 50	2	7 58	66 0	2 0	16.00
CM 14C	43 00	45 50	50	2 25	32 50	14 45	26.50	5 33	57 50	3 0	15 50
CM 88	61 50	72 00	21 00	3 50	92 50	26.71	34 50	11 74	83 50	2 5	16 00
CM 89	57 00	61 00	0	3 00	47	6. 3		7 9	67 0	3 5	16.00
CM 91	53 00	61 50	22 00	2 85	44 25	15 97	42 50	12 08	97 50	0	21 25
CM 93	49 00	59 00	24 50	2 42	46.00	18 99	37 00	12 35	84 50	1 5	16.00
CM 95	56.50	60 50	24 00	2 75	56.50	20 57	33 00	6 69	53 50	2 0	20 50
CM 102	44 50	55 00	22 00	3 50	45 25	12 92	2 00	9 44	62 50	2 0	16.50
CM 103	54 00	60 00	28 00	2 75	63 00	23 13	3 00	11 55	80 50	2 5	21 00
CM 104	57 50	65 00	22 50	2 80	50 0	18 01	29 00	8 00	52 50	1 5	13 75
CM 106	61 50	63 50	24 0	2 25	35 83	16.07	41 50	6 80	52 00	4 0	12 7
CM 107	62 00	68 50	6 00	3 50	66.00	18 88	48 9	8 83	74 00	5	13 25
CM 108	53 50	63 00	9 0	2 58	72 50	28 19	27 50	7 77	77 00	2 5	10 50
CM 109	51 50	55 00	7 50	3 50	51 00	14 92	40 00	12 0	79 50	1 5	17 50
CM 111	49 50	4 00	19 00	3 50	41 75	11 93	25 50	8 46	67 50	3 0	20 00
CM 113	55 00	48 50	18 50	3 00	44 50	14 83	29 0	10 64	76 50		17 50
CM 2	8 00	59 00	27 00	3 10	65 00	21 04	5 00	9 33	87 00	1 0	1 50
CM 126	46.00	62 00	21 00	3 00	62 00	20 65	24 00	6.83	81 50	2 0	15 50
CM 131	55 00	67 50	2 50	2 55	47 50	18 65	32 00	8 82	70 00	2 5	18 50
CM 133	62 50	61 00	23 00	3 75	75 00	0 02	38 0	9 90	64 00	3 0	16.00
CM 135	41 50	41 00	19 50	4 25	58 75	13 85	34 00	7 8	86. 0	2 0	00
CM 36	3 00	58 0	3 00	3 75	89 00	23 79	7 50	13 99	116.00	3 0	0 5
CM 139	52 50	61 00	23 00	3 00	45 00	15 00	59 0	10 63	82 50	2	8 00
CM 147	51 50	4 00	2 00	4 50	65 00	14 28	55 00	9 74	103 00	5	17 0
CM 148	54 50	62 00	22 00	2 75	44 50	16.33	34 00	12 06	74 50	2 0	21 0
CM 149	50 50	50 00	9 50	2 83	44 50	15 79	32 00	9 33	95 00	2 0	11 75
CM 153	50 50	60 0	20 50	3 00	42 17	14 00	42 50	9 14	67 00	1 5	13 00
CM 154	54 00	66 00	20 00	4 00	71 08	17 84	37 00	8 45	73 50	3 5	16 00
CM 15	58 00	61 50	22 00	2 25	43 67	19 43	5 0	7 74	95 0	4 0	14
CM 60	52 50	65 00	21 00	3 00	8 50	16.17	34 50	10 56	85 00	1 5	19 0
CM 162	5 00	61 0	23 00	3 80	61 50	16.21	34 0	9 29	80 50	2 0	20 75
CM 163	52 50	62 50	23 00	4 00	84 00	21 00	26 00	6.75	60 50	3 0	0 0
CM 1 5	73 00	78 00	23 00	5 00	62 50	12 42	49 00	12 03	99 0	2 0	21 50
CM 167	48 00	60 00	24 00	3 25	61 0	18 97	27 00	8 14	71 00	2 5	17 00
CM 71	00	59 00	22 00	3 00	4 75	14 91	29 50	10 50	76.00	2 5	17 00
CM 5	1 50	50 00	19 00	3 00	51 7	17 25	30 0	9 30	83 50	3 5	17 00
CM 7	50	63 50	27 00	3 7	5 00	17 28	44	0 18	9 00	4 00	13 75
M 177	00	60 50	29 00	4 50	71 25	15 78	34 00	7 10	4 50	4 0	16.00
CM 179	48 00	57 50	27 50	3 25	53 25	16.56	38 00	11 79	117 00	3 0	14 50
CM 180	45 50	61 50	25 00	2 75	40 25	14 67	29 50	8 50	45 00	3 5	18 00
CM 182	55 00	59 50	23 00	2 75	59 00	21 83	28 00	8 95	78 50	3 5	13 50
CM 183	57 00	63 50	21 50	2 75	63 25	22 77	44 00	10 47	75 50	2 0	16 50
CM 18	45 00	7 00	20 00	3 00	48 00	16.00	0	7 7	48 00	3 0	21 50
CM 188	42 50	43 50	15 50	3 00	46.50	15 50		8 39	75 50	3 0	12 25
CM 189	56. 0	59 50	21 00	3 00	44 50	14 83	24 00	9 67	57 00	2 0	20 25
M 192	41 00	44 00	20 00	2 67	49 00	18 70	31 50	7 90	87 00	2 5	18 25
CM 193	48 00	45 50	19 50	2 75	39 00	14 27	32 0	6.81	77 50	0	16.7
M 201	68 00	84 0	2 00	3 00	65 50	21 83	7 0	13 65	110 00	2 0	11 50
M 210	58 50	6 0	2 00	2 55	49 0	19 25	30 0	78	6 0	2 5	17 7

t x 2 ((rtd)

Fr ductive br tes/plart	Fru ts/ plant	Average frut weight (kg)	Length of the frut (cm)	Diameter of the fruit (c r)	Flest thickness	S eds/ fruit	100 seed w ight (g)	Yield/ plat (kg)
1 5	2 5	2 40	20 25	17 0	2 7	33› 00	11 10	5 ‹0
1 0	2 0	3 30	‹4 50	24 ›0	2 45	573 00	14 45	6 60
3 5	1 5	2 85	16 25	21 7›	2 50	649 00	7 0›	3 90
4 5	2 0	3 4›	12 25	16.7	3 50	350 00	‹ 45	6 90
3 0	2 0	3 ‹0	25 00	16.30	3 05	631 50	16 80	7 20
3 5	2 0	2 ‹0	28 75	17 00	3 75	381 50	12 6›	4 20
3 5	2 0	2 25	15 25	18 75	2 90	565 00	14 90	4 50
2 0	3 0	2 45	24 2›	16.25	3 15	495 00	12 40	7 40
4 0	2 0	2 90	17 50	16.75	3 85	255 00	11 30	5 80
5 0	2 0	‹ 75	20 50	21 00	4 00	205 00	15 20	7 50
3 0	2 5	2 5 0	26 25	18 75	2 75	›86 50	7 60	6 50
2 5	1 5	1 60	20 50	12 13	2 05	432 50	9 75	2 40
9 5	2 5	1 55	16 75	12 30	2 55	380 00	5 35	3 80
6 0	1 0	3 40	15 25	21 75	3 55	365 00	11 10	3 40
3 5	1 5	2 55	13 25	19 00	4 18	401 50	5 63	3 60
4 0	2 0	1 70	20 00	11 75	2 00	317 00	12 65	3 40
‹ 5	1 0	4 20	19 25	14 00	3 05	516.50	7 00	4 ›0
5 0	2 0	2 10	14 00	19 00	3 25	514 00	12 20	4 20
4 0	1 5	4 80	24 00	21 25	3 10	661 50	12 20	7 30
10 5	2 0	2 35	26.25	14 00	3 35	218 50	10 65	4 70
4 5	2 0	2 45	13 25	22 25	2 45	392 00	11 55	5 00
3 5	3 0	1 55	19 75	17 25	2 ›5	422 00	10 90	4 80
4 0	‹ 0	1 30	16 50	13 25	1 80	379 00	11 20	1 30
7 0	2 0	2 ›0	15 75	16 25	2 15	332 ›0	11 30	4 40
5 0	4 0	1 20	13 50	9 75	2 85	313 50	5 40	4 80
7 0	2 0	3 75	21 50	19 50	3 15	504 50	11 35	7 50
›5	2 0	3 35	20 00	15 25	2 65	484 00	9 75	6.70
3 5	1 5	5 90	22 50	25 00	4 00	717 50	13 10	9 ‹0
3 0	2 5	3 00	32 75	16.25	3 20	450 00	9 53	8 70
5 5	1 0	0 90	22 00	10 35	1 90	202 50	6.25	0 90
6 0	2 5	1 97	18 75	15 50	2 10	607 50	15 13	5 ‹0
7 5	2 5	1 80	15 50	19 00	1 95	360 00	‹0 10	4 50
3 5	2 0	3 30	17 50	19 75	2 35	448 50	10 26	6.60
4 5	2 0	2 00	18 75	13 25	1 95	277 50	8 75	4 00
4 0	1 5	‹ 10	14 50	21 00	2 15	526 00	10 45	3 40
4 5	1 0	5 10	23 ›5	18 00	3 80	653 50	10 93	5 10
2 0	2 0	2 45	15 00	23 00	4 50	566.00	12 10	4 90
9 0	1 5	2 ›5	14 7›	21 90	3 50	624 50	9 98	3 20
3 0	2 0	6 70	21 50	27 00	4 08	678 00	13 43	13 40
5 0	1 5	2 10	11 50	16.50	3 00	106.00	13 14	2 90
4 0	2 5	3 30	26.00	17 25	3 20	418 00	13 58	8 60
3 5	1 0	3 20	15 25	20.75	2 95	350 00	13 95	3 20
1 0	1 5	3 10	26 50	16.00	2 70	536 50	18 90	4 80
3 5	1 0	2 70	1› 25	18 25	3 10	62 50	6 60	2 70
2 5	1 0	3 30	20 25	16.25	4 65	186 50	8 20	3 30
5 0	2 0	4 50	26.00	18 7›	‹ 65	439 00	13 38	‹ 00
4 0	1 5	1 ‹5	14 50	16.25	2 50	339 50	8 10	2 50
3 5	1 5	1 50	15 G0	13 00	1 45	285 00	8 30	2 60
6 5	2 0	2 10	20 00	11 75	3	102 50	10 40	4 20
3 5	1 5	2 70	25 ›0	18 00	3 35	662 50	14 48	4 00

DIVERGENCE STUDIES IN PUMPKIN

(Cucurbita moschata Poir*)*

BY

SURESH BABU, V.

ABSTRACT OF THESIS

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ABSTRACT

The present investigation on "Divergence studies in pumpkin (Cucurbita moschata Poir) was conducted at the College of Horticulture, Vellanikkara, Trichur during June 1988 - March 1989.

Seventy one pumpkin genotypes collected from different parts of India and abroad were utilized for the study. The extent of variability and divergence among 50 selected genotypes were assessed and grouped into 5 clusters based on Mahalanobis D^2 statistic. Cluster I, II, III, IV and V contained 2, 7, 9, 12 and 20 genotypes respectively. Intercluster distance was maximum between clusters I and II and was minimum between clusters III and V. Cluster I showed maximum average intercluster distance with any other cluster.

Screening 71 genotypes for resistance/tolerance to pumpkin mosaic and yellow vein mosaic diseases revealed that all genotypes except CM 214 were susceptible. Artificial inoculation studies confirmed immunity of CM 214 (Nigerian Local) to pumpkin mosaic virus and yellow vein mosaic virus.