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Assessment of genetic divergence in pumpkin (*Cucurbita moschata*)

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Abstract

Eighteen diverse genotypes of pumpkins (*Cucurbita moschata* Duch expoiq.) were evaluated for phenotypical variations and assessment of genetic diversity during the kharif season 2022 at Vegetable Research Farm, Banda University of Agriculture and Technology, Banda, Uttar-Pradesh. Randomized Complete Block Design with three replications was used for divergence, 18 genotypes were grouped into 4 clusters using Tocher's method. Out of the 6 clusters, cluster I was the largest, comprising 8 genotypes, followed by cluster III, comprising 5 genotypes, cluster IV, 4 genotypes, and cluster II with 1 genotype only. Based on distances between clusters, i.e. inter-cluster distances, maximum divergence was observed between cluster III and cluster IV. Maximum inter-cluster D^2 values between clusters indicated that genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population. The maximum intra-cluster D^2 values were observed for cluster I. Maximum intra-cluster distance indicates that genotypes are very diverse. Presence of sufficient phenotypic and genotypic diversity showed the scope in pumpkin for further improvement.

Key words: Cluster, Diversity, Inter, Intra, Phenotypic variation, Divergence

Vegetables are essential for human nutrition, offering key nutrients such as vitamins, minerals, fiber, and antioxidants that promote health (Pandey *et al.* 2024). Pumpkin (Cucurbita moschata Duch. ex. Poir.) is also highly nutritious and a cucurbitaceous vegetable of significant economic importance. It belongs to the Cucurbitaceae family and has a somatic chromosome number of 2n=4x=40. The genus *Cucurbita* consists of 27 species, with five cultivated species under the *Cucurbita* genus. China and India lead in global pumpkin production, followed by countries U S, Egypt, Mexico, Ukraine, Cuba, Italy, Iran, and Turkey (Ferriol and Pico, 2008). India has a rich germplasm source for various vegetable crops (Tripathi and Yogeesha, 2018) despite the vast diversity of local pumpkin cultivars in India, which exhibit variations in fruit size, shape, and colour, limited attention has been given to genetic improvement. Pumpkin has received less focus in crop improvement in comparison to other cucurbitaceous vegetables.

The concept of D^2 statistics, initially developed by P.C. Mahalanobis in 1928, is widely used in plant breeding and genetics to study genetic divergence. Precise information about genetic divergence is critical because phenotypic selection depends upon the range of genetic diversity (Singh *et al.* 2023), as genetically diverse plants have been shown to produce high heterotic effects and yield desirable segregates. It helps assess the relative distance between strains for the characters under study and provides essential information for launching viable improvement programs. Successful breeding programs require a reasonable range of genetic diversity among parents, and understanding the nature of gene effects for yield and associated characters facilitates the selection of effective and efficient breeding methods.

The study was carried out at College of Horticulture, Banda University of Agriculture and Technology, Banda, Uttar Pradesh, India, during *kharif* 2022-23. The observations were recorded for node number at first male flower appear, node number at first female flower appear, internodal length (cm) , days for first male flower anthesis , days for first female flower anthesis, days for first fruit harvesting, number of primary branches/plant, vine length (cm), leaf area (cm^2), male/female bud ratio, average fruit weight (kg), number of fruits/plant, peripheral thickness of fruit (cm), fruit polar diameter, fruit pericarp thickness (cm), pericarp/seed ball ratio, fruit yield (q/ha) and TSS. The observations recorded were statistically analyzed for different characters.

By using the pivotal condensation approach to convert correlated variables to uncorrelated ones, the evaluation of D^2 is made simpler (Singh and Chaudhary 1977). The actual values of D^2 were obtained by taking sum of square of differences of values of transformed uncorrelated variable for two genetic stocks thus the total D^2 values for all possible pairs from 18 genotypes were obtained. The genetic divergence among genotypes was estimated by using D^2 statistics (Mahalanobis, 1936). All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952).

Out of four clusters formed, cluster I was the largest group comprising 8 genotypes, followed by cluster III with 5 genotypes, cluster IV with 4 genotypes and clusters

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II was monotypic or solitary. Although, genotypes of the same origin or geographic region were also found to be grouped together in the same cluster, the instances of grouping of genotypes of different origin or geographic region in the same cluster were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity. Therefore, selection of parental materials for hybridization programme, simply based on geographic diversity may not be successful experience. The choice of suitable distinct parent selected on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity. This finding is in agreement with those of Hossain *et al.*, (2010); Naik and Prasad (2015); and Sundaram and Vadivel, (2007). The D^2 values revealed that genotypes of the same cluster had little divergence from each other with respect to aggregate effect of 18 characters under study (Table 1). Therefore choice of obtaining good recombinants in segregating generations by crossing member of the same cluster is very low. It is therefore, suggested that crosses should be between the genotypes belonging to cluster separated by large inter-cluster distances.

The average intra cluster distance ranged from 1.52 (cluster II) to 3.706 (cluster I), suggesting that genotypes in cluster I were relatively more diverse than the genotypes in other clusters. Maximum intra cluster distance was recorded in cluster I (3.706), followed by cluster III (3.352), cluster IV (3.322) and cluster II (1.520). The maximum inter cluster distance was between cluster IV and cluster II (5.885), followed by that between cluster II and cluster I (5.379), cluster II and III (4.737), cluster III and IV (3.818) and cluster IV and I (3.676), suggesting a large difference between these groups. On the other hand, minimum distance was recorded between cluster III and cluster I (3.60).

The average intra cluster distance ranged from cluster II to cluster I, suggesting that genotypes in cluster I were relatively more diverse than the genotypes in other clusters. Maximum intra cluster distance was recorded in cluster I, followed by cluster III, cluster IV and cluster II. The maximum inter cluster distance was between cluster IV and cluster II, followed by cluster II and cluster I, cluster II and III, cluster III and IV and cluster IV and I, suggesting a large difference between these groups. Thus crossing between genotypes belonging to cluster pairs separated by very high inter-cluster distance as discussed above may be through desirable deviant segregates. On the other hand, minimum distance observed between cluster III and cluster I, indicated that genotypes present in these cluster pair were genetically closed to each other. The crosses between genotypes belonging to clusters separated by low inter-cluster distances are unlikely to produce promising recombinant in segregating generations. Similar reports were also made by (Masud *et al.*, 1995; and Rahman 2006).

Cluster I showed maximum mean value for fruit harvest (78.18), days for first female flower anthesis (53.76), fruit polar diameter (12.36) and internodal length (11.06). Cluster II showed maximum mean value for leaf area (337.52), days for first male flower anthesis (50.67), pericarp/seed ball ratio (11.78), node number, at first male flower appear (9.80), TSS (4.86), number of primary branches/plant (4.07), pericarp thickness (3.16), and fruit weight (2.50). Cluster III showed maximum mean value for node number, at first female flower appear (22.68) and number of fruits/plant (6.16). Cluster IV showed maximum mean value for fruit yield (235.79), vine length (227.68), peripheral thickness of fruit (53.29) and male/female bud ratio (11.87). Cluster I showed maximum mean value for days for first fruit harvesting, days for first female flower anthesis, fruit polar diameter and internodal length. Cluster II showed maximum mean value for leaf area, days for first male flower anthesis, pericarp/seed ball ratio, node number at first male flower appear ,TSS, number of primary branches per plant, fruit pericarp thickness, and fruit weight. Cluster III showed maximum mean value for node number at first female flower appear and number of fruits/plant. Cluster IV showed maximum mean value for fruit yield, vine length, peripheral thickness of fruit and male:female bud ratio. Similar finding was also observed by (Muralidhara *et al.*, 2014 and Shivanandha *et al.*, 2013).

Table 1: Cluster mean values for eighteen characters of 18 pumpkin genotypes: -

Cluster	I	II	III	IV
Primary branches	3.73	4.07	3.70	3.81
Male/female bud ratio	6.80	5.96	5.90	11.87
Internodal length	11.06	10.80	10.07	10.60
Node no, at first female flower appear	20.49	21.73	22.68	20.95
Node no, at first male flower appear	9.07	9.80	8.80	7.73
Fruit weight (kg)	1.69	2.50	1.68	1.62
Pericarp/seed ball ratio	8.24	11.78	9.86	5.76
Vine length (cm)	169.48	226	220.67	227.78
Leaf area (cm^2)	298.77	337.52	262.3	335.29
Days for first male flower anthesis	48.08	50.67	41.11	40.52
Days for first female flower anthesis	53.76	48.27	51.68	48.27
No of fruits per plant	5.67	6.13	6.16	5.98
TSS (^{o}brix)	4.31	4.86	4.84	4.16
Fruit polar diameter (cm)	12.36	11.26	10.35	11.87
Peripheral thickness (cm)	45.20	52.67	52.43	53.29
Days for first fruit harvest	78.18	64.33	75.67	69.23
Pericarp thickness (cm)	2.28	3.16	2.54	2.29
Fruit yield (q/ha)	200.44	161.61	202.39	235.79

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