International Journal of Advanced Biochemistry Research 2024; 8(12): 618-622

International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2024; 8(12): 618-622
www.biochemjournal.com
Received: 18-10-2024
Accepted: 22-11-2024

Samita Shivaji Gavali
M.sc Students, Department of Agriculture Botany, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

SR Karad
Maize Breeder, AICRP on Maize, Maize Improvement Project, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

MS Mote
Associate Professor, Department of Agriculture Botany, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

SN Sathe
M.sc Students, Department of Agriculture Economics, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

SS Jadhav
M.sc Students, Department of Agriculture Botany, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Nireekshitha MK
M.sc Students, Department of Agriculture Botany, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

DR Kshirsagar
M.sc Students, Department of Entomology, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Corresponding Author:
Samita Shivaji Gavali
M.sc Students, Department of Agriculture Botany, RCSM College of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

Genetic diversity studies on yield and yield attributing traits of quality protein maize (*Zea mays* L.)

Samita Shivaji Gavali, SR Karad, MS Mote, SN Sathe, SS Jadhav, Nireekshitha MK and DR Kshirsagar

DOI: https://doi.org/10.33545/26174693.2024.v8.i12h.3225

Abstract
The present study on "Genetic diversity studies on yield and yield attributing traits of Quality Protein Maize (*Zea mays* L.)" was carried out at AICRP on Maize, Maize Improvement Project, Kasba Bawada, Kolhapur during *rabi 2*023. Fourty-two maize (*Zea mays* L.) genotypes were evaluated to measure genetic diversity. The 42 genotypes were grouped into eleven clusters in which six clusters are solitary. Cluster I contained maximum genotypes (18) followed by cluster V which contained 10 genotypes, cluster VI contained 4 genotypes and cluster VIII had 3 genotypes. The maximum inter cluster distance was observed between cluster VI and cluster VIII (D^2= 75.17) followed byclusters V and VI (D= 57.73), clusters VIII and IX (D = 54.36), clusters III and VIII (D=47.67) and clusters I and VIII (D=46.26) indicated that these genetically heterogeneous clusters of genotypes may be utilized in a hybridization program to further improvement in maize. The majority of the characters desirable mean values were found in cluster V and VIII. Thus, it would be possible to combine the desirable traits of several accessions by recombination breeding between genotypes of distinct clusters. It was observed under study that thousand kernel weight (g) contributed highest (68.99%) for diversity indicating scope for development for these personalities.

Keywords: Quality protein maize, *Zea mays* L., cluster, divergence, genetic diversity

Introduction
Maize (*Zea mays* L.) is a member of the tribe Maydae within the family Poaceae and originated in Mexico and Central America. Often referred to as the "queen of cereals," it is recognized for having the highest genetic yield potential. Classified as a "C4" plant, maize thrives in warm climates with adequate rainfall, predominantly being cultivated in humid subtropical and warmer temperate regions.

In India, maize ranks as the third most important food crop after rice and wheat. It has a somatic chromosome number of 20, a genome size of 2.3 gigabases, and contains over 32,000 genes. This versatile crop demonstrates wide adaptability and is unique among food cereals for its ability to be grown in various seasons, ecologies, and for multiple uses. However, it is sensitive to waterlogging conditions.

Globally, approximately 1,016.73 million metric tonnes of maize are produced annually, the highest output among major staple cereals. There are several types of maize, including normal yellow/white grains, sweet corn, baby corn, popcorn, waxy corn, high amylase corn, high oil corn, and quality protein maize. Additionally, maize serves as a significant industrial raw material, offering substantial opportunities for value addition.

Globally, maize is cultivated on over 160 million hectares across 166 countries, showcasing a wide range of soil types, climates, biodiversity, and management practices. It contributes significantly to global food production, accounting for about 40% (over 800 million tonnes) of total food cereal crop output. Among the world's maize-producing countries, the "United States" is the largest producer, contributing nearly 35% of total global maize production, while "China" follows with over 20% of production, despite having similar acreage. In the U.S., maize is a key driver of agricultural productivity, achieving over 101 tonnes per hectare, which is double the global average of 5.3 tonnes per hectare. In contrast, India's productivity is roughly half of the world average.

Quality Protein Maize (QPM) refers to a group of maize varieties that contain a recessive gene called opaque-2, which enhances the protein quality in the maize grain's endosperm. QPM grains provide nearly twice the amounts of lysine and tryptophan, two essential amino acids that are often limited in grains but are crucial for human health and for monogastric animals. Amino acids are the building blocks of protein, and the deficiency of tryptophan and lysine in normal maize results in lower protein quality. Diets that rely heavily on normal maize without high-quality protein sources can lead to protein malnutrition. Severe protein deficiency in children can cause kwashiorkor, often referred to as “weaning disease.” Substituting normal maize with QPM can enhance dietary quality and help combat malnutrition. Research has shown that poultry and pigs experience improved growth rates when fed QPM compared to normal maize. Thus, rural smallholder pig and poultry producers could greatly benefit from using QPM, particularly in areas lacking access to high-quality protein supplements.

Genetic diversity refers to the variability present among different genotypes within a species. A method developed by Mahalanobis (1936), known as Mahalanobis D^2 Statistics, is commonly used to assess genetic diversity in available germplasm. This technique evaluates the forces of differentiation at both intra-cluster and inter-cluster levels, aiding in the selection of genetically diverse parents for use in hybridization programs. Additionally, the D^2 statistics measure the degree of diversification and determine the relative contribution of each component character to the overall divergence in Quality Protein Maize (QPM).

Materials and Methods

The experimental material for the variability studies comprised of 42 genotypes of Maize. Field study was conducted at AICRP on Maize, Kasba Bawada farm, Kolhapur, *rabi* 2023. The experiment was laid out in a randomized block design with two replications. The analysis of divergence was carried out by D^2 statistics of Mahalanobis as described by Rao (2017) [15]. Cluster formation was done as per Tocher’s method as described by Rao (2017) [15]. Diagrammatic representation of cluster divergence showing different genotypes was obtained with the help of D^2 values between (inter-cluster distances) and within (intra-cluster distance) clusters.

Results and Discussion

A. Cluster formation

A method of determining the genotypes relative genetic proximity is clustering. When compared to the genotype of another cluster, the genotypes within the same cluster are thought to be more closely connected by origin and ancestry. In order to achieve transgressive breeding and diverse parent combinations, clustering is crucial for crop development. It is recommended that parents be chosen from several clusters. Finding the intra- and inter-cluster distances is the fundamental concept behind cluster formation. This serves as a guide for parents from different backgrounds. In the present experimental study, the 38 genotypes of kodo millet were grouped into eight clusters respectively. The cluster formation was done by using Tocher’s method as described by Rao (2017) [15]. These clusters in addition with genotypes included under them are presented in Table No. 1.

Among eleven clusters, Cluster I was the largest, containing 18 genotypes, followed by cluster V with 10 genotypes, cluster VI with 4 genotypes, and cluster VIII with 3 genotypes (including 1 genotype and 2 checks). Clusters II, III, IV, VII, IX, X, and XI were monogenotypic.

These results are in accordance with Patil *et al.*, (2017) [12], Bhusal *et al.,* (2016) [3], Bhadru *et al*., (2020) [2] who reported that cluster I had maximum number of genotypes and these genotypes are less divergent. Similarly observed that cluster I is the largest cluster and cluster II, III, IV, VII, IX, X, XI were monogenotypic and cluster V has highest intra cluster distance this indicates the presence of wide genetic diversity among the genotypes present within this cluster and Bhadru *et al*., (2020) [2], Patil *et al*., (2017) [12] reported that cluster II, III, IV, VII were monogenetic.

According to Islam *et al*., (2020) [6] who reported that the greater the distance between two clusters, the wider the genetic diversity between the genotypes. Similarly Bhusal *et al*., (2016) [3] and Bhadru *et al*., (2020) [2] reported that cluster IV, V, VI IX, X are solitary in nature

B. Intra and inter cluster distances

D^2 values from the divergence analysis were used to calculate the intra- and inter-cluster D^2 values. These values are presented in Table 2.

The highest intra-cluster distance was noted in cluster VIII (D^2 = 16.57), followed by cluster VI (D^2 = 15.71), cluster V (D^2 = 14.15), and cluster I (D^2 = 13.31), indicating significant genetic diversity among genotypes within these clusters. Here is an opportunity for improvement through other selection techniques because the high intra-cluster distance suggested the presence of a significant degree of heterogeneity inside the cluster. Conversely, the lowest intra-cluster distance was observed in cluster I (D^2 = 13.31). Clusters II, III, IV, VI, IX, X, and XI showed no intra-cluster distances due to being mono-genotypic in nature.

The maximum inter-cluster distance was recorded between clusters VII and VIII (D^2 = 75.17), followed by clusters V and VI (D^2 = 57.73), clusters VIII and X (D^2 = 54.36), clusters III and VIII (D^2 = 47.67) and clusters I and VIII (D^2 = 46.26) indicated that these genetically heterogeneous clusters of genotypes may be utilized in a hybridization program to further improve maize crops. Therefore, in hybridization programs aimed at creating high-yielding varieties, the genotypes of the most varied cluster may be utilized as parents. While, the minimum inter-cluster distances were observed between clusters II and III (D^2 = 7.56), followed by clusters II and IV (D^2 = 9.22), clusters VII and IX (D^2 = 13.19), and clusters I and I (D^2 = 13.31) reflecting their proximity to each other. For hybridization work, selecting parents based on substantial intra- and inter-cluster distances yields a variety of beneficial combination. According to the feature under consideration, the inter-cluster distance was greater than the intra-cluster distance, indicating more genetic diversity between genotypes of different clusters. Therefore, by hybridizing genotypes throughout the clusters, a combination with a wide heterotic response and improved recombination may be discovered.

C. Cluster means

Cluster means for yield and yield contributing characters of 42 maize genotypes are written below in Table 3.

On the basis of cluster means, the genotypes in the clusters X and I had superior results with a shorter number of days required for the character days to 50% tasseling. The genotypes in the clusters X and IV showed fewer days to silking in terms of 50% days to silking. In terms of the characteristic plant height, the genotypes from clusters III and VI were shown to be better. Plant height character were found in the genotypes from clusters X and XIII, and this is a desirable trait. The genotypes from clusters VII and VI have a minimum cob height therefore selection of genotypes will be helpful for the future breeding purpose. The genotypes from clusters VIII and V have maximum cob length and this is suitable character for selection. The genotypes belonging to clusters V and VIII had a highest cob width and thousand kernel weight. The genotypes with the highest protein % are found in clusters II and III. The genotypes with the highest yield per plant belonged to the V and VIII clusters. The majority of the characters' desirable mean values were found in cluster V and VIII. Thus, it would be possible to combine the desirable traits of several accessions by recombination breeding between genotypes of distinct clusters.

.

Table 1: Distribution of 42 genotypes of maize into different clusters

Cluster	Number of genotypes included	Name of genotypes
I	18	Hyd 09R-366, Hyd-18227, QPM 10273, Hyd 08R-2453-2, 52095, Hyd 08R-2526-17, N-8211-14, QPM Hyd 10152, 52346, Hyd R14-40228, GPM-532, 71642, QPM-10044-2, Hyd 09R-2168-1, Hyd-10108, Hyd 08R-435-1, Hyd 08R-3782, Z-485-2.
II	1	QPM-10051
III	1	IC-75119
IV	1	71245
V	10	70290, 70328, DMWNY-4091-2, 71025, Hyd 08R-1033-1, Hyd 08 R-2407-3, Hyd 06R-2169-1, QPM Hyd 10278, 70923, A2-9.
VI	4	Hyd-19082, N-8201-45, N-8211-1, 71030
VII	1	Hyd 08R-2437-1
VIII	3	71266, phule maharshi (C), vivek QPM 9 (C)
IX	1	VL-13672
X	1	71523
XI	1	71563

Table 2: Average intra and inter cluster D^2 and D values of eleven clusters formed from 42 genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	13.31 (3.64)	16.57 (4.07)	17.10 (4.13)	16.86 (4.10)	27.85 (5.27)	34.71 (5.89)	17.67 (4.20)	46.26 (6.80)	18.64 (4.31)	17.24 (4.15)	21.76 (4.66)
II		0.00	7.56 (2.74)	9.22 (3.03)	29.05 (5.39)	34.77 (5.89)	21.05 (4.58)	44.39 (6.66)	19.52 (4.41)	19.08 (4.36)	25.19 (5.01)
III			0.00	15.13 (3.89)	32.92 (5.73)	30.73 (5.54)	23.95 (4.89)	47.67 (6.90)	21.28 (4.61)	16.29 (4.03)	24.35 (4.93)
IV				0.00	22.27 (4.71)	41.79 (6.46)	17.47 (4.18)	38.61 (6.21)	15.43 (3.92)	23.89 (4.88)	25.03 (5.00)
V					14.15 (3.76)	57.73 (7.59)	20.80 (4.56)	26.33 (5.13)	20.76 (4.55)	37.67 (6.13)	26.66 (5.16)
VI						15.71 (3.96)	44.88 (6.69)	75.17 (8.67)	46.13 (6.79)	24.71 (4.97)	43.64 (6.60)
VII							0.00	39.72 (6.30)	13.19 (3.63)	28.58 (5.34)	26.65 (5.16)
VIII								16.57 (4.07)	36.27 (6.022)	54.36 (7.37)	38.00 (6.16)
IX									0.000	27.86 (5.27)	23.22 (4.81)
X										0.00	21.37 (4.62)
XI											0.00

Table 3: Mean performance of 11 clusters for 11 characters in maize.

Cluster	Days to 50 percent tasseling	Days to 50 percent silking	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob width (cm)	Number of kernel rows per cob	Cob weight (g)	Thousand kernel weight (g)	Grain yield per plant (g)	Protein percent
I	66.63	66.27	124.13	58.38	13.98	13.46	13.33	86.63	203.94	95.36	9.14
II	70.50	72.50	125.00	59.50	15.75	13.90	14.00	90.50	202.00	97.55	12.26
III	70.50	72.50	108.50	66.00	12.15	13.90	14.00	89.00	187.50	82.58	12.12
IV	66.00	68.00	131.00	57.50	16.40	14.70	14.00	112.00	225.50	111.83	11.82
V	67.25	69.25	148.80	71.65	17.81	15.71	14.20	151.85	268.75	122.45	9.23
VI	69.62	71.62	105.66	48.87	11.45	12.01	12.00	68.12	111.58	67.43	9.86
VII	73.50	75.50	130.00	42.00	12.50	13.00	12.00	78.50	252.00	88.05	8.71
VIII	71.50	73.50	193.33	110.16	17.43	15.81	15.33	169.83	297.16	132.35	10.87
IX	69.00	71.00	108.50	60.00	9.85	10.50	16.00	60.00	250.50	85.50	10.08
X	64.00	66.00	167.50	75.50	13.60	12.60	12.00	76.50	155.00	73.90	9.20
XI	67.00	69.00	179.50	107.50	14.50	12.90	14.00	87.50	192.50	86.00	8.15

Table 4: Percent contribution of 11 characters for divergence in maize.

Sr. No.	Source	Times ranked 1st	Contribution (%)
1	Days to 50 percent tasseling	13	1.51
2	Days to 50 percent silking	0	0.00
3	Plant height (cm)	4	0.46
4	Cob height (cm)	58	6.74
5	Cob length (cm)	35	4.07
6	Cob width (cm)	3	0.35
7	Number of kernel rows per cob	1	0.12
8	Cob weight (g)	0	0.00
9	Thousand kernel weight (g)	594	68.99
10	Protein percent	153	17.77
11	Grain yield per plant (g)	0	0.00
		Total	100.00

Conclusions

The 42 genotypes grouped into eleven clusters in which six clusters are solitary. Cluster I contained maximum genotypes (14). The majority of the characters' desirable mean values were found in cluster V and VIII. Thus, it would be possible to combine the desirable traits of several accessions by recombination breeding between genotypes of distinct clusters. According to the traits under consideration, the inter-cluster distance was greater than the intra-cluster distance, indicating more genetic diversity between genotypes of different clusters. It was observed under study that thousand kerel weight (g) contributed highest (68.99%) for diversity indicating scope for development for these personalities.

Acknowledgement

The Authors are thankful to AICRP on Maize, Kasba Bawada, Kolhapur for providing maize genotypes to conduct the experiment.

References

1. Aboyi IK, Ojo AA, Kalu BA, Adeyemo MO. Genetic variability, heritability, and genetic advance in S1 progenies of extra-early and early maize (*Zea mays* L.) populations. J Sustain Agric Environ. 2004;6(2):179-184.
2. Bhadru D, Swarnalatha V, Mallaiah B, Sreelatha D, Kumar MVN, Reddy ML. Study of genetic variability and diversity in maize (*Zea mays* L.) inbred lines. Curr J Appl Sci Technol. 2020;39(38):31-39.
3. Bhusal TN, Lal GM, Marker S, Synrem GJ. Discrimination of maize (*Zea mays* L.) inbreds for morpho-physiological and yield traits by D statistics and principal component analysis (PCA). Asian J Bio Sci. 2016;11(1):77-84.

4. Ghosh A, Subba V, Roy A, Ghosh A, Kundagrami S. Genetic variability and character association of grain yield components in some inbred lines of maize (*Zea mays* L.). J Agroecol Nat Resour Manag. 2014;1(2):34-39.
5. Grace B, Marker S, Rajasekhar D. Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). J Pharmacogn Phytochem. 2018;7(1):2813-2816.
6. Islam NU, Ali G, Dar ZA, Maqbool S, Kumar B, Bhat A. Genetic divergence in maize (*Zea mays* L.) inbred lines. Int J Chem Stud. 2020;8(1):425-428.
7. Kandel M, Ghimire SK, Ojha BR, Shrestha J. Analysis of genetic diversity among the maize inbred lines (*Zea mays* L.) under sand heat stress condition. J Maize Res Dev. 2017;3(1):86-97.
8. Khumkar MS, Singh RD. Divergence analysis of elite inbred lines of maize (*Zea mays* L.). Ann Agric Res. 2002;23:595-601.
9. Mallikarjuna S. Study of genetic diversity in elite inbred lines of maize (*Zea mays* L.). PhD Thesis. Acharya NG Ranga Agricultural University, Guntur; 2019.
10. Matin MQI, Uddin MS, Rohman MM, Amiruzzaman M, Azad AK, Banik BR. Genetic variability and path analysis studies in hybrid maize (*Zea mays* L.). Am J Plant Sci. 2017;8(12):3101-3109.
11. More AJ, Bhoite KD, Pardeshi SR. Genetic diversity studies in forage maize (*Zea mays* L.). Res Crops. 2006;7(3):728.
12. Patil SM, Jakhar DS, Kumar K, Meena S. Genetic diversity studies in maize (*Zea mays* L.) germplasm from India. Int J Plant Soil Sci. 2017;14(6):1-6.
13. Priyanka J, Banshidhar SRA, Singh R. Estimation of genetic parameters for yield-related traits and grain zinc concentration in biofortified inbred lines of maize (*Zea mays* L.). Pharma Innov J. 2019;8(3):87-91.
14. Reddy KHP, Agrawal BD. Estimation of genetic variation in an improved population of maize (*Zea mays* L.). Madras Agric J. 2012;79(12):714-719.
15. Suryanarayana L, Sekhar MR, Babu DR, Ramana AV, Rao VS. Genetic divergence studies in maize (*Zea mays* L.). Int J Curr Microbiol Appl Sci. 2017;6(7):360-365.
16. Tang H, Huang YQ, Yan JB, Liu ZH, Tang JH, Zheng YL, *et al*. Genetic analysis of yield traits with elite maize hybrids. Acta Agron Sin. 2004;30(9):922-926.