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AR Patil

PG Scholar, Department of
Genetics and Plant Breeding,
RCSM College of Agriculture,
Kolhapur, Maharashtra, India

Dr. MS Kamble

Assistant Professor,
Department of Agricultural
Botany, RCSM College of
Agriculture, Kolhapur,
Maharashtra, India

Dr. SR Karad

Maize Breeder, AICRP on
Maize, Kolhapur,
Maharashtra, India

Dr. PN Gajbhiye

Assistant Professor,
Department of Soil Science and
Agricultural Chemistry, RCSM
College of Agriculture,
Kolhapur, Maharashtra, India

Dr. SJ Waghmare

Assistant Professor,
Department of Plant
Pathology, RCSM College of
Agriculture, Kolhapur,
Maharashtra, India

KA Wagh

Ph.D., Research Scholar,
Department of Genetics and
Plant Breeding, Post Graduate
Institute, MPKV, Rahuri,
Maharashtra, India

ON Ragade

PG Scholar, Department of
Genetics and Plant Breeding,
RCSM College of Agriculture,
Kolhapur, Maharashtra, India

Corresponding Author:

AR Patil

PG Scholar, Department of
Genetics and Plant Breeding,
RCSM College of Agriculture,
Kolhapur, Maharashtra, India

Genetic diversity and trait variability in maize: A study across drought and normal environmental conditions

AR Patil, MS Kamble, Dr. SR Karad, PN Gajbhiye, SJ Waghmare, KA Wagh and ON Ragade

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Abstract

This study investigates the genetic diversity of 17 maize (*Zea mays* L.) genotypes under drought and normal conditions using cluster analysis. Tocher's method was employed to classify the genotypes, revealing nine clusters under drought conditions and five clusters under normal conditions. The findings indicate that Cluster I under drought contained the largest group, suggesting shared adaptive traits among the genotypes. Intra-cluster distance analysis revealed substantial genetic variability within certain clusters, particularly for clusters I and IV under drought and cluster V under normal conditions. Inter-cluster distances highlighted significant genetic divergence between clusters, guiding the selection of parental lines for hybridization. The analysis of cluster means demonstrated variability in traits such as days to flowering, plant height, cob length, and kernel traits, indicating potential for selection in breeding programs. Notably, protein and proline content emerged as key contributors to genetic divergence, underscoring their relevance for drought resilience. These results provide critical insights for breeders in developing improved maize varieties adapted to varying environmental conditions.

Keywords: Maize, genetic diversity, clusters, drought, normal

Introduction

Maize (*Zea mays* L.) is a staple food crop globally, contributing significantly to food security and agricultural sustainability. Its cultivation is increasingly challenged by climate variability, particularly drought, which adversely affects growth, yield and nutritional quality. Understanding the genetic diversity of maize genotypes is crucial for developing effective breeding strategies that enhance resilience to environmental stresses. Genetic diversity influences the adaptability and productivity of maize, enabling breeders to select for traits that confer tolerance to drought and other abiotic stresses (Hallauer & Miranda, 1988; Reif *et al.*, 2005) [5, 30].

Cluster analysis, particularly Tocher's method, is a valuable tool for categorizing genotypes based on their genetic similarities and differences, allowing breeders to identify diverse parental lines for hybridization. The insights gained from this analysis not only elucidate the genetic relationships among genotypes but also inform breeding strategies aimed at enhancing drought tolerance and overall performance (Murthy and Arunachalam, 1966; Venkatesan and Subramanian, 2000) [22, 43].

In this study, 17 maize genotypes were tested under drought and normal conditions, assessing genetic divergence, intra and inter-cluster distances, cluster means and the percent contribution of various characters to total genetic divergence. The findings reveal significant variability in the traits associated with drought resistance and adaptability, emphasizing the need for targeted breeding programs that can optimize yield and resilience in the face of climate change (Singh *et al.*, 2015; Reddy *et al.*, 2004) [40, 29]. By integrating insights from cluster analysis and genetic diversity assessments, this research aims to guide maize improvement efforts and contribute to the development of varieties that thrive both under drought and normal growing conditions.

Materials and Methods

The experimental material for the variability studies comprised of 17 genotypes of maize. The experimental material has been obtained from Maize Improvement Project, Kasba Bawda, Kolhapur, Maharashtra. Field study was conducted at Maize Improvement Project, Kasba Bawda, Kolhapur during *Rabi*, 2023. The experiment was laid out in a randomized block design with three replications. The analysis of divergence was carried out by D^2 statistics of Mahalanobis as described by Rao (1952) [26]. Cluster formation was done as per Tocher's method as described by Rao (1952) [26]. 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

Understanding genetic diversity is crucial for effective breeding strategies in maize (*Zea mays* L.), particularly in the context of climate variability and the increasing prevalence of drought conditions. Genetic diversity within and among maize genotypes influences adaptability, resilience and yield potential under various environmental stresses. Cluster analysis serves as a valuable tool for categorizing genotypes based on their genetic similarities and differences, enabling the identification of diverse parental lines for hybridization. This method allows breeders to select genotypes that exhibit desirable traits, ultimately leading to improved maize varieties that can withstand adverse conditions.

In this study, we employed Tocher's method to group 17 maize genotypes based on their genetic divergence both under drought and normal conditions. The insights gained from this analysis not only provide a clearer understanding of the genetic relationships among the genotypes but also inform breeding strategies aimed at enhancing drought tolerance and overall performance. The contrasting cluster formations under drought and normal conditions highlight the genotypic responses to varying environmental factors, which is critical for developing effective breeding programs tailored to specific conditions.

Drought Condition

Under drought conditions, the genotypes were grouped into nine distinct clusters. Cluster I emerged as the largest, containing seven genotypes, demonstrating their genetic similarity under drought stress. This grouping suggests that these genotypes share similar adaptive mechanisms to drought. Clusters III and IV each contained two genotypes, while clusters II, V, VI, VII, VIII and IX were solitary clusters, indicating that the genotypes in these clusters are highly divergent from others (Rao, 1952; Bhatt, 1970; Murthy and Arunachalam, 1966; Venkatesan and Subramanian, 2000) [26, 3, 22, 43]. The formation of solitary clusters under drought conditions highlights the distinctiveness of certain genotypes that may possess unique traits enabling them to cope with drought stress (Singh *et al.*, 2015; Sharma *et al.*, 2013) [40, 37].

Normal Condition

In normal conditions, the 17 genotypes were grouped into five clusters, with Cluster I containing the largest number of genotypes (10), showing genetic similarities under

favourable conditions. Cluster V comprised four genotypes, while clusters II, III and IV were solitary, containing only one genotype each (Rao, 1952; Murthy & Arunachalam, 1966; Roy & Panwar, 1993) [26, 22, 31]. The formation of larger clusters in normal conditions reflects reduced genetic divergence among the genotypes compared to the drought condition. This reduced divergence may indicate shared growth traits among the genotypes under optimal growing conditions (Bhatt, 1970; Jambhulkar *et al.*, 2018) [3, 8].

The clear differences in cluster formation between drought and normal conditions suggest that specific genotypes have adapted more effectively to stress environments, which could be exploited for breeding programs aimed at drought tolerance (Venkatesan and Subramanian, 2000; Reddy *et al.*, 2004) [43, 29].

B. Intra and Inter Cluster Distances

The evaluation of intra and inter cluster distances is vital for understanding the genetic diversity among maize genotypes, which can significantly influence breeding strategies. Intra-cluster distance reflects the genetic variability within a cluster, while inter-cluster distance indicates the divergence between different clusters. This information is essential for breeders aiming to enhance specific traits in maize through hybridization.

Intra-cluster distance

Drought Condition

In drought conditions, the highest intra-cluster distance was observed for Cluster I ($D^2 = 9.13$), followed by Cluster IV ($D^2 = 8.75$). This indicates a significant level of genetic variability among the genotypes within these clusters, suggesting that they may possess diverse adaptive traits beneficial for drought tolerance (Mather & Jinks, 1982; Rao, 1952; Singh *et al.*, 2015) [18, 26, 40]. Conversely, the lowest intra-cluster distance was recorded for Cluster III ($D^2 = 7.45$), which may imply a narrower genetic base among the genotypes in this cluster (Mishra *et al.*, 2016) [21]. Notably, the solitary clusters II, V, VI, VII, VIII and IX exhibited no intra-cluster distances, reflecting their mono-genotypic nature, which limits their potential for hybridization.

Normal Condition

Under normal conditions, the highest intra-cluster distance was recorded for Cluster V ($D^2 = 9.73$), while Cluster I had the lowest ($D^2 = 9.13$). This pattern indicates that while, certain genotypes cluster closely, others exhibit more substantial genetic variability, which is crucial for selecting parents for hybridization aimed at improving yield and stress resistance (Murthy and Arunachalam, 1966; Venkatesan and Subramanian, 2000) [22, 43]. The solitary clusters (II, III and IV) again showed no intra-cluster distance, emphasizing their uniqueness.

Inter Cluster Distance

Inter-cluster distances provide critical insights into the genetic divergence between different clusters, guiding the selection of diverse parental lines. In drought conditions, the maximum inter-cluster distance was observed between Clusters VII and IX ($D^2 = 31.91$), indicating substantial genetic divergence. This was followed by Clusters IV and IX ($D^2 = 27.96$) and Clusters I and IX ($D^2 = 27.43$), suggesting that these genotypes can be utilized as parents for hybridization to develop drought-resistant varieties

(Bhatt, 1970; Reddy *et al.*, 2004) [3, 29]. In normal conditions, the highest inter-cluster distance was recorded between Clusters III and V ($D^2 = 17.96$), followed by Clusters I and V ($D^2 = 13.14$) and Clusters II and V ($D^2 = 12.68$). The minimum inter-cluster distances in drought conditions were found between Clusters V and II ($D^2 = 9.19$) and between Clusters VI and II ($D^2 = 11.36$), indicating closer genetic relationships that may limit their effectiveness as diverse parents in breeding programs (Khan *et al.*, 2014; Mather & Jinks, 1982) [12, 18]. Similarly, in normal conditions, the least distance was recorded between Clusters IV and II ($D^2 = 6.57$), underscoring the genetic proximity among these genotypes (Rao, 1952; Venkatesan and Subramanian, 2000) [26, 43].

The significant variation in both intra and inter-cluster distances emphasizes the necessity of selecting genetically diverse parents for hybridization. Genotypes with larger inter-cluster distances are more likely to produce offspring with enhanced traits, such as improved drought resistance and overall yield potential.

C. Cluster Means

The analysis of cluster means for the 15 characters evaluated in maize genotypes demonstrated considerable variability, emphasizing their potential for selection in breeding programs under both drought and normal conditions. For days to 50 per cent tasselling, cluster I exhibited the earliest flowering, taking only 58.14 days under drought conditions, while cluster IV required significantly longer, at 68.50 days. In contrast, under normal conditions, cluster III emerged as the earliest flowering group at 60.00 days compared to cluster V, which took 70.17 days (Sahu *et al.*, 2020; Kumar *et al.*, 2021) [32, 14, 16]. Similar trends were observed for days to 50 per cent silking, where cluster I showed the earliest silking at 60.71 days under drought, whereas cluster IV needed the most time, at 71.50 days. Under normal conditions, cluster III again showed earlier silking at 62.00 days, contrasting with cluster V, which required 73.08 days (Mishra *et al.*, 2019; Singh *et al.*, 2022) [21, 41].

In terms of plant height, solitary cluster VII recorded the tallest plants at 166.67 cm under drought, whereas cluster IX was the shortest at 135.00 cm. In normal conditions, cluster V exhibited the maximum height at 172.67 cm, while cluster III was the shortest at 148.67 cm (Patel *et al.*, 2021; Yadav *et al.*, 2022) [23, 46]. Cob height followed a similar trend; cluster IX had the shortest height at 58.33 cm under drought, while cluster VII reached a maximum of 90.67 cm. Under normal conditions, cluster V recorded the highest cob height at 78.83 cm, in contrast to the shortest height of 68.00 cm in cluster IV (Sharma *et al.*, 2020; Raut *et al.*, 2023) [35, 28].

Regarding days to 75 per cent dry husk, cluster VIII required the least time under drought (102.00 days), while cluster IV needed the most (111.50 days). In normal conditions, cluster III demonstrated the shortest duration at 105.33 days, compared to cluster V, which took 113.67 days (Jha *et al.*, 2019; Mehta *et al.*, 2021) [10, 20]. Cob length results indicated that cluster VII had the longest cob at 16.43 cm under drought, while cluster V was the shortest at 12.27 cm. In normal conditions, cluster IV achieved the maximum cob length at 18.93 cm, whereas cluster III recorded the shortest at 14.90 cm (Jaiswal *et al.*, 2020; Kumar *et al.*, 2022) [7, 13].

For cob width, cluster VII displayed the maximum width of 14.00 cm in drought, while cluster V recorded the minimum at 11.67 cm. Under normal conditions, cluster IV exhibited the largest cob width at 14.22 cm, with cluster I having the smallest at 13.22 cm (Verma *et al.*, 2020; Singh and Kaur, 2023) [44, 38]. The number of cobs per plot was highest in cluster VII at 30.00 under drought, while cluster III had the lowest at 19.33. In normal conditions, cluster IV had the maximum number of cobs at 29.00, compared to the minimum of 23.33 in cluster III (Bansal *et al.*, 2021; Yadav *et al.*, 2023) [2, 47].

Furthermore, solitary cluster VII exhibited the highest number of kernel rows per cob at 17.33 under drought, while clusters II and V had the lowest at 11.33. In normal conditions, cluster IV had the maximum number of kernel rows per cob at 16.67, while cluster II had the minimum at 12.67 (Patel *et al.*, 2022; Kumar *et al.*, 2023) [17, 24]. Regarding the number of kernels per row, cluster VII achieved the highest at 35.33 in drought, while cluster V showed the lowest. Under normal conditions, cluster IV recorded the maximum number of kernels per row at 38.33, with cluster III at the minimum (Sharma *et al.*, 2021; Raut *et al.*, 2022) [36, 27].

Cob weight was highest in solitary cluster VII at 146.33 g in drought, while cluster II had the lowest at 107.87 g. In normal conditions, cluster II achieved the maximum cob weight at 158.37 g, while cluster I recorded the minimum at 132.19 g (Singh *et al.*, 2020; Jha *et al.*, 2021) [39, 9]. For 100 kernel weight, solitary cluster VII recorded the highest at 27.03 g under drought, while cluster V was the lowest at 20.26 g. In normal conditions, cluster IV showed the maximum at 27.87 g, with cluster III at the minimum weight of 22.39 g (Mehta *et al.*, 2022; Sharma & Singh, 2023) [34, 19]. The proline content was highest in cluster VII at 0.64 mg/g under drought, while cluster VIII had the lowest at 0.42 mg/g. In normal conditions, cluster II had the maximum proline content at 0.48 mg/g, while cluster I recorded the minimum at 0.40 mg/g (Kumar *et al.*, 2020; Yadav *et al.*, 2021) [15, 45]. Lastly, protein content was highest in cluster IX at 16.10 per cent under drought, with cluster I showing the lowest at 9.26 per cent. Under normal conditions, cluster I recorded a high protein content of 9.42 per cent, while cluster III had the lowest at 7.72 per cent (Bansal *et al.*, 2020; Jaiswal *et al.*, 2022) [1, 6].

This comprehensive examination of cluster means illustrates the diverse performance of maize genotypes under varying conditions, providing valuable insights for breeders in selecting suitable parents for hybridization strategies.

D. Percent contribution of various characters for divergence

Understanding the percent contribution of various traits to total genetic divergence in maize is pivotal for breeding programs, particularly in developing resilient varieties suited for varying environmental conditions. This analysis aids in identifying key traits that could be targeted for selection, facilitating improved yields and better adaptation to stress conditions.

In the context of drought conditions, protein content was identified as the largest contributor to divergence, accounting for 64.71 per cent of total variance. This suggests that higher protein content may be linked to better performance under stress, supporting findings by Velu *et al.* (2018) [42] and Shakoor *et al.* (2019) [33], who highlighted

protein's role in physiological adaptations. The second most significant contributor was proline content, with a 15.44 per cent share, indicating its importance in osmotic adjustment and stress tolerance (Jinks, 1986; Ranjan *et al.*, 2022) [11, 25]. Other notable contributors included days to 50 per cent tasselling (5.88%) and 100 kernel weight (4.41%), both critical for yield stability (Zhang *et al.*, 2020; Kumar *et al.*, 2021) [14, 16]. Conversely, traits like number of kernel rows per cob, cob weight and yield per plant contributed minimally (0.74% each), suggesting that these traits might be less influential in drought conditions (Shakoor *et al.*, 2019) [33]. In normal conditions, the contribution of protein content remained significant, accounting for 36.03 per cent of the divergence, followed by proline (25.00%) and days to 50 per cent tasselling (11.75%). These findings are corroborated by research from Gaffney *et al.* (2019) [4] and

Singh *et al.* (2020) [39], which emphasizes the importance of these traits in promoting genetic diversity and adaptability. Additionally, the number of kernel per row contributed 10.29 per cent, highlighting its potential role in enhancing yield in favourable conditions. However, traits such as cob height (0.74%) and days to 50 per cent silking (0.00%) showed negligible contributions, indicating less relevance in normal growth conditions (Kumar *et al.*, 2021; Ranjan *et al.*, 2022) [14, 16].

These results underscore the necessity of incorporating traits like protein and proline content into breeding strategies aimed at improving both yield and resilience in maize. The differential contributions observed under drought and normal conditions indicate that breeding programs should focus on selecting for these traits to achieve optimal performance across various environments.

Table 1: Distribution of 17 genotypes of maize into 9 different clusters in drought condition

Clusters	No. of genotypes included	Name of genotypes	Specific Character
I	7	DMRH-1305, PMH 7-222, 11242 X LM16, 11328 X V373, 11341 X LM16, Rajarshi and Phule Maharshi	DFT, DFS, DDH
II	1	11197 X LM16	Lowest CW
III	2	11023 X LM15 and 11289 X LM16	PH, CH, CL. Low NCPP and NKRC
IV	2	11687 X LM16 and DKC 7074	PT and high values for DFT, DFS and DDH
V	1	11399 X LM15	Lowest NKR and HKW
VI	1	11260 X LM16	Low YPP
VII	1	DKC 9164	Highest YPP
VIII	1	IMH-221	-
IX	1	11370 X V391	Highest PR

DFT= Days to 50 per cent tasselling, DFS= Days to 50 per cent silking, PH= Plant height, CH= Cob height, DDH= Days to 75 per cent dry husk, CL= Cob length, CW= Cob width, NCPP= Number of cobs per plot, NKRC= Number of kernel rows per cob, NKR= Number of kernel per row, CWE= cob weight, HKW= 100 kernel weight, PL= Proline, PT= Protein and YPP= Yield per plant.

Table 2: Distribution of 17 genotypes of maize into 9 different clusters in normal condition

Clusters	No. of genotypes included	Name of genotypes	Specific Character
I	10	DMRH-1305, PMH 7-222, 11197 X LM16, 11242 X LM16, 11260 X LM16, 11289 X LM16, 11328 X V373, 11370 X V391, 11399 X LM15 and Phule Maharshi	DFT, DFS, DDH, PH, CH, CL and CW. Highest PT content.
II	1	11023 X LM15	Highest PL
III	1	Rajarshi	Lowest CL, CW, NCPP, NKRC, NRK and HKW.
IV	1	IMH-221	Highest NKRC and NKR
V	4	11341 X LM16, 11687 X LM16, DKC 9164, DKC 7074	Highest Cob length, CW, NCPP, CWE, HKW and low PT content.

DFT= Days to 50 per cent tasselling, DFS= Days to 50 per cent silking, PH= Plant height, CH= Cob height, DDH= Days to 75 per cent dry husk, CL= Cob length, CW= Cob width, NCPP= Number of cobs per plot, NKRC= Number of kernel rows per cob, NKR= Number of kernel per row, CWE= cob weight, HKW= 100 kernel weight, PL= Proline, PT= Protein and YPP= Yield per plant.

Table 3: Average intra and intercluster D² and D values (in parenthesis) of maize in drought condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	9.13 (3.02)	11.66 (3.41)	21.28 (4.61)	13.13 (3.62)	18.44 (4.29)	16.94 (4.11)	14.71 (3.83)	13.49 (3.67)	27.43 (5.23)
Cluster II		0.00 (0.00)	16.62 (4.07)	11.70 (3.42)	9.19 (3.03)	11.36 (3.37)	16.82 (4.10)	15.42 (3.92)	19.95 (4.46)
Cluster III			7.45 (2.72)	21.74 (4.66)	18.29 (4.27)	13.79 (3.71)	21.62 (4.64)	18.29 (4.27)	17.66 (4.20)
Cluster IV				8.75 (2.95)	15.46 (3.93)	18.92 (4.34)	16.33 (4.04)	19.00 (4.35)	27.96 (5.28)
Cluster V					0.00 (0.00)	10.87 (3.29)	24.21 (4.92)	20.11 (4.48)	15.33 (3.91)
Cluster VI						0.00 (0.00)	22.82 (4.77)	13.80 (3.71)	11.45 (3.38)
Cluster VII							0.00 (0.00)	18.88 (3.34)	31.91 (5.64)
Cluster VIII								0.00 (0.00)	23.89 (4.88)
Cluster IX									0.00 (0.00)

Table 3: Average intra and intercluster D² and D values (in parenthesis) of maize in normal condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	9.12 (3.01)	11.11 (3.33)	12.15 (3.48)	11.18 (3.34)	13.14 (3.62)
Cluster II		0.00 (0.00)	11.73 (3.42)	6.57 (2.56)	12.68 (3.56)
Cluster III			0.00 (0.00)	10.47 (3.23)	17.96 (4.23)
Cluster IV				0.00 (0.00)	12.72 (3.56)
Cluster V					9.73 (3.11)

Table 4: Mean performance of 9 clusters for 15 characters in 17 genotypes of maize in drought condition

	DFT	DFS	PH	CH	DDH	CL	CW	NCPP	NKRC	NKR	CWE	HKW	PL	PT	YPP
Cluster I	58.14	60.61	144.48	66.19	102.57	13.78	12.33	22.48	13.24	28.48	112.66	22.71	0.49	9.26	92.83
Cluster II	60.67	63.00	156.00	79.67	104.67	12.80	11.77	20.00	11.33	26.67	107.87	20.54	0.52	12.00	89.85
Cluster III	60.00	62.67	146.00	66.17	102.67	15.43	12.73	19.33	16.00	32.00	129.98	24.55	0.56	13.28	105.33
Cluster IV	68.50	71.50	151.50	63.67	111.50	14.28	12.78	23.00	14.00	29.50	131.32	23.24	0.56	10.50	110.08
Cluster V	65.33	67.67	153.00	59.33	109.33	12.27	11.67	19.67	11.33	26.00	109.20	20.26	0.51	13.87	92.21
Cluster VI	59.00	61.33	134.33	58.67	102.33	14.47	12.53	24.33	14.67	29.67	110.23	23.37	0.48	13.20	89.45
Cluster VII	60.00	63.00	166.67	90.67	105.33	16.43	14.00	30.00	17.33	35.33	146.33	27.03	0.64	9.50	124.41
Cluster VIII	60.67	63.00	150.33	63.33	102.00	16.07	12.50	28.33	16.67	34.00	125.87	26.31	0.42	9.90	100.25
Cluster IX	58.67	61.00	135.00	58.33	104.00	14.00	12.10	23.33	13.33	28.67	113.53	22.92	0.49	16.10	91.85

Table 5: Mean performance of 9 clusters for 15 characters in 17 genotypes of maize in normal conditions

	DFT	DFS	PH	CH	DDH	CL	CW	NCPP	NKRC	NKR	CWE	HKW	PL	PT	YPP
Cluster I	62.633	65.333	154.633	72.033	107.133	15.747	13.220	24.433	14.667	30.600	132.194	23.537	0.402	9.417	111.211
Cluster II	64.667	67.000	157.000	72.000	107.333	16.933	13.543	26.333	16.000	33.333	158.367	24.947	0.480	8.633	135.220
Cluster III	60.000	62.000	148.667	70.333	105.333	14.900	12.500	23.333	12.667	29.333	139.533	22.393	0.410	7.720	120.867
Cluster IV	63.667	66.000	163.667	68.000	108.33	18.933	14.230	29.000	16.667	38.333	152.150	27.867	0.440	7.800	128.307
Cluster V	70.167	73.083	172.667	78.833	113.667	17.025	13.669	26.333	14.833	33.917	154.131	25.378	0.423	8.617	130.926

Table 6: Per cent contribution of 15 characters for divergence of maize in drought condition

Sr. No.	Source	Times Ranked 1 st	Contribution %
1	Days to 50 per cent tasselling	8	5.88
2	Days to 50 per cent silking	0	0.00
3	Plant height (cm)	0	0.00
4	Cob height (cm)	0	0.00
5	Days to 75 per cent dry husk	0	0.00
6	Cob length (cm)	0	0.00
7	Cob width (cm)	2	1.47
8	Number of cobs per plot	5	3.68
9	No. of Kernel Rows per cob	1	0.74
10	No. of Kernel per row	3	2.21
11	Cob weight (g)	1	0.74
12	100 kernel weight (g)	6	4.41
13	Proline (mgg ⁻¹)	21	15.44
14	Protein (%)	88	64.71
15	Yield per plant (g)	1	0.74

Table 7: Per cent contribution of 15 characters for divergence of maize in normal condition

Sr. No.	Character	Times Ranked 1 st	Contribution %
1	Days to 50 per cent tasselling	16	11.76
2	Days to 50 per cent silking	0	0.00
3	Plant height (cm)	0	0.00
4	Cob height (cm)	1	0.74
5	Days to 75 per cent dry husk	0	0.00
6	Cob length (cm)	4	2.94
7	Cob width (cm)	0	0.00
8	Number of cobs per plot	8	5.88
9	No. of Kernel Rows per cob	0	0.00
10	No. of Kernel per row	14	10.29
11	Cob weight(g)	6	4.41
12	100 kernel weight (g)	2	1.47
13	Proline (mgg ⁻¹)	34	25.00
14	Protein (%)	49	36.03
15	Yield per plant (g)	2	1.47

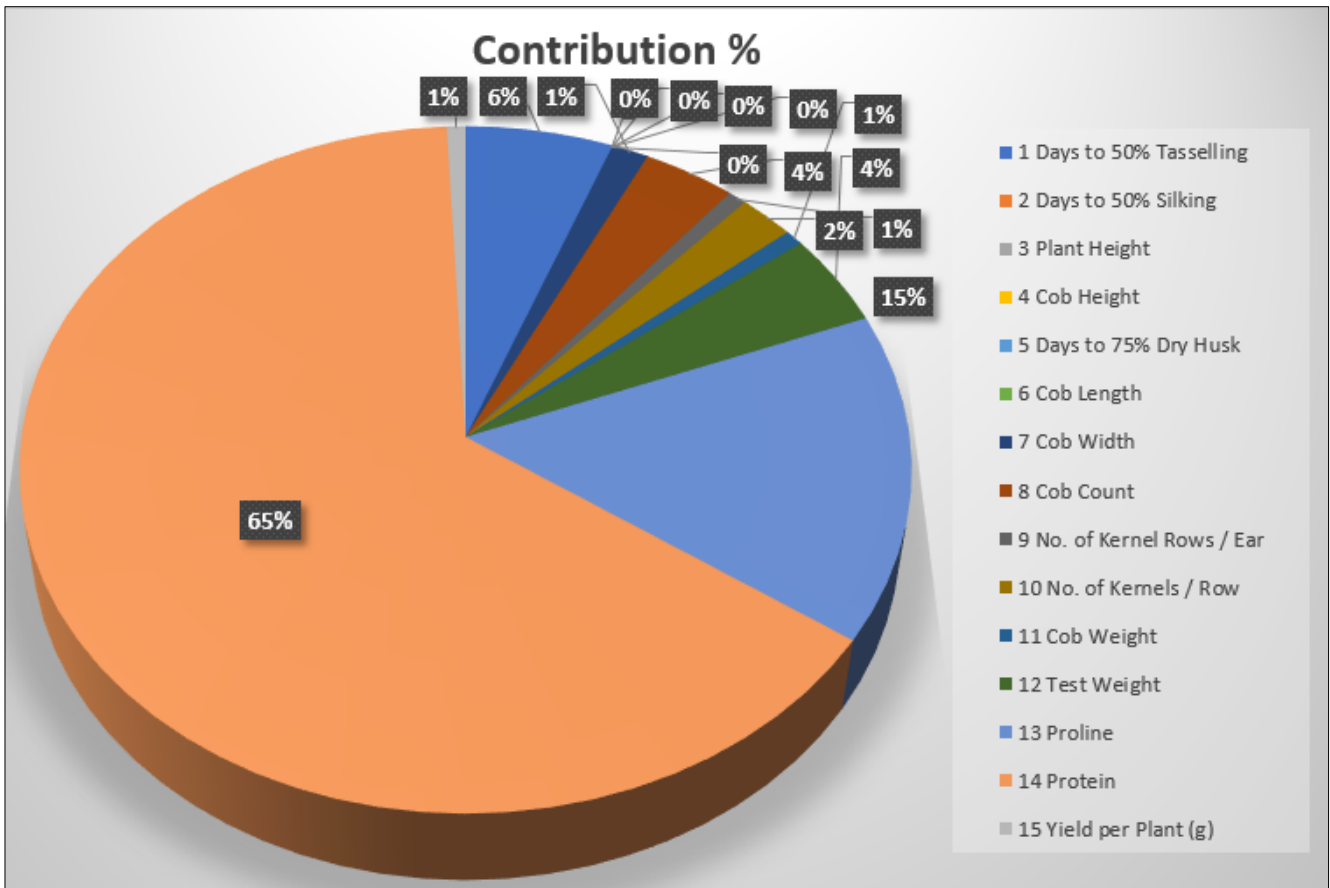


Fig 1: Per cent contribution of 15 characters to divergence in drought condition

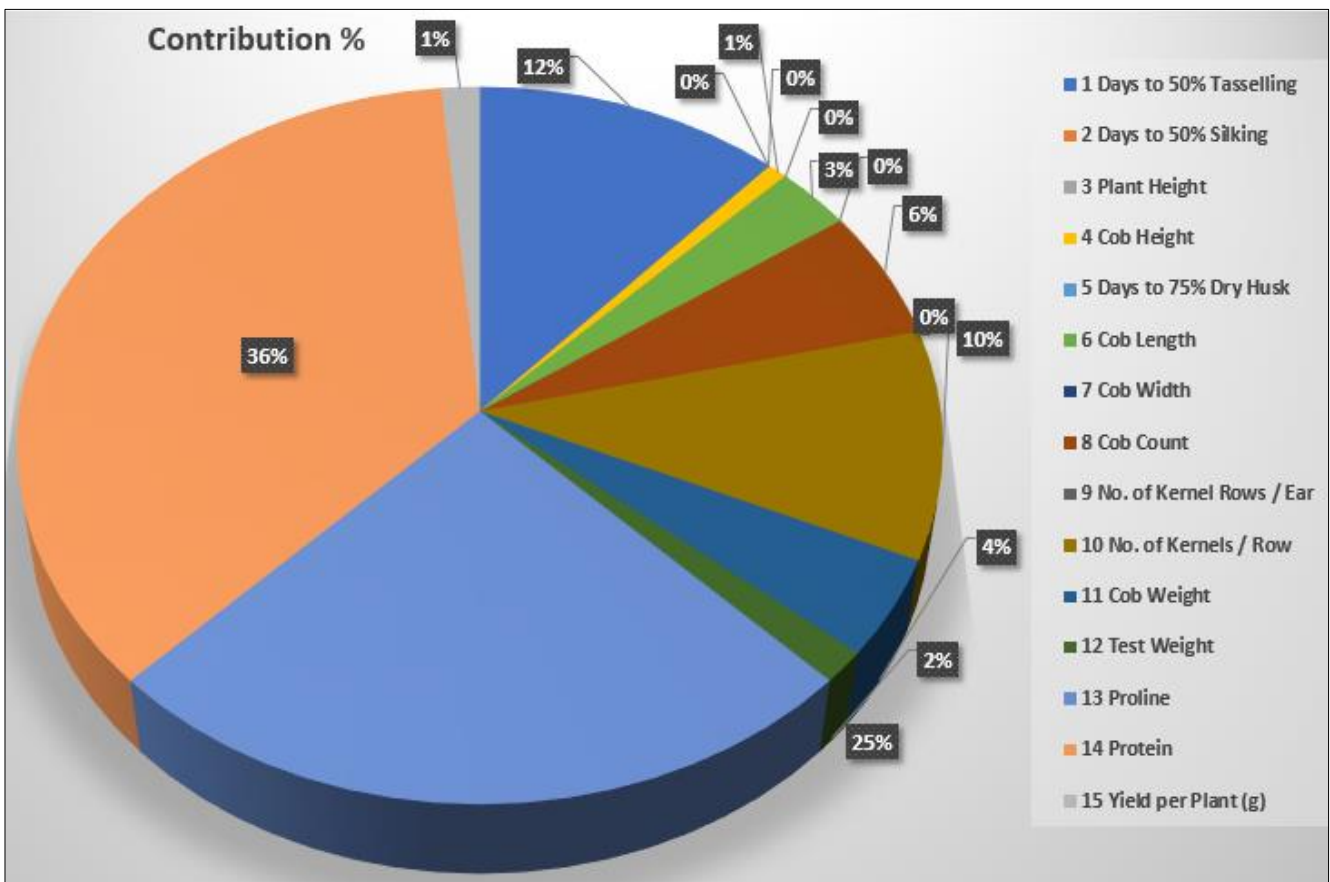


Fig 2: Per cent contribution of 15 characters to divergence in normal condition

Conclusion

The investigation of genetic diversity among maize genotypes under both drought and normal conditions has unveiled critical insights for breeding programs. The distinct cluster formations indicate that certain genotypes exhibit more effective adaptation to drought stress, while others thrive in optimal conditions. The evaluation of intra and inter-cluster distances reinforces the importance of selecting genetically diverse parents to enhance desirable traits such as drought resistance and yield potential.

The analysis of cluster means illustrates significant variability in agronomic traits, emphasizing the potential for selecting superior parents for hybridization. Additionally, the per cent contribution of traits such as protein and proline content to genetic divergence highlights their essential roles in breeding for resilience. This research underscores the necessity of integrating genetic diversity assessments into maize breeding strategies, paving the way for the development of varieties that are not only high-yielding but also resilient to the challenges posed by climate variability. Future breeding efforts should prioritize these traits to ensure sustainable maize production and food security in the face of ongoing environmental changes.

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