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Genetic divergence of elite maize (*Zea mays* L.) genotypes under rice-fallow zero tillage conditions

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ABSTRACT

Abstract: In maize, the assessment of genetic parameters and genetic diversity is essential for understanding the extent of heritable variation and identifying genetically diverse and superior genotypes for effective selection and hybridization. The present study was conducted at Agricultural Research Station, Ragolu, involving 42 maize hybrids. High genotypic coefficient of variation (GCV), high heritability coupled with high genetic advance as per cent of mean were observed for grain yield, ear placement height, days to 50% anthesis, days to 50% silking and plant height, indicating the predominance of additive gene effects and the effectiveness of phenotypic selection for these traits. Based on Tocher's method, the 42 hybrids were grouped into eight clusters, with Cluster IV being the largest (16 genotypes), followed by Cluster III (8) and Clusters I and II (6 genotypes each), indicating the presence of genetic similarity among genotypes within clusters. Considering cluster means and inter-cluster distances, crosses between genetically divergent clusters with desirable trait combinations were identified. Cluster II × Cluster III, involving PHM 19, PHM 14, PHM 17, PHM 9, P 3396 and DKC 9120 with genotypes of Cluster III, along with Cluster II × Cluster VIII (Bharathi 99) and Cluster II × Cluster V (PH 423217), may be utilized in hybridization programmes to generate greater variability and desirable transgressive segregants. These crosses may serve as useful source material for combining high yield potential with desirable maturity duration in subsequent breeding generations.

Keywords: Genetic Parameters, Genetic diversity analysis, Heritability, Maize, Variability

Introduction

Maize (*Zea mays* L.), popularly known as the 'Queen of Cereals', is one of the most important cereal crops grown worldwide and serves as a major source of food, feed, fodder and industrial raw material. In India, maize ranks third among the major cereal crops after rice and wheat with an area of 9.5 million ha and annual production of 24.5 million tonnes and has gained increasing importance owing to its diverse applications in food, livestock and poultry feed, starch industries, biofuel production and other value-added products (Sanodiya *et al.*, 2023) [1]. Despite its wide adaptability and high yield potential, the productivity of maize in India remains lower than that of several major maize-producing countries, emphasizing the need for continuous genetic improvement through the development and identification of superior genotypes with high yield potential, desirable maturity duration and wider adaptability (Maazou *et al.*, 2016) [2].

In rice-based cropping systems, rice-fallow conditions offer considerable potential for intensifying maize production, particularly in areas where residual soil moisture after rice harvest can be effectively utilized. Zero-tillage maize provides an opportunity for timely establishment of the succeeding crop while reducing tillage operations, production costs and turnaround time between rice and maize (Reddy *et al.*, 2012) [3]. However, maize grown under rice-fallow zero-tillage conditions may encounter several production constraints, including variable soil moisture availability, narrow sowing windows and other environmental stresses. Therefore, identification of genetically diverse and agronomically superior maize genotypes adapted to such conditions is essential for sustaining productivity and strengthening rice-based cropping systems (Rao *et al.*, 2011) [4].

The magnitude and nature of genetic variability present in a breeding population determine the effectiveness of selection and the success of crop improvement programmes. Genetic divergence analysis provides valuable information on the extent of diversity among genotypes and helps in identifying genetically distinct parents possessing desirable attributes (Kumar *et al.*, 2022) [5]. In hybrid maize breeding, the choice of diverse and agronomically superior parental materials is particularly important because the exploitation of heterosis depends, among other factors, on the genetic constitution and divergence of the parents. Hence, characterization of elite genotypes for genetic divergence can assist breeders in selecting suitable parents and broadening the genetic base of future breeding populations (Madhukumar *et al.*, 2023) [6].

Mahalanobis' D² statistic (Mahalanobis, 1936), as described in the multivariate approach of Tocher's method (Rao, 1952) [7], provides an effective means of quantifying genetic divergence among genotypes based on multiple correlated traits simultaneously. The method enables the grouping of genotypes into distinct clusters

and facilitates the assessment of intra- and inter-cluster distances. Genotypes belonging to clusters separated by larger inter-cluster distances may represent greater genetic divergence and, when combined with desirable cluster means, can provide useful parental combinations for hybridization. Such information is particularly valuable for identifying genotypes that can contribute favourable combinations of high grain yield, desirable maturity and other important agronomic traits under specific production environments (Duppala *et al.*, 2024) [8].

The amount and nature of genetic diversity among genotypes significantly influence the breeding strategies employed to enhance a crop's genetics. Maize is one such crop wherein hybrids are the commercial requirement (Banakara *et al.*, 2024) [9]. To develop high yielding hybrids, understanding and harnessing the genetic variability for the identification of candidate lines and including them in crop improvement for enhancement of existing germplasm is the key strategy (Reif *et al.*, 2005 and Hallauer *et al.*, 1988) [10]. The success of any breeding program relies on the level of useful variability within the population and the degree to which desirable traits are inherited (Manojkumar *et al.*, 2024).

Therefore, the present investigation was undertaken to assess the genetic divergence among elite maize genotypes under rice-fallow zero-tillage conditions at Agricultural Research Station, Ragolu, with the objective of identifying genetically diverse and agronomically desirable genotypes and clusters that could serve as potential parental sources in future maize improvement programmes. The study also aimed to examine the clustering pattern and inter-cluster divergence and to identify promising combinations of genetically divergent genotypes with desirable trait performance for developing superior maize hybrids and segregating populations suited to rice-fallow zero-tillage conditions.

Materials and Methods

The experimental material used in the study comprised of 42 hybrids obtained from different Research Centres of Acharya N. G. Ranga Agricultural University (ANGRAU), Guntur. (Table 1). The seeds were sown in a randomized complete block design (RCBD) with three replications at the Agricultural Research Station, Ragolu. The entries were sown paddy fallow Zero tills age with spacing of 60 cm and 20 cm between rows and between plants respectively. The crop was raised as per the recommended package of practices to obtain proper plant stand in the experiment.

The data on Plant Height, Ear placement height, Cob Length (cm), Cob Girth (cm), No. of kernel rows, No. of kernels per row, No. of kernels per cob and Grain yield were recorded on 10 randomly selected competitive plants for each treatment in each replication except for days to 50% anthesis and days to 50% silking which were recorded on then plot basis. Standard statistical procedure was used for analysis of variance and for genotypic and phenotypic coefficient of variation (Burton *et al.*, 1953) [11], heritability (Hanson *et al.*, 1956) [12] and genetic advance. Multivariate analysis was done as per Mahalanobis's D^2 statistics and the genotypes were grouped into different clusters following Tochers's method (Rao, 1952) [7].

Results and Discussion

Analysis of variance revealed that the mean sum of squares of genotypes for all the 10 characters studied were significant indicating the existence of considerable variability among the hybrids for all the characters under investigation. Based on the results of the analysis of variance, D^2 analysis was carried out. The clustering pattern, average intra and inter cluster distances, cluster means for different characters and number of hybrids included in different clusters determined separately were presented in Fig. 1 to 2 and Table 1 to 4. The results obtained are presented hereunder.

4.1 Variability, heritability and genetic advance

The estimates of environmental coefficient of variation (ECV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) for ten quantitative traits are presented in Table 1.

The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters, indicating that environmental factors had a relatively small influence on the expression of these traits. The narrow differences between PCV and GCV observed for most traits suggested that the observed variability was predominantly genetic in nature, making these characters amenable to effective selection (Satyanarayana *et al.*, 2023) [13].

Among the traits studied, grain yield exhibited the highest genotypic coefficient of variation (25.761%) and phenotypic coefficient of variation (29.056%), indicating the existence of substantial genetic variability for this trait. Ear placement height also recorded high GCV (19.292%) and PCV (21.340%), suggesting considerable scope for genetic improvement through selection. Similar findings were reported by Reddy *et al.*, 2024, Antony, B. J., *et al.*, 2024, Bharathi *et al.*, 2021 [14], for grain yield and Ear placement height.

Moderate GCV and PCV values were observed for plant height (12.835% and 14.402%), days to 50% anthesis (12.683% and 12.821%) days to 50% silking (12.298% and 12.428%) and number of kernels per cob (9.559% and 12.252%). These findings are in agreement with the findings of Fekadu Korsa *et al.*, 2024 [15], Reddy *et al.*, 2024, Pradhan *et al.* (2022) [16] for plant height, Sondaarava *et al.*, 2025 [17], Ochigbo *et al.*, 2021 [18] for days to 50% anthesis and days to 50% silking

In contrast, number of kernel rows (7.874% and 9.280%), number of kernels per row (7.887% and 9.882%), cob length (4.231% and 7.074%) and cob girth (3.853% and 4.962%) exhibited relatively low GCV and PCV, indicating limited genetic variability for these traits. Similar results were reported by Antony, B. J., *et al.*, 2024, Fekadu Korsa *et al.*, 2024 [15], Jilo, *et al.*, 2018 [19] for Number of kernel rows and number of kernels per row: Sondaarava *et al.*, 2025 [17], Ochigbo *et al.*, 2021 [18] for cob length and Fekadu Korsa *et al.*, 2024 [15], Gokulakrishnan *et al.*, 2021 [20], for cob girth.

Broad-sense heritability estimates ranged from 35.8% for cob length to 97.9% for both days to 50% anthesis and days to 50% silking. Very high heritability was observed for days to 50% anthesis (97.9%) and days to 50% silking (97.9%), followed by ear placement height (81.7%), plant height (79.4%) and grain yield (78.6%), number of kernel rows (72.0%), number of kernels per row (63.7%), number of kernels per cob (60.9%) and cob girth (60.3%) indicating that these traits were largely governed by genetic factors with comparatively less environmental influence. Similar findings have been reported by Fekadu Korsa *et al.*, 2024 [15], Reddy *et al.*, 2024, Pradhan *et al.* (2022) [16] and Gokulakrishnan *et al.*, 2021 [20] whereas cob length showed low heritability (35.8%), indicating greater environmental influence on its expression. Sondaarava *et al.*, 2025 [17], reported low heritability for cob length.

Genetic advance as per cent of mean (GAM) ranged from 5.213% for cob length to 47.052% for grain yield. Grain yield recorded the highest GAM (47.052%), followed by ear placement height (35.927%), days to 50% anthesis (25.847%), days to 50% silking (25.071%) and plant height (23.561%). These traits, coupled with high heritability estimates, suggest the predominance of additive gene action and indicate that direct selection would be highly effective for their improvement. Similar results were reported by Reddy *et al.* (2024) [16] for the characters like yield and ear height, Jilo *et al.*, 2018 [19] for ear placement height, plant height and grain yield. Moderate GAM was observed for number of kernels per cob (15.364%), number of kernel rows (13.765%) and number of kernels per row (12.966%), indicating moderate genetic gain through selection. Jilo *et al.*, 2018 [19] for number of kernels per row. On the other hand, cob girth (6.163%) and cob length (5.213%) exhibited low GAM (Gokulakrishnan *et al.*, 2021) [20]

20], suggesting limited response to selection due to the influence of non-additive gene action and environmental effects.

Overall, the combination of high GCV, high heritability and high genetic advance as per cent of mean for grain yield, ear placement height, days to 50% anthesis, days to 50% silking and plant height indicated that these traits are predominantly controlled by additive gene effects and can be effectively improved through simple phenotypic selection. In contrast, cob length and cob girth exhibited comparatively lower variability, lower genetic advance and lower to moderate heritability, suggesting that improvement of these traits through direct selection may be less effective.

4.2 Genetic divergence based on cluster distances

The 42 hybrids were grouped in to eight clusters (Table 2-3 & Fig. 1-2), out of which cluster IV was the largest, having sixteen genotypes followed by cluster III with eight genotypes, cluster II and I with six genotypes and cluster VII with three genotypes indicating the genetic similarity among the genotypes present in these clusters. Remaining three clusters V, VI and VIII are the solitary clusters having only one hybrid indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes present study. The clustering pattern revealed that the hybrids showed considerable genetic diversity among themselves by occupying eight different clusters.

The average intra- and inter-cluster distances among the eight clusters are presented in Table 3. The intra-cluster distance reflects the genetic diversity among genotypes within a cluster, whereas the inter-cluster distance indicates the extent of genetic divergence between different clusters. The intra-cluster distances ranged from 0.00 to 13.24. Cluster 3 recorded the highest intra-cluster distance (13.24), followed by Cluster 7 (11.26), Cluster 1 (9.20) and Cluster 2 (8.43), indicating the presence of relatively higher genetic variability among the genotypes within these clusters. In contrast, Clusters 5, 6 and 8 exhibited an intra-cluster distance of 0.00, suggesting that each of these clusters contained a single genotype and, therefore, no genetic divergence existed within them.

The inter-cluster distances were consistently greater than the corresponding intra-cluster distances, indicating substantial genetic divergence among the clusters. The highest inter-cluster distance was observed between Cluster 2 and Cluster 3 (228.78), followed by Cluster 2 and Cluster 8 (183.07), Cluster 2 and Cluster 5 (155.83) and Cluster 1 and Cluster 2 (143.00). The large genetic distances between these cluster pairs indicate the presence of wide genetic divergence among their constituent genotypes. Therefore, the hybrids in these cluster could be used as parents for inbred line development which can be used for new hybrids. In this context, hybrids from cluster I, II, III, V and VIII should be selected as parents for development of new inbreds to be used in new hybrid program of maize. These finding were supported by with Zaman *et al.*, (2013) [21], Rathod *et al.* (2021) [22], Hussain *et al.* (2021) [23] and Banakara *et al.* (2024) [9].

The lowest inter-cluster distance was observed between Cluster 1 and Cluster 6 (16.79), followed by Cluster 4 and Cluster 5 (18.06), Cluster 3 and Cluster 8 (24.03), Cluster 1 and Cluster 4 (24.11) and Cluster 1 and Cluster 5 (24.49). The relatively smaller distances among these cluster pairs indicate close genetic similarity among the constituent genotypes. Consequently, crosses involving genotypes from these clusters may offer comparatively limited scope for generating desirable variability.

Overall, the wide range of inter-cluster distances observed in the present study demonstrates the existence of considerable genetic diversity among the evaluated maize genotypes. Selection of parents from clusters exhibiting maximum inter-cluster distances, particularly Clusters 2 and 3, Clusters 2 and 8 and Clusters 2 and 5, could be used as parents for inbred line development. The cluster distances and Tocher's clustering pattern indicated substantial genetic divergence among the studied maize genotypes, which can be effectively exploited in a crossing programme. The, genotypes belonging to these highly divergent clusters may be selected as parents to generate

greater genetic variability and to facilitate the recovery of desirable recombinants in subsequent generations.

Based on the cluster composition, promising crosses may include Cluster II $\times$ Cluster III involving genotypes such as PHM 19, PHM 14, PHM 17, PHM 9, P 3396 and DKC 9120 with genotypes from Cluster III such as HQPM 5, P 3546, PH 421266, IQMH 2107, PDMH 1449, DHM 117, PH 1534 and PDMH 171213. Similarly, Cluster II $\times$ Cluster VIII, particularly involving Cluster VIII's Bharathi 99 and Cluster II $\times$ Cluster V, involving PH 423217, may also be considered. The cluster diagram further supports the distinct placement of these clusters, while Cluster IV comprised the largest group of genotypes, suggesting considerable diversity within the material. Thus, crosses between geographically or genetically divergent clusters, particularly Cluster II $\times$ Cluster III, Cluster II $\times$ Cluster VIII and Cluster II $\times$ Cluster V, should receive priority in the hybridization programme, with final parent selection based on the specific breeding objectives and per se performance of the genotypes.

4.3 Cluster mean analysis

The cluster mean values for ten quantitative traits are presented in Table 4. The cluster means provide an estimate of the average performance of the genotypes grouped within each cluster and aid in identifying clusters possessing desirable values for specific traits. Considerable variation in cluster means was observed for all the characters, indicating the presence of substantial genetic diversity among the maize genotypes.

For days to 50% anthesis, the lowest mean value was recorded by Cluster 3 (55.25 days), followed by Cluster 8 (59.67 days) and Cluster 5 (60.33 days), indicating their suitability as sources of earliness. The highest mean was observed in Cluster 2 (81.67 days), followed by Cluster 7 (71.67 days), representing late-maturing genotypes. Similarly, for days to 50% silking, Cluster 3 (57.00 days) exhibited the lowest mean, followed by Cluster 8 (61.67 days) and Cluster 5 (62.67 days), while Cluster 2 (83.83 days) recorded the highest mean, indicating delayed flowering. With respect to cob length, Cluster 5 (20.03 cm) recorded the highest mean value, followed by Cluster 7 (19.87 cm) and Cluster 4 (19.56 cm). The lowest cob length was observed in Cluster 8 (18.19 cm).

For plant height, the highest mean was observed in Cluster 8 (255.87 cm), followed by Cluster 4 (238.14 cm) and Cluster 3 (224.08 cm), whereas Cluster 1 (192.47 cm) recorded the lowest mean plant height. With respect to ear placement height, Cluster 6 (118.60 cm) recorded the highest mean, closely followed by Cluster 8 (116.93 cm), while Cluster 5 (57.73 cm) exhibited the lowest ear placement height. For cob length, Cluster 5 (20.03 cm) recorded the highest mean value, followed by Cluster 7 (19.87 cm) and Cluster 4 (19.56 cm). The lowest cob length was observed in Cluster 8 (18.19 cm). Regarding cob girth, the highest mean was recorded by Cluster 4 (4.94 cm), followed by Cluster 7 (4.93 cm) and Cluster 6 (4.82 cm), whereas Cluster 1 (4.68 cm) showed the lowest mean. For number of kernel rows per cob, Cluster 8 (18.00) recorded the highest mean, closely followed by Cluster 6 (17.67). The lowest mean was observed in Cluster 5 (14.27). The highest mean for number of kernels per row was recorded by Clusters 2 and 6 (39.67), followed by Cluster 7 (38.40), whereas Cluster 8 (32.60) exhibited the lowest mean. For number of kernels per cob, Cluster 6 (700.19) recorded the highest mean, followed by Cluster 7 (607.84) and Cluster 2 (588.27). The lowest mean was observed in Cluster 5 (511.23). Among all the clusters, Cluster 6 recorded the highest grain yield (153.30 g), followed by Cluster 1 (143.43 g) and Cluster 4 (139.14 g), indicating that these clusters comprised high-yielding genotypes. In contrast, Cluster 2 (71.94 g) and Cluster 7 (75.90 g) exhibited the lowest grain yield.

The cluster mean analysis indicated that Cluster 6 possessed superior mean performance for economically important traits such as grain yield, ear placement height, number of kernel rows, number of kernels per row and number of kernels per cob, making it a valuable source for yield improvement. Cluster 3 was characterized by early

flowering and silking, while Cluster 5 exhibited the longest cobs and the lowest ear placement height. Cluster 8 possessed the tallest plants and the highest number of kernel rows per cob. Considering both cluster mean performance and inter-cluster distances, hybridization between genetically divergent clusters with desirable trait combinations, particularly Cluster 2 and Cluster 3, Cluster 2 and Cluster 8 and Cluster 2 and Cluster 5, as well as involving the high-yielding Cluster 6, could be utilized as source materials for getting desirable transgressive segregants and having maximum yield along with short duration. These findings were in line with Zaman, & Islam, (2013) [21], Rathod *et al.* (2021) [22], Supriya *et al.* (2025) [24], Greeshma *et al.* (2025) [25].

Conclusion

Genetic diversity was studied to find out the more diverse maize hybrids. There was significant difference between genotypes for all the characters studied. high GCV, high heritability and high genetic ad-

vance as per cent of mean for grain yield, ear placement height, days to 50% anthesis, days to 50% silking and plant height indicated that these traits are predominantly controlled by additive gene effects and can be effectively improved through simple phenotypic selection. The 42 hybrids were grouped into eight clusters, out of which cluster IV was the largest, having sixteen genotypes followed by cluster III with eight genotypes, cluster II and I with six genotypes and cluster VII with three genotypes indicating the genetic similarity among the genotypes present in these clusters. Considering both cluster mean performance and inter-cluster distances, hybridization between genetically divergent clusters with desirable trait combinations, particularly Cluster 2 and Cluster 3, Cluster 2 and Cluster 8 and Cluster 2 and Cluster 5, as well as involving the high-yielding Cluster 6, could be utilized as source materials for getting desirable transgressive segregants and having maximum yield along with short duration.

Table 1. Genetic Parameters with respect to yield and yield contributing traits maize (*Zea mays* L)

	Days to 50% Anthesis	Days to 50% silking	Plant Height	Ear place- ment height	Cob Length (cm)	Cob Girth (Cm)	No. of kernel rows	No. of kernels per row	No. of kernels per cob	Grain Yield
GCV	12.683	12.298	12.835	19.292	4.231	3.853	7.874	7.887	9.559	25.761
PCV	12.821	12.428	14.402	21.340	7.074	4.962	9.280	9.882	12.252	29.056
ECV	1.874	1.789	6.535	9.123	5.669	3.127	4.910	5.955	7.664	13.438
h^2 (Broad Sense)	0.979	0.979	0.794	0.817	0.358	0.603	0.720	0.637	0.609	0.786
Genetic Advancement 5%	16.850	16.963	51.533	32.230	1.005	0.297	2.098	4.894	88.238	55.212
Gen. Adv as % of Mean 5%	25.847	25.071	23.561	35.927	5.213	6.163	13.765	12.966	15.364	47.052

Table 2. Clustering of forty-two maize genotypes based on D^2 analysis.

Cluster	No. of genotypes	Genotypes
I	6	PH 420009, PH 420147, PH 420016, BIO 9544, PDMH 16921, PH 423220
II	6	PHM 19, PHM 14, PHM 17, PHM 9, P 3396, DKC 9120
III	8	HQPM 5, P 3546, PH 421266, IQMH 2107, PDMH 1449, DHM 117, PH 1534, PDMH 171213
IV	16	PH 423218, PH 421343, PDMH 1222, PH 421473, Kaveri 50, PDMH 1540, PDMH 1829, PH 421449, PH 422024, PDMH 153227, P 3567, PH 422092, DHM 121, PH 423216, PH 423225, PH 423222
V	1	PH 423217
VI	1	PH 420205
VII	3	PHM 8171, PHM 66, PHM 18
VIII	1	Bharathi 99

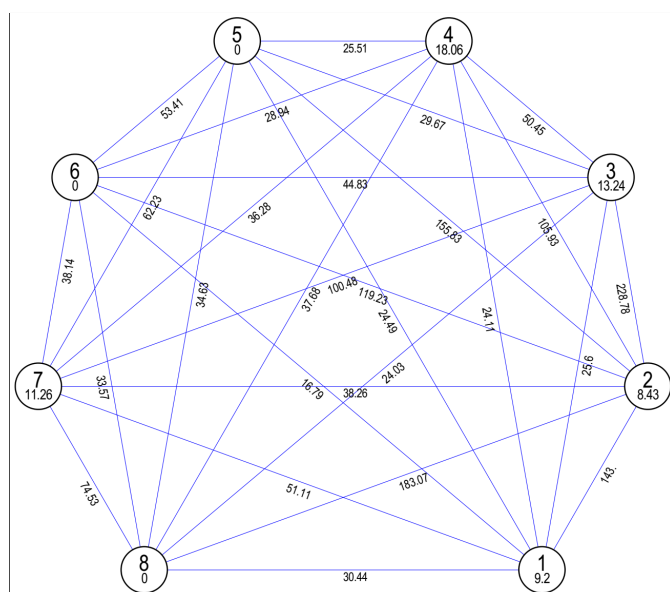
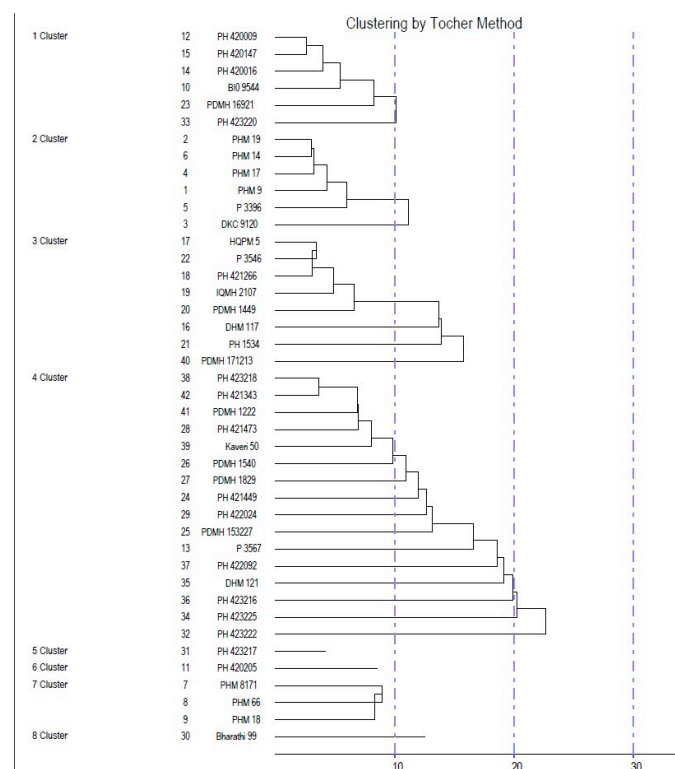
Table 3. Inter and intra-cluster distances among the maize hybrids

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	9.20	143.00	25.60	24.11	24.49	16.79	51.11	30.44
Cluster 2		8.43	228.78	105.93	155.83	119.23	38.26	183.07
Cluster 3			13.24	50.45	29.67	44.83	100.48	24.03
Cluster 4				18.06	25.51	28.94	36.28	37.68
Cluster 5					0.00	53.41	62.23	34.63
Cluster 6						0.00	38.14	33.57
Cluster 7							11.26	74.53
Cluster 8								0.00

(continued on next page)

Table 4. Cluster Means among the maize hybrids

Cluster	Days to 50% Anthesis	Days to 50% silking	Plant Height	Ear placement height	Cob Length (cm)	Cob Girth (Cm)	No. of kernel rows	No. of kernels per row	No. of kernels per cob	Grain Yield
Cluster 1	61.22	64.17	192.47	84.58	18.92	4.68	15.07	38.24	576.56	143.43
Cluster 2	81.67	83.83	193.50	81.02	18.51	4.73	14.82	39.67	588.27	71.94
Cluster 3	55.25	57.00	224.08	99.32	19.39	4.74	15.28	37.05	565.02	105.60
Cluster 4	65.00	67.81	238.14	88.12	19.56	4.94	15.07	37.38	561.90	139.14
Cluster 5	60.33	62.67	220.93	57.73	20.03	4.79	14.27	35.87	511.23	88.69
Cluster 6	63.67	66.67	205.73	118.60	19.11	4.82	17.67	39.67	700.19	153.30
Cluster 7	71.67	73.89	195.00	92.16	19.87	4.93	15.80	38.40	607.84	75.90
Cluster 8	59.67	61.67	255.87	116.93	18.19	4.79	18.00	32.60	586.80	95.51

**Figure 1.** Mahalanobis D² Euclidean distances between the clusters**Figure 2.** Clustering by Tocher's optimization method

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