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Genetic Divergence Analysis over Seasons in Single Cross Hybrids of Maize (*Zea mays* L.)

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ABSTRACT

D2 analysis in single cross hybrids of maize over seasons indicated the influence of seasons on clustering patterns based on morpho-physiological and yield components. The cluster analysis assigned the 45 hybrids of maize single cross hybrids into five, six and seven major clusters in rabi, summer, and kharif, respectively based on the quantitative characters indicating the importance of phenotypic descriptors to differentiate between them. The component characters viz., cob girth, kernel weight, and days to 50% tasseling contributed much to the clustering pattern of hybrids in all three seasons, while number of kernel rows cob-1, number of kernels row-1, cob length, SPAD meter reading, days to 50% silking and specific leaf weight contributed much less to the genetic diversity. Cluster means for different yield contributing characters also varied across seasons maximum being in rabi, kharif, and summer, respectively, while morpho-physiological characters were high in kharif followed by rabi and summer emphasizing the need for multi-environment testing for the identification of stable and superior hybrids. High levels of intra and inter-cluster distances indicated the presence of broad genetic variation between and within a cluster and utilization of them in crop improvement programmes. The top high-yielding hybrids viz., BML 7 × DFTY, BML 15 × PDM 1474, DFTY × Heypool and DFTY × PDM 145 consistently were included in the same clusters over seasons indicating their genetic similarities and stability in performance.

Keywords: *Maize (Zea mays L.), D2 analysis, Genetic Diversity and Yield and Yield Components*

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important staple food crop among all the cereals in the present world agriculture scenario due to its several uses and wider adaptability to different environments. It is used as food grain, animal feed, fodder and in industries for various purposes, chiefly for starch. It plays a significant role in human and livestock nutrition worldwide and has greater nutritional value, as it contains about 72% starch, 10% proteins, 8.5% fibre, 4.8% oil, 3% sugar and 1.7% ash, [1]. Maize occupies the third place at the global level after wheat and rice due its high production potential and broad resilience [3]. It contributes maximum among the cereal food crops (38%) annually to the global food production as compared to wheat (30%) and rice (20%) [3]. Maize accounts 21.5 million tonnes of annual production in India. It is greatly preferred by farmers for its versatility and good yield potential. Maize is predominantly cultivated as a *kharif* crop in India. The use of genetically diverse parents is essential to generate a genetic variation for the successful selection of genotypes in a breeding program [4]. An assessment of the nature and magnitude of diversity between genotypes will help to choose better ones to produce superior genotypes. The determination of genetic diversity in crop plant is either from pedigree data [5] or morphological characters [6]. Multivariate analysis (D^2 statistics) developed by [7] is the most powerful tool for quantifying genetic diversity among the specified set of genotypes [8]. Genetic divergence for metric traits to a great extent is subjective to an environment. The present study was aimed at determining the genetic diversity among single cross hybrids of maize over three environments (seasons) based on morpho-physiological and yield contributing components.

MATERIALS AND METHODS

The 45 single cross hybrids made involving 10 promising inbred lines in a half diallel fashion excluding reciprocals were evaluated in three seasons *viz*., *rabi*, *summer* and *kharif* from 2016-17 to 2017-18 in a randomized block design with three replications at the experimental farm of Agricultural Research Station, Perumallapalli, Chittoor, A.P. Seeds of each hybrid were sown in five meters long one row plot with a spacing of 75 × 20 cm in *kharif* and 60 × 20 cm in *rabi* and *summer* between rows and hills, respectively. One plant per hill was kept after proper thinning. Recommended doses of fertilizers were applied. Necessary intercultural operations and irrigations were accorded during the crop growth period to ensure normal growth, and development of the plants and to raise a uniform crop. Fifteen morpho-physiological and yield contributing characters were recorded in all three seasons. Data for days to 50% tasseling, days to 50% silking and days to maturity were recorded on a whole plot basis. Five randomly selected plants were used for recording observations on plant height, leaf area, leaf weight, SPAD meter readings, cob length, cob girth, number of kernel rows cob^{-1}, number of kernels row^{-1}, 100 kernel weight and kernel yield plant^{-1}. Anthesis-silking interval was determined as the deviation of days to 50% silking from days to 50% tasseling, whereas specific leaf area and specific leaf weight were worked out as ratios of leaf area and leaf weight and vice versa. Harvest index was calculated as the ratio of kernel yield to total dry matter/plant. Analysis of variance was carried out following standard statistical techniques to establish significance levels among the hybrids [9-10]. Data collected on 15 characters were subjected to [11]. D^2 statistic to calculate intra and inter-cluster genetic distance values and clustering was carried out adopting Tocher's method [12] using INDOSTAT version 8.1.

RESULTS AND DISCUSSION

Analysis of variance revealed that the mean sum of squares of genotypes for all the 15 characters studied were significant in all three seasons *viz*., *rabi*, *summer*, and *kharif* indicating the existence of considerable variability among the single cross hybrids for all the characters under investigation. Based on the results of the analysis of variance, D^2 analysis was carried out for each season. The clustering pattern, average intra and inter cluster distances, cluster means for different characters and number of hybrids included in different clusters determined separately for each season were presented in Fig. 1 to 6 and Table .1 to 6**.** The results obtained are presented on season- wise hereunder.

The cluster analysis grouped all the 45 single cross hybrids of maize into five major clusters in *rabi* based on the quantitative characters indicating the importance of phenotypic descriptors to differentiate between them (Fig. 1). Cob girth (36.77%), days to 50% silking (19.20%), days to maturity (11.21%), 100 kernel weight (11.11%), SPAD meter reading (8.38), days to 50% tasseling (6.97%), kernel yield (6.26%) and harvest index (5.25%) in that order contributed much to the clustering pattern. Cluster II and cluster I were the largest having 22 and 20 hybrids indicating genetic similarity among them, whereas clusters III, IV and V had one hybrid each (Fig. 2). All the 11 top high yielding hybrids *viz*., BML 2 × Heypool, BML 6 × PDM 1474, BML 7 × DFTY, BML 15 × Heypool, BML 15 × PDM 1474, Heypool × PDM 1574, BML 6 ×DFTY, BML 15 × PDM 1452, DFTY × Heypool, DFTY × PDM 1452 and PDM 1452 × PDM 1474 were included in cluster I, while only one hybrid BML 2 × BML 7 was included in the cluster III.

The intra and inter-cluster distances among the five clusters were presented in Table 1. The intra-cluster distances were lower than the inter-cluster distances. The inter-cluster distance varied from 22.23 (cluster I and III) to 131.88 (cluster V and IV), while the intra cluster distance varied from 0.00 (cluster III and V) to 11.18 (cluster IV and V). The low intra cluster distance indicates that these are solitary clusters with single genotypes in them. Cluster means for various characters studied indicate that Clusters III and I possessed higher values for SPAD meter readings, specific leaf area, cob length, cob girth, number of kernels cob^{-1}, number of kernels row^{-1}, 100 kernel weight and kernel yield and moderate values for days to 50% tasseling, days to % silking, anthesis to silking

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Table 1. Average intra and inter cluster D^2 and D (in bracket) values of five clusters formed from 45 single cross hybrids of maize in *rabi* season

Clusters	I	II	III	IV	V
I	15.29 (3.91)	38.29 (6.19)	22.23 (4.71)	58.68 (7.66)	91.70 (9.58)
II	38.29 (6.19)	15.55 (3.94)	44.91 (6.70)	38.06 (6.17)	48.80 (6.99)
III	22.23 (4.71)	44.91 (6.70)	0.00 (0.00)	78.19 (8.84)	82.26 (9.07)
IV	58.68 (7.66)	38.06 (6.17)	78.19 (8.84)	0.00 (0.00)	131.88 (11.48)
V	91.70 (9.58)	48.80 (6.99)	82.26 (9.07)	131.88 (11.48)	0.00 (0.00)

interval, days to maturity and plant height. Clusters V recorded lower mean values for kernel yield and yield components and higher means for days to 50% tasseling, days to % silking, anthesis to silking interval, days to maturity and plant height (Table 2). During *summer*, anthesis–silking interval (53.43%), days to 50% tasseling (13.43%), cob girth (6.67%), 100 kernel weight (6.46%), plant height (6.36%) contributed maximum to the clustering pattern compared to other characters. Maximum inter-cluster distance (96.66) was noted between clusters I and VI and minimum distance between clusters (IV and V). Intra cluster distances ranged from 0.00 (Cluster III, IV and VI) to 9.83 (cluster V) (Fig. 3 and Table 3). Cluster I contained a maximum number of hybrids (25) followed by cluster II (11) and cluster V (6). Clusters III, IV, and VI were the minor clusters and together consisted three hybrids (Fig. 4). Single cross hybrids *viz*., DFTY × Heypool, DFTY × PDM 1452, Heypool × PDM 1474, BML 2 × PDM 1474, BML 6 × DFTY, BML 7 × DFTY and BML 15 × PDM 1474 in cluster I and BML 6 × PDM 1474 and BML 2 × Heypool were included in cluster V. Cluster mean values were found higher in cluster V and cluster I for most of the characters along with low mean values for developmental characters. All other clusters registered lower means for kernel yield and yield contributing characters (Table 4).

Table 2 . Cluster means for kernel yield and yield contributing characters in *rabi* season

Clusters	**DT**	**DS**	**ASI**	**DM**	**PH**	**SP AD**	**SLA**	**SL W**	**CL**	**CG**	**NK RC**	**NK PR**	**KW**	**HI**	**KY**
I	61.28	64.68	3.47	101.17	191.86	52.91	89.24	1.13	18.63	15.57	15.19	40.52	35.90	38.27	138.55
II	62.32	65.70	3.38	102.58	191.24	50.17	86.46	1.15	17.06	14.52	14.11	37.95	33.79	37.62	122.29
III	60.33	63.67	3.44	102.67	183.53	53.45	89.46	1.12	18.40	16.00	14.37	41.00	35.53	36.31	142.73
IV	61.33	62.33	1.00	98.00	195.93	49.95	85.88	1.17	17.18	14.50	14.27	38.67	33.20	37.43	137.53
V	65.33	69.67	4.78	106.67	176.30	51.27	84.55	1.18	17.30	13.97	13.70	37.67	31.93	37.20	103.93

Table 3. Average intra and inter cluster D2 and D (in bracket) values of six clusters formed from 45 single cross hybrids of maize in *summer* season

Clusters	I	II	III	IV	V	VI
I	22.53 (4.75)	35.19 (5.93)	45.57 (6.75)	41.83 (6.47)	41.83 (6.47)	96.66 (9.83)
II	35.19 (5.93)	30.98 (5.57)	36.90 (6.07)	43.51 (6.60)	47.30 (6.88)	68.62 (8.28)
III	45.57 (6.75)	36.90 (6.07)	0.00 (0.00)	23.14 (4.81)	31.63 (5.62)	71.61 (8.46)
IV	41.83 (6.47)	43.51 (6.60)	23.14 (4.81)	0.00 (0.00)	18.99 (4.36)	43.39 (6.59)
V	41.83 (6.47)	47.30 (6.88)	31.63 (5.62)	18.99 (4.36)	24.59 (4.96)	62.42 (7.90)
VI	96.66 (9.83)	68.62 (8.28)	71.61 (8.46)	43.39 (6.59)	62.42 (7.90)	0.00 (0.00)

All the 45 hybrids were grouped in to seven clusters during *kharif* season (Fig.6). Anthesis–silking

Table 4. Cluster means for kernel yield and yield contributing characters in *summer* season

Clusters	**DT**	**DS**	**ASI**	**DM**	**PH**	**SP AD**	**SLA**	**SL W**	**CL**	**CG**	**NK RC**	**NK PR**	**KW**	**HI**	**KY**
I	60.73	63.32	2.59	98.57	170.23	51.30	81.98	1.22	17.49	13.55	14.40	35.76	30.73	37.65	108.70
II	61.52	64.12	2.61	99.82	180.26	49.68	80.23	1.25	16.41	12.76	13.71	33.00	28.49	37.22	98.75
III	64.33	67.00	2.67	102.00	153.67	49.60	81.34	1.23	16.10	12.97	13.23	32.67	27.63	37.22	90.07
IV	60.33	62.33	2.00	98.00	158.33	51.77	81.74	1.22	17.53	13.35	14.00	35.67	29.67	36.45	92.47
V	61.78	64.44	2.67	98.35	177.92	51.28	82.26	1.22	17.80	13.63	14.45	36.20	30.78	37.15	108.86
VI	58.33	60.67	2.33	98.00	202.15	50.47	81.17	1.23	16.60	12.34	13.00	30.67	24.73	37.26	93.63

Table 5. Average intra and inter cluster D2 and D (in bracket) values of seven clusters formed from 45 single cross hybrids of maize in *kharif* season

Clusters	I	II	III	IV	V	VI	VII
I	16.93 (4.11)	41.38 (6.43)	44.85 (6.70)	29.37 (5.42)	30.29 (5.50)	52.76 (7.26)	49.38 (7.03)
II	41.38 (6.43)	18.37 (4.29)	78.11 (8.84)	72.50 (8.51)	32.75 (5.72)	52.23 (7.23)	100.53 (10.03)
III	44.85 (6.70)	78.11 (8.84)	23.79 (4.88)	80.67 (8.98)	72.92 (8.54)	132.16 (11.50)	116.13 (10.78)
IV	29.37 (5.42)	72.50 (8.51)	80.67 (8.98)	0.00 (0.00)	44.06 (6.64)	39.38 (6.28)	24.71 (4.97)
V	30.29 (5.50)	32.75 (5.72)	72.92 (8.54)	44.06 (6.64)	0.00 (0.00)	43.11 (6.57)	65.31 (8.08)
VI	52.76 (7.26)	52.23 (7.23)	132.16 (11.50)	39.38 (6.28)	43.11 (6.57)	0.00 (0.00)	48.22 (6.94)
VII	49.38 (7.03)	100.53 (10.03)	116.13 (10.78)	24.71 (4.97)	65.31 (8.08)	48.22 (6.94)	0.00 (0.00)

Table 6. Cluster means for kernel yield and yield contributing characters in *kharif* season

Clus-ters	DT	DS	ASI	DM	PH	SP AD	SLA	SL W	CL	CG	NK RC	NK PR	KW	HI	KY
I	64.40	68.12	3.72	105.22	197.55	51.22	84.96	1.17	17.76	14.55	14.03	38.40	34.52	37.55	127.26
II	64.87	68.75	3.88	105.65	203.55	51.51	84.40	1.19	17.77	14.19	13.83	37.67	33.79	37.30	120.32
III	62.82	66.41	3.59	103.36	189.64	52.92	88.13	1.14	19.12	15.77	15.04	40.79	36.06	37.95	136.27
IV	64.33	68.33	4.00	105.33	210.00	51.07	81.79	1.22	17.17	14.38	13.92	37.67	33.83	37.01	96.27
V	64.67	68.33	3.67	105.00	174.53	50.80	86.78	1.20	17.97	13.83	13.45	36.00	35.60	38.01	105.87
VI	66.67	71.67	5.00	108.33	214.20	50.27	87.79	1.14	17.17	14.50	13.48	32.67	31.93	37.73	102.30
VII	66.33	70.67	4.33	104.00	192.07	51.33	85.74	1.17	17.43	13.80	13.65	38.33	31.57	37.95	113.43

DT=Days to tasseling; DS=Days to silking; ASI=Anthesis-silking interval; DM=Days to maturity; PH=Plant height; SPAD=SPAD meter readings; SLA=Specific leaf area; SLW=Specific leaf weight; CL=Cob length; CG=Cob girth; NKRC=Number of kernel rows cob^{-1}; NKPR=Number of kernels row^{-1}; KW=100 kernel weight; HI=Harvest index; KY=Kernel yield plant^{-1}

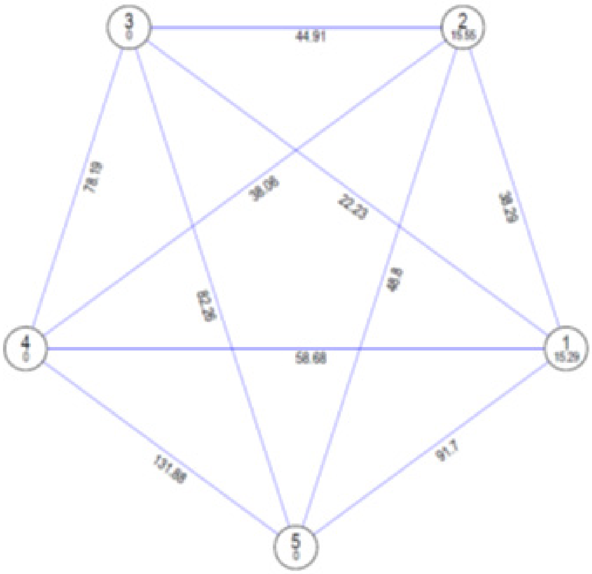

Fig. 1. Clustering of 45 single cross hybrids of maize by Tocher method for *rabi* season

interval (43.23%) followed by cob girth (20.51%), 100 kernel weight (9.09), days to maturity (6.87%), days to 50 %tasseling (6.06 %) and kernel yield (5.05%) contributed maximum to the differentiation of hybrids and inclusion in different clusters.

The highest inter-cluster distance of 132.16 was observed between clusters III and VII followed by 116.13 between clusters III and VI and 100.53 between clusters II and VI suggesting more genetic diversity among the hybrids included in different clusters (Table 5). The largest major cluster I consisted 20 hybrids followed by cluster III (13) and cluster II (8). Clusters IV, V, VI and VII contained one hybrid each (Fig.5). Top yielding hybrids *viz.*, BML 2 × BML 6, BML 6 × PDM 1416, BML 7 × Heypool, BML 15 × DFTY, DFTY × PDM 1428 in cluster I; BML 7 × DFTY, BML 15 × PDM 1452, BML 15 × PDM 1474, DFTY × Heypool, DFTY × PDM 1452, Heypool × PDM 1452 and Heypool × PDM 1474 in cluster III and BML 6 × DFTY in cluster II were included. Cluster mean values were higher in cluster III followed by cluster I and II for most of the yield components and yield and lower mean values for maturity (Table 6). Next best cluster was cluster I for yield and yield components. The clusters *viz.*, IV, V, VI and VII registered low values for all the characters studied. The hybrids belonging to the clusters separated by high statistical distance could be selected for further improvement.

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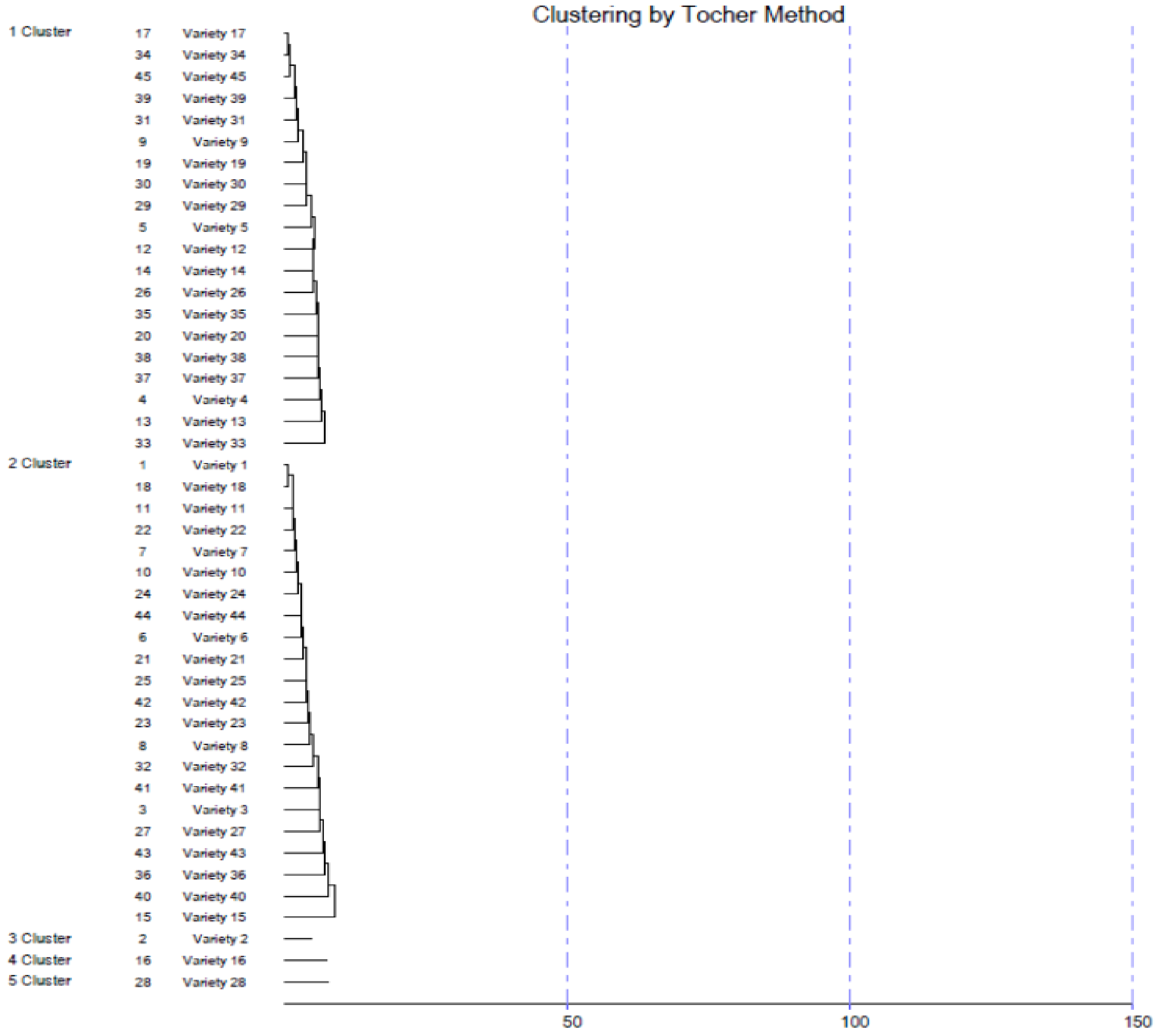

Fig 2. Distribution of 45 single cross hybrids of maize in to different clusters for *rabi* season

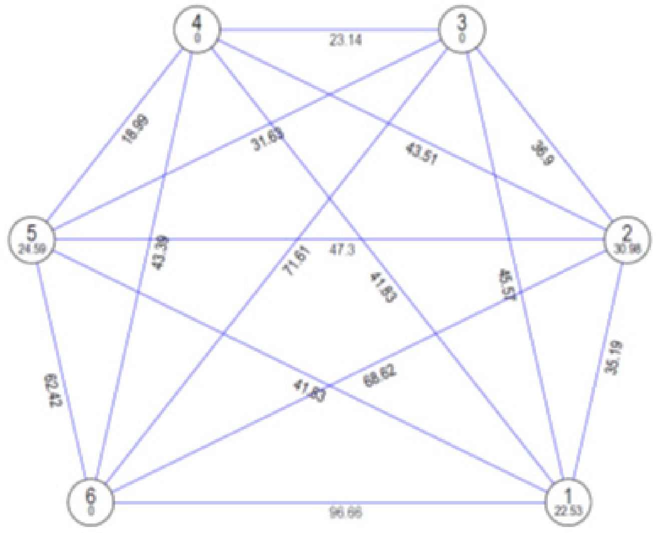

Fig.3. Clustering of 45 single cross hybrids of maize by Tocher method for *summer* season

Similar results on the clustering pattern of maize genotypes based on quantitative characters through multivariate analysis such as D^2 analysis and cluster analysis were reported in maize [13-17]

The hybrids *viz.*, BML 7 × DFTY, BML 15 × PDM 1474, DFTY × Hey pool and DFTY × PDM 1452 were included in the same cluster in all the seasons revealing that they are more similar and stable over seasons. The clusters having the largest number of hybrids indicate genetic similarity among the hybrids. The highest inter-cluster distances also suggest more variability in the genetic makeup of the hybrids included in the clusters and the genotypes from those clusters may be utilized for advanced crop development programme. Out of 15 characters studied, the number of kernels per row, test weight, days to 50% tasseling and yield per plant contributed to high genetic divergence.

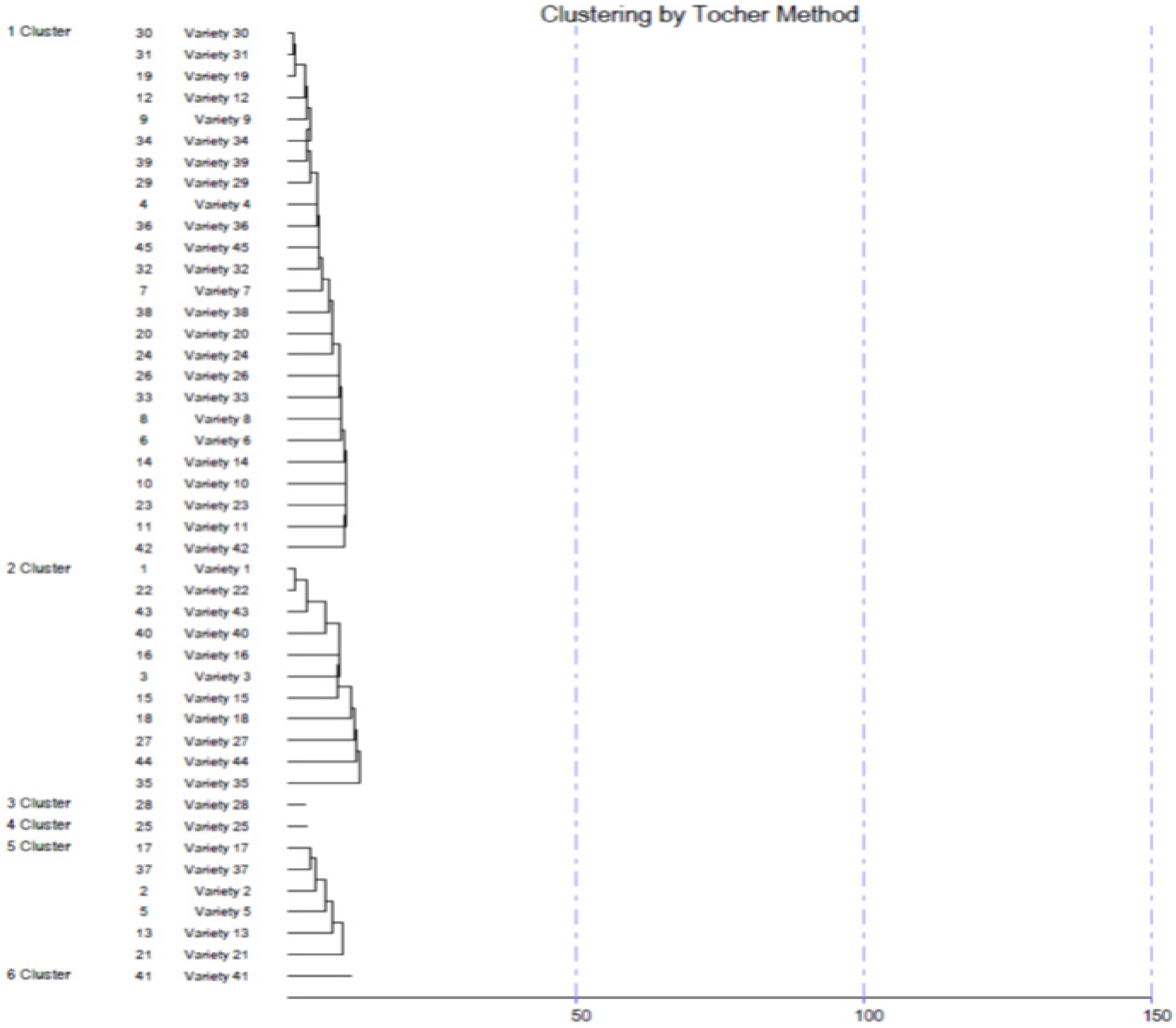

Fig 4. Distribution of 45 single cross hybrids of maize in to different clusters for *summer* season

Fig 5. Clustering of 45 single cross hybrids of maize by Tocher method for *kharif* season

CONCLUSIONS

Cluster analyses based on the characters studied indicated the presence of enough variability among the hybrids considered under this investigation. Cluster analysis assigned the 45 hybrids of maize single cross hybrids grouped into five, six and seven major clusters in *rabi*, *summer,* and *kharif*, respectively based on the quantitative characters clearly indicating the impact of seasons on clustering pattern and the importance of phenotypic descriptors to differentiate between them. High levels of intra and inter-cluster distances indicate the presence of broad genetic variation between and within a cluster. Therefore, the present investigation could be helpful in a reliable selection of single cross hybrids as well as for the development of high-yielding varieties for further breeding programs. The characters *viz.*, cob girth, kernel weight and days to 50% tasseling

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contributed much to the clustering pattern of hybrids in all three seasons, while the number of kernel rows cob^{-1}, number of kernels row^{-1}, cob length, SPAD meter reading, days to 50% silking and specific leaf weight contributed much less to the genetic diversity. Among the top high-yielding hybrids *viz*., BML 7 × DFTY, BML 15 × PDM 1474, DFTY × Heypool and DFTY × PDM 145 consistently were included in the same clusters over seasons indicating their genetic similarities and stability in performance.

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