



## ASSESSMENT OF GENETIC DIVERSITY IN INDIGENOUS GENOTYPES OF TIKHUR (*CURCUMA ANGUSTIFOLIA* ROXB.)

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### Abstract

An investigation was conducted to assess the genetic divergence of quantitative characters under Bastar Plateau of Chhattisgarh, India. The experiment was conducted during *kharif* seasons 2010-11 & 2011-12 at S.G. College of Agriculture and Research Station (IGKV), Jagdalpur, Bastar (C. G.), India. The experiment was laid out in Randomized Complete Block Design (RCBD) with 20 genotypes of tikhur with 03 replications. The genotypes were grown randomly in each replication in a total of 60 plots of 3.0 m × 2.4 m each containing 60 plants per plot. Observations were recorded from ten randomly selected sample plants in each treatment and observed mean value used for statistical analysis. In the pooled analysis, highest intra cluster distance was observed in cluster V and lowest was in cluster III. The highest inter cluster distance was observed between cluster I and V and lowest between cluster II and III. Cluster IV had the highest number of genotypes (6) and lowest was in cluster I (2) genotypes. cluster IV had the highest mean values for leaf area index, weight of mother rhizome per plant, weight of primary finger rhizome per plant, weight of secondary finger rhizome per plant, number of primary finger rhizome, thickness of primary finger rhizome per plant and total rhizome yield t/ha. Cluster V had maximum mean values for plant height, leaf length leaf breadth and dry matter per cent. Cluster I had highest mean value for number of leaves per plant, harvest index, and thickness of mother rhizome per plant and cluster II had maximum mean values for days to maturity, number of mother rhizome per plant and starch recovery per cent. Based on inter cluster distance and cluster means, it can be concluded that genotypes of the cluster V and II could be select for hybridization programme as they are expected to produce high heterogenic crosses. Based on D<sup>2</sup> studies genotypes IGBT-10-1, IGKOT-10-1, IGDNT-10-1, IGBT-10-4, IGDNT-10-1, IGSJT-10-1 and IGSJT-10-2 have been selected for hybridization and tikhur improvement programme. For hybridization programme parents of tikhur should not be selected from same cluster. On the basis of the above analysis, genotypes IGBT-10-4 and IGSJT-10-2 is recommended to be used as parents for starch recovery per cent and total rhizome yield.

**Key words :** Tikhur, *Curcuma angustifolia* Roxb., genetic divergence, cluster mean, indigenous genotypes.

### Introduction

Tikhur (*Curcuma angustifolia* Roxb.) is an important annual herb of family Zingiberaceae. It is an important starchy plant. Simultaneously it is used as a medicine by tribal people of Chhattisgarh. It occurs abundantly found in *Sal* forest especially near the streams is a rich source of starch, and has good demand by the industries as well as for human consumption especially in festivals in recent past. In Chhattisgarh, it is found abundantly in the hilly tracts and forests of Bastar, Dantewada, Bijapur, Narayanpur, Kanker, Rajnandgaon, Kawardha, Dhamtari,

Bilaspur, Raipur, Korba, Korea and Surguja districts. The total collection of tikhur rhizome as a minor forest produce in Chhattisgarh is 1,90.00 tonnes. Bastar and Bilashpur divisions are the major potential area of the state for tikhur (Anonymous, 2005). Two types of tikhur are found in the Bastar division; one with creamy white flowers and another having light pink coloured flowers (Singh *et al.*, 1999). It is found that over exploitation of the species that resulted in bringing it in valuable category of IUCN. Thus, it has necessitated the cultivation of this species in the farmer's field. Growing demand for various pharmaceutical and food industries for a quality raw

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material rich in starch contents, require thorough studies for selection of best genotype and varieties which have high starch content, thus can only be met by selection of better natural source and then attempt for breeding better variety. Tikhur rhizomes are used as appetizer reducing burning sensations and stomach pains, removal of stone from kidney, useful for ulcer patient (Sharma, 2003) and rhizome pulp is used for treatment of headache as well as it gives cooling effect (Nag *et al.*, 2006). The rhizome pulp is a remedy for fever, joint pains and leucorrhoea. The starch obtained from the rhizomes is highly nutritious and easily digestible, therefore, it is recommended for infants, weak children and invalids. The starch of tikhur is used for the preparation of many sweet meals and herbal dishes like *halwa*, *barfi*, *jalebi* etc. It is used specially during fast (*Vrata*, *Upwas*). Farmers also prepare herbal drink “*sarbat*” through tikhur starch during summer due to its cooling effect (Singh and Palta, 2004). In the past, Tikhur was occurring to a large extent throughout the *Sal forest* of Chhattisgarh. But at present the unscientific manner of harvesting and over exploitation have brought its occurrence to the restricted patches. In spite of being an important medicinal herb, information on its superior genotypes, starch extraction technique and value added product is lacking. No research work has been carried out to screen superior genotypes assessing its genetic diversity and variation. The success of breeding programme depends on the nature and magnitude of variability available in any crop and germplasm serves as the most valuable natural resources in providing needed attributes for engineering successful varieties (Hawkes, 1981). Availability of sufficient genetic diversity in the indigenous genotypes collection, which the breeder is handling, is the basis of breeding program. The assessment of genetic divergence in the present investigation is based on the phenotypic divergence of the genotypes.

Looking to the importance of the crop for people of the Chhattisgarh an investigation entitled “Assessment of genetic diversity in indigenous genotypes of Tikhur (*Curcuma angustifolia* Roxb.)” was undertaken during the year of *kharif* seasons 2010-11 & 2011-12 at Shaheed Gundadhoor College of Agriculture and Research Station (IGKV) Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, India.

### Materials and Methods

The investigation was conducted at IGKV, Shaheed Gundadhoor College of Agriculture & Research Station (SG CARS), Kumhrawand, Jagdalpur, Bastar, Chhattisgarh during *Kharif* seasons of 2010-11 and 2011-12. Twenty indigenous genotypes [(1) IGBT-10-1, (2)

IGKOT-10-1, (3) IGDMT-10-1, (4) IGDMT-10-2, (5) IGMOT-10-1, (6) IGSJT-10-1, (7) IGJT-10-1, (8) IGSJT-10-2, (9) IGSJT-10-3, (10) IGKT-10-1, (11) IGSJT-10-4, (12) IGBLT-10-1, (13) IGBT-10-2, (14) IGBT-10-3 (Local Check), (15) IGNT-10-1, (16) IGBT-10-4, (17) IGBLT-10-2, (18) IGKNT-10-1, (19) IGDNT-10-1 and (20) IGBT-10-1] of tikhur (*Curcuma angustifolia* Roxb.) collected from different districts of Chhattisgarh during March 2010 to June 2010. The experiment was laid out in Randomized Complete Block Design (RCBD) with 20 genotypes of tikhur with three replications. The experimental field was prepared and FYM thoroughly mixed with soil as pH of soil was slightly basic in nature. The genotypes were grown randomly in each replication in a total of 60 plots of 3.0 m x 2.4 m each containing 60 plants per plot and spacing was 60x20 cm. Applied manure and fertilizers FYM: 20 tones/ha, N: 60 kg/ha, P<sub>2</sub>O<sub>5</sub>: 40 kg/ha, K<sub>2</sub>O: 60 kg/ha during the crop season. Full dose of FYM mixed in plots during field preparation. Half dose of N and full dose of P and K was mixed in the plots before planting (basal dose) and remaining half dose was applied 45 days after planting during intercultural operation and earthing-up. The crop was grown under rainfed conditions. The data were recorded on 10 randomly selected plants for each genotype for each replication. The 19 growth and yield attributing characters like plant height (cm), number of leaves per plant, leaf length (cm), leaf breadth (cm), leaf area index (LAI), days to maturity, harvest index (%), weight of mother rhizome per plant (g), weight of primary finger rhizome/plant (g), weight of secondary finger rhizome/plant (g), number of mother rhizome/plant, number of primary finger rhizome / plant, number of secondary finger rhizome / plant, thickness of mother rhizome / plant (cm), thickness of primary finger rhizome/plant (cm), thickness of secondary finger rhizome/plant (cm), dry matter per cent of rhizome/plant, starch recovery (%) and total rhizome yield t/ha were recorded in experimental field. The harvested rhizomes were cleaned up and mother rhizomes and finger rhizomes were separated. The flesh colour of rhizomes, dry matter and starch recovery per cent were estimated in Horticulture laboratory. All the observations were taken from sprouting of rhizomes and up to maturity for estimation genetic divergence. Data recorded from 19 growth and yield attributing characters were submitted to analysis of variance and mean compared by Panse and Sukhatme (1978). Multivariate analysis was used to evaluate divergence between genotypes, employing Canonical Variables Analysis and clustering based on Mahalanobis Generalized Distance (D<sup>2</sup>). Genotypes clustering were performed by using Optimization Method

proposed by Rao (1952) to clustering in Tocher's method. The data are analyzed by using software like MS-EXCEL and Statistical Analysis System (SAS). It measures group distance based on multiple characters. The genotypes were grouped in to number of clusters following Tochers method as described by Rao (1952). Clustering was done by looking to the values of any two genotypes belonging to the same cluster showing least average small  $D^2$  value than those belonging to different clusters.

## Results and Discussion

### Intra and inter cluster distance (year: 2010-11)

In the year 2010-11, 20 genotypes were grouped in to 5 clusters. The inter and intra cluster  $D^2$  Values are presented genetic distance are showed in Figs. 1 & 2. Cluster II had the highest intra cluster distance of 690.883 followed by cluster III (674.939), cluster I (406.971) and cluster IV (392.01). Cluster number II had the highest 8 genotypes followed by cluster number III (6 genotypes), cluster number IV (3 genotypes), cluster number I (2 genotypes) and lowest was in cluster number V (1 genotype). The inter cluster distance was observed highest in between cluster I and V (6741.68). The inter cluster  $D^2$  values were also high between cluster I and IV (6294.28) cluster I and III (4586.78), cluster II and V (3685.544), Cluster II and IV (3045.84) Cluster III and V (2514.91) cluster II and III (1959.93), I and II (1290.74), cluster IV and V (1244.594). The lowest inter cluster  $D^2$  value was found between cluster III and IV (994.36).

### Intra cluster means (year: 2010-11)

The intra cluster means for nineteen characters given in table 1 revealed marked difference between the five clusters in respect of cluster means for different characters. The cluster mean for plant height was the highest for cluster V (95.40 cm) followed by cluster II (73.89 cm) cluster I (73.80 cm) and cluster IV (64.38 cm). The lowest cluster mean for plant height showed by cluster III (54.85 cm). In case of character, number of leaves per plant the highest cluster mean was obtained for cluster I (10.53) followed by cluster II (8.05), cluster IV (7.49), cluster V (7.13) and cluster III (6.48) showed the lowest cluster mean value. The highest cluster mean for leaf length was observed for cluster V (51.80 cm) followed by cluster II (37.08 cm) cluster I (36.17 cm) and cluster IV (35.62 cm). The lowest cluster mean for leaf length was observed in cluster III (29.61 cm). Cluster V (20.75 cm) showed the highest cluster mean for leaf breadth followed by cluster IV (17.29 cm), cluster III (15.74 cm) and cluster II (14.79 cm). The lowest cluster mean was observed in cluster II (14.79).

The highest cluster mean value for leaf area index was observed for cluster V (3.50 cm) followed by cluster IV (3.48 cm) cluster III (3.20 cm) and cluster II (2.64 cm). The lowest cluster mean was observed for cluster I (2.04). Cluster V has the highest treatment mean for days to maturity (177.67) followed by cluster IV (172.11), cluster I (171.33) and cluster II (168.42). The lowest cluster mean was observed for cluster II (168.42). Cluster III had the highest treatment mean for harvest index per cent (89.72) followed by cluster IV (88.41) cluster II (88.25) and cluster I (87.65). The lowest cluster mean was observed for cluster V (85.62). The highest cluster mean for weight of mother rhizome per plant was observed for cluster III (49.77g) followed by cluster I (48.31), Cluster II (48.08g) and cluster IV (42.55 g). The lowest cluster mean was observed the cluster V (35.86 g). Cluster II had the highest treatment mean for weight of primary finger rhizome per plant (138.75 g) followed by cluster III (117.69) cluster I (99.77 g) and cluster IV (99.52 g). The lowest cluster mean was showed by cluster V (85.67 g). Cluster III had the highest treatment mean for weight of secondary finger rhizome per plant (51.18 g) followed by cluster II (44.37 g), cluster IV (31.22 g) and cluster V (24.79). The lowest cluster treatment mean was showed by cluster I (22.02 g). Cluster III had the highest treatment mean for number of mother rhizome per plant (1.89) followed by cluster II (1.73), cluster IV (1.64) and cluster I (1.23). The lowest cluster mean was showed by cluster V (1.07). The highest cluster mean for number of primary finger rhizome per plant was observed for cluster II (7.89) followed by cluster IV (7.11) cluster III (6.87) and cluster I (5.80). The lowest cluster mean was showed by cluster V (4.67). The highest cluster mean for number of secondary finger rhizome per plant was recorded for cluster III (9.96) followed by cluster V (9.60), cluster II (8.47) and cluster IV (6.76). The lowest cluster mean was showed by cluster I (5.47). Cluster V (3.79 cm) showed the highest cluster mean for thickness of mother rhizome per plant followed by cluster I (3.47 cm) cluster II (3.18 cm) and cluster III (2.98 cm). The lowest cluster mean was showed by cluster IV (2.95 cm). The highest cluster means for thickness of primary finger rhizome per plant was observed for cluster II (1.90 cm) followed by cluster I (1.77 cm), cluster III (1.70 cm) and cluster V (1.71 cm). The lowest cluster mean was showed by cluster IV (1.59 cm). The highest cluster means for thickness of secondary finger rhizome per plant was observed for cluster V (1.61 cm) followed by cluster I (1.46.cm), cluster II (1.41 cm) and cluster IV (1.35 cm). The lowest cluster mean was showed by cluster III (1.17 cm). Cluster IV had the highest treatment means

for dry matter per cent of rhizome per plant (31.98) followed by cluster I (27.75), cluster V (25.30) and cluster III (25.21). The lowest cluster mean was showed by cluster II (25.14). Cluster II has the highest treatment means for starch recovery per cent (13.52) followed by cluster V (12.34), Cluster IV (11.91) and cluster III (11.85). The lowest cluster mean was showed in cluster I (11.62). The highest cluster means for total rhizome yield t/ha was observed for cluster II (18.14 t/ha) followed by cluster III (17.95 t/ha) cluster IV (12.31 t/ha) and cluster I (11.78 t/ha). The lowest cluster mean was showed by cluster I (11.78).

#### **Intra and inter cluster distance (year: 2011-12)**

In the year 2011-12, 20 genotypes were grouped in to 5 clusters. The inter and intra cluster  $D^2$  value are presented and genetic distance are showed in Fig 3 & 4. Cluster IV had the highest intra cluster distance of 513.35 followed by cluster III (399.38) cluster V (385.41) cluster II (344.12) and cluster I (376.74). Cluster V had the highest number of genotypes (9) followed by cluster number III (5 genotypes), cluster number IV (4 genotypes), cluster number II (3 genotypes) and lowest 2 genotypes had cluster number I. The inter cluster distance was observed highest between cluster I and IV (12487.29). The inter cluster  $D^2$  values were also high between cluster I and V (8648.03), cluster II and IV (7598.36), cluster and V (4638.36), cluster III and IV (4217.42) cluster I and III (2684.46), Cluster III and V (2206.58), cluster I and II (926.36) and cluster II and III (916.29). The lowest inter cluster  $D^2$  value was found between cluster IV and V (873.39).

#### **Intra- Cluster means (2011-12)**

Cluster means for the nineteen characters are presented in table 2. Cluster IV had the highest treatment means for plant height (11.02 cm) followed by cluster III (111.14 cm) cluster II (108.22 cm) cluster I (106.34 cm) and cluster V with the lowest treatment mean (97.56) for plant height. Cluster I had the highest treatment means for number of leaves per plants (15.13) followed by cluster III (14.67), cluster IV (12.70), cluster II (11.91) and cluster V with the lowest treatment means (11.44). Cluster IV had the highest treatment means for leaf length (43.22) followed by cluster II (41.97 cm) cluster III (41.27cm) cluster I (39.41 cm) and cluster V with the lowest treatment mean (35.31). Again cluster IV had the highest treatment mean for leaf breadth (18.56 cm) followed by cluster V (16.76), cluster III (15.07), cluster II (14.34) and cluster I with the lowest treatment mean (13.45 cm). Cluster IV had the highest treatment mean for leaf area index (3.49) followed by cluster V (3.27) cluster III (2.71),

cluster II (2.41) and cluster I with the lowest treatment mean (2.05). Again cluster IV had the highest treatment mean for days to maturity (171.33) followed by cluster I (168.00) cluster II (167.78), cluster III (166.67) and cluster V with the lowest treatment mean (166.61). Cluster I had the highest treatment mean for harvest index (85.22) followed by cluster III (84.04), cluster V (81.68) cluster IV (81.32) and cluster II with the lowest treatment mean (80.27). The highest cluster mean for weight of mother rhizome per plant was observed for cluster V (58.16g) followed by cluster I (48.93), cluster III (46.99) and cluster IV (44.06). The lowest cluster mean was showed by cluster II (43.07). The highest cluster mean for weight of primary finger rhizome per plant was observed for cluster II (152.11) followed by cluster V (150.33 g) cluster III (134.86 g) and cluster I (131.85 g). The lowest cluster mean was showed by cluster IV (102.97g). Cluster V has the highest treatment mean for weight of secondary finger rhizome per plant was observed for cluster V (48.02g) followed by cluster II (45.46g) cluster III (33.47), cluster IV (33.17). The lowest cluster mean was showed by cluster (25.34g). Cluster III had the highest treatment mean for number of mother rhizome per plant (2.00) followed by cluster V (1.86) cluster IV (1.65) cluster I (1.50) and cluster II with the lowest treatment mean (1.40). Cluster V had the higher treatment mean for number of primary finger rhizome per plant (9.02) followed by cluster II (7.96), cluster III (7.77), cluster I (7.13) and cluster IV with the lowest treatment mean. Cluster II had the highest treatment mean for number of secondary finger rhizome per plant (12.11) followed by cluster V (10.40) cluster III (5.54), cluster IV (7.62) and cluster I with the lowest treatment mean (6.60). Cluster I had the highest treatment mean for thickness of mother rhizome per plant (3.55cm) followed by cluster IV (3.52 cm) cluster III (3.51 cm) cluster II (3.20 cm) and cluster V with the lowest treatment mean (3.18 cm). Cluster IV had the highest treatment mean for thickness of primary finger rhizome per plant (1.93) followed by cluster II (1.81) and cluster I, III & III with the lowest treatment mean (1.80 cm). Again cluster II had the highest treatment mean for thickness of secondary finger rhizome per plant (1.61 cm) followed by cluster I (1.50), cluster IV (1.46), cluster III (1.25) and cluster V with the lowest treatment mean (1.21). Cluster IV (30.37) showed the highest cluster mean for dry matter per cent of rhizome followed by cluster III (27.88) cluster I (27.67), cluster II (24.50). The lowest cluster mean was showed by cluster V (23.21). The highest cluster means for starch recovery per cent was showed by cluster III (14.49) followed by

cluster V (13.93) cluster I (13.11) and cluster (12.60). The lowest cluster mean was showed by cluster IV (12.22). Cluster V (20.66 t/ha) had showed the highest treatment mean for total rhizome yield t/ha followed by cluster II (19.07 t/ha) cluster III (15.75 t/ha), cluster I (14.88 t/ha) and cluster IV with the lowest treatment mean (13.69 t/ha).

#### **Intra and inter cluster distance (Pooled analysis: 2010-12)**

Diversely in 20 collected genotypes were grouped into 5 clusters. The intra and inter cluster  $D^2$  values are given and genetic distances are depicted in figs. 5 & 6. Cluster V had the highest intra cluster distance of 182.81 followed by cluster II (168.22), cluster IV (135.62), cluster I (113.76) the lowest intra cluster distance observed in cluster III (88.12). Cluster IV had the highest number of genotypes (6) followed by cluster number II (5 genotypes), cluster number V (4 genotypes), cluster number III (3 genotypes) and lowest 2 genotypes had cluster number I. The highest inter cluster distance was observed between cluster I and V (3011.82) followed by cluster I and IV (2091.94) cluster III and V (1744.70) cluster II and V (1073.02), cluster III and IV (1049.37) cluster I and III (286.27). The lowest inter cluster distance was observed between cluster II and III (240.81).

#### **Intra cluster mean (Pooled analysis 2010-12)**

Cluster mean for the nineteen characters are presented in table 3. Cluster V had the highest cluster mean has plant height (93.07 cm) cluster II (92.05 cm) cluster III (90.40 cm) cluster I (90.07 cm) and cluster IV with the lowest treatment mean (76.92 cm). Cluster I had the highest treatment means for number of leaves per plant (12.83) followed by cluster II (12.09), cluster V (10.05), cluster III (9.02) and cluster IV with the lowest treatment mean (8.83). Cluster V had the highest treatment mean for leaf length (41.44 cm) followed by cluster III (39.52 cm) cluster II (38.75 cm) cluster I (37.79 cm) and cluster IV with the lowest treatment mean (32.82cm). Again cluster V had the highest treatment mean for leaf breadth (18.36 cm) followed by cluster IV (16.56 cm) cluster II (14.83 cm) cluster III (14.11 cm) and cluster I with the lowest cluster mean (13.30 cm). The highest cluster mean for leaf area index (3.49) followed by cluster IV (3.27) cluster II (2.70), cluster III (2.40). The lowest cluster mean was showed by cluster II (2.70). The highest cluster mean for days to maturity was observed for cluster II (172.42) followed by cluster I (169.67) cluster III (169.28), cluster II (167.13) and cluster IV with the lowest cluster mean (165.72). Cluster I had the highest treatment mean for harvest index per

cent (86.44) followed by cluster II (86.19), cluster IV (85.78), cluster V (84.52) and cluster III with the lowest treatment mean (84.03). Cluster IV had the highest treatment mean for weight of mother rhizome per plant (56.23 g) followed by cluster I (48.62 g), cluster II (48.45 g), cluster V (42.44 g) and cluster III with the lowest treatment mean (39.02 g). Again cluster IV had the highest treatment mean for weight of primary finger rhizome per plant (143.49 g) followed by cluster II (134.50 g), cluster III (130.31) cluster I (115.81 g) and cluster V with the lowest treatment mean (99.51 g). The highest cluster means for weight of secondary finger rhizome per plant in cluster IV (50.62 g) followed by cluster III (49.66 g) cluster II (34.85) and cluster V (31.39). The lowest cluster mean was showed by cluster I (23.68). The highest cluster means for number of mother rhizome per plant (1.94) for cluster II followed by cluster IV (1.92), cluster II (1.75) and cluster I (1.37). The lowest cluster mean was showed by cluster III (1.36). Cluster IV had the highest treatment mean for number of primary finger rhizome per plant (8.26) followed by cluster II (8.15), cluster III (6.77) cluster I (6.47) and cluster V with the lowest treatment mean (6.33). Cluster III had the highest treatment mean for number of secondary finger rhizome per plant (10.00) followed by cluster IV (9.91), cluster II (9.00), cluster V (7.54) and cluster I with the lowest treatment mean (6.03). Cluster I had the highest treatment mean for thickness of mother rhizome per plant (3.51 cm) followed by cluster V (3.34 cm), cluster III (3.29), cluster II (3.27 cm) and cluster IV with the lowest treatment mean (3.34 cm). Cluster IV had the highest treatment mean for thickness of primary finger rhizomes per plant (1.82 cm) followed by cluster II (1.81 cm), cluster III (1.79 cm), cluster I (1.78 ) and cluster V with the lowest treatment mean (1.77 cm). The highest treatment mean for thickens of secondary finger rhizome per plant was observed for cluster III (1.60 cm) followed by cluster I (1.48 cm) cluster V (1.43 cm) and cluster II (1.26 cm). The lowest treatment mean of cluster was showed by cluster IV (1.21 cm). The highest treatment mean for dry matter per cent was observed for cluster V (30.33) followed by cluster II (27.89), cluster I (27.71) and cluster III (24.49). The lowest treatment mean was recovered for cluster IV (23.22). Cluster II had the highest treatment mean for starch recovery per cent (13.99) followed by cluster IV (13.43), cluster I (12.37), cluster V (12.12) and cluster III with the lowest treatment mean (11.99). Cluster IV had the highest treatment mean for total rhizome yield t/ha (20.49 t/ha) followed by cluster III (17.42 t/ha) cluster II (16.21 t/ha) cluster I (13.33 t/ha) and cluster V with the lowest treatment mean (12.86t/ha).

**Table 1** : Mean value for rhizome yield and its components in various clusters (Year: 2010-11).

S. no.	Observations/characters	Cluster number					Mean	Range	
		I	II	III	IV	V		Min.	Max.
1.	Plant height (cm)	73.80	73.89	54.85	64.38	95.40	72.46	54.85	95.40
2.	Number of leaves per plant	10.53	8.05	6.48	7.49	7.13	7.94	6.48	10.53
3.	Leaf length (cm)	36.17	37.08	29.61	35.62	51.80	38.06	29.61	51.80
4.	Leaf Breadth (cm)	13.14	14.79	15.74	17.29	20.75	16.34	13.14	20.75
5.	Leaf area index (LAI)	2.04	2.64	3.20	3.48	3.50	2.97	2.04	3.50
6.	Days to maturity	171.33	168.42	165.33	172.11	177.67	170.97	165.33	177.67
7.	Harvest index (%)	87.65	88.25	89.72	88.41	85.62	87.93	85.62	89.72
8.	Weight of mother rhizome per plant (g)	48.31	48.08	49.77	42.55	35.86	44.91	35.86	49.77
9.	Weight of primary finger rhizome/plant (g)	99.77	138.75	117.69	99.52	85.67	108.28	85.67	138.75
10.	Weight of secondary finger rhizome/plant (g)	22.02	44.37	51.18	31.22	24.79	34.72	22.02	51.18
11.	Number of mother rhizome /plant	1.23	1.73	1.89	1.64	1.07	1.51	1.07	1.89
12.	Number of primary finger rhizome/plant	5.80	7.89	6.87	7.11	4.67	6.47	4.67	7.89
13.	Number of secondary finger rhizome/plant	5.47	8.47	9.96	6.76	9.60	8.05	5.47	9.96
14.	Thickness of mother rhizome / plant (cm)	3.47	3.18	2.98	2.95	3.79	3.27	2.95	3.79
15.	Thick. of primary finger rhizome/plant (cm)	1.77	1.90	1.70	1.59	1.71	1.73	1.59	1.90
16.	Thick. of secondary finger rhizome/plant (cm)	1.46	1.41	1.17	1.35	1.61	1.40	1.17	1.61
17.	Dry matter per cent of rhizome/plant	27.75	25.14	25.21	31.98	25.30	27.08	25.14	31.98
18.	Starch recovery (%)	11.62	13.52	11.85	11.91	12.34	12.25	11.62	13.52
19.	Total rhizome yield t/ha	11.78	18.14	17.95	12.31	11.17	14.27	11.17	18.14

## Discussion

The ultimate objective of plant breeder is to the collection of population which have genetic variability is much important for breeder which exploits such variability for crop improvement. The genetic information has been obtained through analysis of genetic variability, heritability, genetic advance, analysis of association existing among the characters and  $D^2$  analysis. An attempt has been made in this investigation to classify the accusable genotype collections of tikhur into different clusters by using multivariate  $D^2$  analysis.

### Genetic divergence

In this study, an attempt was made to know the genetic diversity of twenty genotypes for nineteen characters. Such an assumption will be helpful for the breeder to chalk out by hybridizations programme involving minimum risk from the point of heterosis. The experimental finding of this study with respect to genetic diversity has been discussed in the following pages. To avoid unnecessary reception, only pooled data of both the years with regard to  $D^2$  analysis have been discussed.

### Cluster distance

On the basis of graphical presentation 20 genotypes were grouped in to five clusters during the year 2010-11. The highest inter cluster distance was observed between

cluster I and V and lowest inter cluster distance was observed between III and IV. Cluster III had the highest inter cluster distance and cluster IV had lowest. Cluster number II had the maximum number of genotypes and cluster number III had lowest. In the year 2011-12 cluster IV had the maximum intra cluster distance and cluster I had lowest. The inter cluster distance was observed highest between cluster I and IV and lowest was between IV and V. Cluster number V had the maximum number of genotypes and cluster number I had lowest (2). In the pooled analysis, highest tetra cluster distance was observed in cluster V and lowest was in cluster III. The highest inter cluster distance was observed between cluster I and V and lowest between cluster II and III. Cluster IV had the highest number of genotypes (6) and lowest was in cluster I (2) genotypes.

### Intra cluster mean

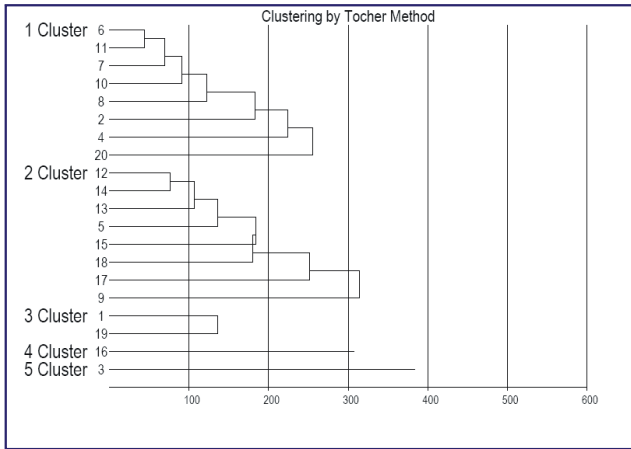
The intra cluster means for nineteen characters for the year 2010-11, 2011-12 and pooled analysis and findings are discussed below. In the year 2010-11, cluster V had the highest mean value for plant height, leaf length leaf breadth, leaf area index, days to maturity thickness of mother rhizome per plant and thickness of secondary finger rhizome per plant, cluster II and highest mean value for weight of primary finger rhizome per plant, number of primary finger, rhizome per plant, thickness of primary

**Table 2 :** Mean value for rhizome yield and its components in various clusters (Year: 2011-12).

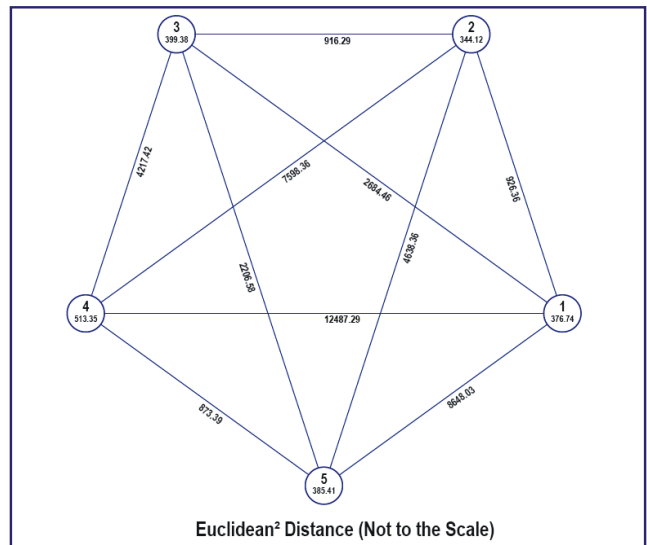
S. no.	Observations/characters	Cluster number					Mean	Range	
		I	II	III	IV	V		Min.	Max.
1.	Plant height (cm)	106.34	108.22	111.14	114.02	97.56	107.46	97.56	114.02
2.	Number of leaves per plant	15.13	11.91	14.67	12.70	11.44	13.17	11.44	15.13
3.	Leaf length (cm)	39.41	41.97	41.27	43.22	35.31	40.24	35.31	43.22
4.	Leaf Breadth (cm)	13.45	14.34	15.07	18.56	16.76	15.64	13.45	18.56
5.	Leaf area index (LAI)	2.05	2.41	2.71	3.49	3.27	2.79	2.05	3.49
6.	Days to maturity	168.00	167.78	166.67	171.33	166.61	168.08	166.61	171.33
7.	Harvest index (%)	85.22	80.27	84.04	81.32	81.68	82.51	80.27	85.22
8.	Weight of mother rhizome per plant (gm)	48.93	43.07	46.99	44.00	58.16	48.23	43.07	58.16
9.	Weight of primary finger rhizome/plant (gm)	131.85	152.11	134.86	102.97	150.33	134.42	102.97	152.11
10.	Weight of secondary finger rhizome/plant (gm)	25.34	45.46	33.47	33.17	48.02	37.09	25.34	48.02
11.	Number of mother rhizome / plant	1.50	1.40	2.00	1.65	1.86	1.68	1.40	2.00
12.	Number of primary finger rhizome / plant	7.13	7.96	7.77	6.17	9.02	7.61	6.17	9.02
13.	Number of secondary finger rhizome / plant	6.60	12.11	8.54	7.62	10.40	9.05	6.60	12.11
14.	Thickness of mother rhizome / plant (cm)	3.55	3.20	3.51	3.52	3.18	3.39	3.20	3.55
15.	Thick. of primary finger rhizome/plant (cm)	1.80	1.80	1.80	1.93	1.81	1.83	1.80	1.93
16.	Thick. of secondary finger rhizome/plant (cm)	1.50	1.61	1.25	1.46	1.21	1.41	1.21	1.61
17.	Dry matter per cent of rhizome/plant	27.67	24.50	27.88	30.37	23.21	26.73	23.21	30.37
18.	Starch recovery (%)	13.11	12.60	14.49	12.22	13.93	13.27	12.22	14.49
19.	Total rhizome yield t/ha	14.88	19.07	15.75	13.69	20.66	16.81	13.69	20.66

**Table 3 :** Mean value for rhizome yield and its components in various clusters (Pooled: 2010-11 & 2011-12).

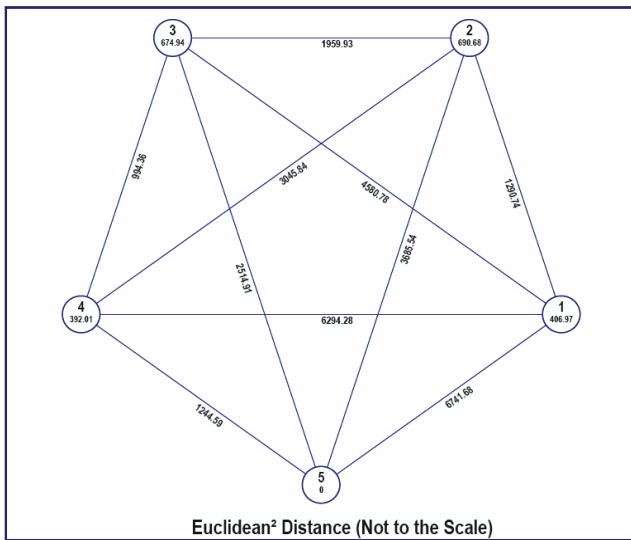
S. no.	Observations/Characters	Cluster number					Mean	Range	
		I	II	III	IV	V		Min.	Max.
1.	Plant height (cm)	90.07	92.05	90.40	76.92	93.07	88.50	76.92	93.07
2.	Number of leaves per plant	12.83	12.09	9.02	8.83	10.05	10.56	8.83	12.83
3.	Leaf length (cm)	37.79	38.75	39.52	32.82	41.44	38.06	32.82	41.44
4.	Leaf Breadth (cm)	13.30	14.83	14.11	16.56	18.36	15.43	13.3	18.36
5.	Leaf area index (LAI)	2.04	2.70	2.40	3.27	3.49	2.78	2.04	3.49
6.	Days to maturity	169.67	167.13	169.28	165.72	172.42	168.84	165.72	172.42
7.	Harvest index (%)	86.44	86.19	84.03	85.78	84.52	85.39	84.03	86.44
8.	Weight of mother rhizome per plant (gm)	48.62	48.45	39.52	56.23	42.44	47.05	39.52	56.23
9.	Weight of primary finger rhizome/plant (gm)	115.81	134.50	130.31	143.49	99.51	124.72	99.51	143.49
10.	Weight of secondary finger rhizome/plant (gm)	23.68	34.85	49.66	50.62	31.39	38.04	23.68	50.62
11.	Number of mother rhizome / plant	1.37	1.94	1.36	1.92	1.57	1.63	1.36	1.94
12.	Number of primary finger rhizome / plant	6.47	8.15	6.77	8.26	6.33	7.20	6.33	8.26
13.	Number of secondary finger rhizome / plant	6.03	9.00	10.00	9.91	7.54	8.50	6.03	10
14.	Thickness of mother rhizome / plant (cm)	3.51	3.27	3.29	3.09	3.34	3.30	3.09	3.51
15.	Thick. of primary finger rhizome/plant (cm)	1.78	1.81	1.79	1.82	1.77	1.79	1.77	1.82
16.	Thick. of secondary finger rhizome/plant (cm)	1.48	1.26	1.60	1.21	1.43	1.40	1.21	1.6
17.	Dry matter per cent of rhizome/plant	27.71	27.89	24.49	23.22	30.33	26.73	23.22	30.33
18.	Starch recovery (%)	12.37	13.99	11.99	13.43	12.12	12.78	11.99	13.99
19.	Total rhizome yield t/ha	13.33	16.21	17.42	20.49	12.86	16.06	12.86	20.49



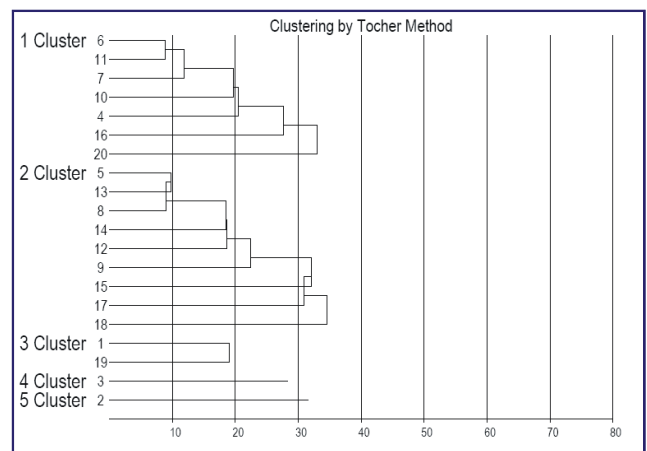
**Fig. 1 :** Composition of clusters and graphical presentation of genetic distance (2010-11).



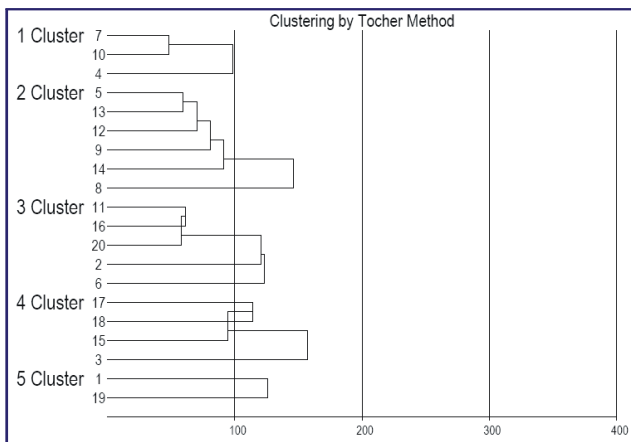
**Fig. 4 :** Intra and inter cluster distance (Year:2011-12).



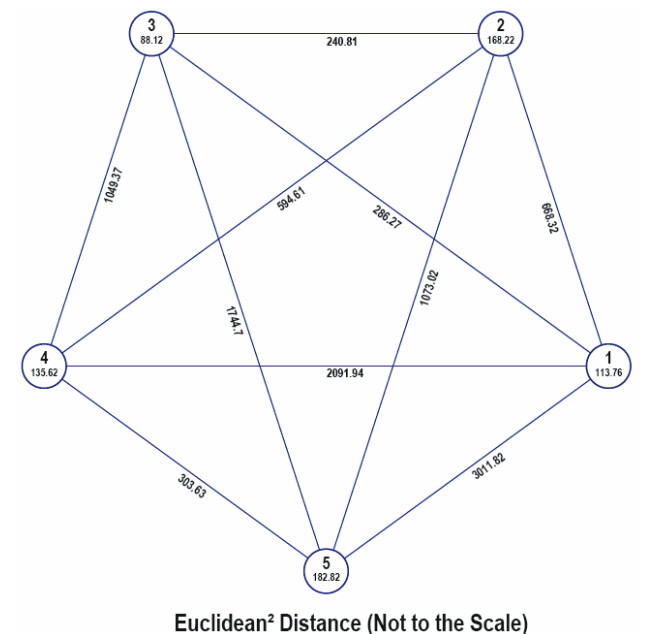
**Fig. 2 :** Intra and inter cluster distance (Year:2010-11).



**Fig. 5 :** Composition of clusters and graphical presentation of genetic distance (Pooled analysis).



**Fig. 3 :** Composition of clusters and graphical presentation of genetic distance (2011-12).



**Fig. 6 :** Intra and inter cluster distance (Year: Pooled analysis)



finger rhizome per plant, starch recovery per cent and total rhizome yield t/ha cluster III had highest mean value for harvest index, weight of mother rhizome per plant, weight of secondary rhizome per plant, number of mother. Rhizome per plant, number of secondary finger rhizome per plant cluster I had number of leaves per plant and cluster IV had dry matter per cent of rhizome per plant for maximum mean values. In the year 2011-12 cluster IV had the highest mean values of plant height, leaf length, leaf breadth, leaf area index days to maturity, thickness of primary finger rhizome per plant and dry matter per cent of rhizome. Cluster V had the highest mean values for weight of mother rhizome per plant, weight of secondary rhizome per plant, number of primary finger rhizome per plant. Cluster I had number of leaves per plant, harvest index and thickness of mother rhizome per plant. Cluster II had weight of primary finger rhizome per plant, number of secondary finger rhizome per plant and thickness of secondary finger rhizome per plant. Cluster III had number of mother rhizome per plant and starch recovery per cent. In the pooled analysis (2010-11 & 2011-12), cluster IV had the highest mean values for leaf area index, weight of mother rhizome per plant, weight of primary finger rhizome per plant, weight of secondary finger rhizome per plant, number of primary finger rhizome, thickness of primary finger rhizome per plant and total rhizome yield t/ha. Cluster V had maximum mean values for plant height, leaf length leaf breadth and dry matter per cent. Cluster I had highest mean value for number of leaves per plant, harvest index, and thickness of mother rhizome per plant and cluster II had maximum mean values for days to maturity, number of mother rhizome per plant and starch recovery per cent.

Based on inter cluster distance and cluster means, it can be concluded that genotypes of the cluster V and II could be select for hybridization programme as they are expected to produce high heterogenic crosses. Based on D<sup>2</sup> studies genotypes IGBT-10-1, IGKOT-10-1, IGDMT-10-1, IGBT-10-4, IGDNT-10-1, IGSJT-10-1 and IGSJT-10-2 have been selected for hybridization and tikhur improvement programme. For hybridization programme parents of tikhur should not be selected form same cluster. On the basis of the above analysis, genotypes IGBT-10-4 and IGSJT-10-2 is recommend to be used as parents for starch recovery per cent and total rhizome yield D<sup>2</sup> analysis has been workout in different crops by several workers. These findings are in agreement with those obtained with root crops by Easwari Amma and Lakshmi (1982) in Asian greater yam Naskar and Srinivasan (1985) in sweet potato and Naskar and Ravindran (1986) in cassava.

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