The Pharma Innovation Journal 2021; 10(12): 889-897

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(12): 889-897

www.thepharmajournal.com
Received: 04-10-2021
Accepted: 10-11-2021

Studies on genetic diversity of selected colocasia germplasm accessions (*Colocasia esculenta* var. *antiquorum* (L.) Schott) of Chhattisgarh

GP Nag, HC Nanda, Deo Shankar, DP Singh, Anurag Kerketta, RK Dewangan and Bhagwat Kumar

GP Nag
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

HC Nanda
College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Deo Shankar
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

DP Singh
Shaheed Gundadhur College of Agriculture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Anurag Kerketta
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

RK Dewangan
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Bhagwat Kumar
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Corresponding Author:
GP Nag
College of Horticulture and Research Station, Jagdalpur, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Abstract

The present investigation was carried out to study the genetic diversity of Colocasia (*Colocasia esculenta* var. *antiquorum* (L.) Schott) involving 24 selected taro (including check) genotypes were evaluated at three locations during summer season of 2018 and 2019. The experiments were conducted at location *viz.*, Jagdalpur, Bastar (L1), Kanker (L2) and Dantewada (L3) of Chhattisgarh in RBD with three replications. Observations were recorded for 16 quantitative traits which included leaf, petiole, corm, cormel and yield. The data was then subjected to D^2 analysis and was concluded from D^2 analysis that, the characters leaf area, corm weight plant^{-1}, cormel weight plant^{-1} and yield plant^{-1} contributed the maximum towards diversity. Studies in this direction are very less and can not to be generalized for every climatic condition and with other genetic materials. Hence, the information in a collection of some indigenous genotypes of taro in order to formulate a sound breeding plan for its improvement has been reviewed here.

Keywords: Colocasia, germplasms, genetic diversity, cluster distance, grouping and cluster mean

Introduction

Colocasia (*Colocasia esculenta* var. *antiquorum* L. Schott) also known as '*Taro*' is one of the oldest known tuber crop and has been grown for more than 10,000 years ago in Tropical Asia (Lebot, 2009) [17]. It is a tropical tuber crop belongs to the monocotyledonous own family *Araceae* of the order *Arales* whose participants are called aroids (Henry, 2001) [14]. *Araceae* includes about 100 genera and 1500 widely distributed species. It has been probably originated as of the wet tropical place flanked by India and Indonesia (Matthews, 2004) [20] and has been cultivated within the South Pacific for hundreds of years (FAO, 1992) [9]. Colocasia grows wild in tropical Asia, extending as far as east as New Guinea region near Indonesia and possibly Northern Australia. Taro serves as staple supply of diet for community in the region of the globe and it is the fourteenth mainly enthusiastic vegetable globally (Rao *et al.*, 2010). Worldwide taro is grown in an area of approximately 1.35 M ha in the midst of a yearly production of 10.2 MT and average productivity of 6.82 t/ha. In Asia, average yields reach 12.6 t ha^{-1} (FAOSTAT, 2019) [10]. It is grown as pure crop or as an intercrop in different farming systems and can tolerate salinity (Grubben and Denton, 2004) [12].

Tuber crops are classified through their hardiness to varying environmental conditions which are in advance global significance among bigger demand to increase diversity to maintain crop production. Further being a wealthy supply of vitamins, carbohydrates, minerals, proteins and dietary fibre (Bradburry and Holloway, 1998) [5], colocasia too possesses therapeutic values in opposition to tuberculosis, fungal infection and ulcers (Singh *et al.*, 2012) [28]. The magnitude of colocasia in the country will become yet greater vital considering about the fact that the main centre of source and diversity is believed to be in the Indo- Malayan area which consists of the North Eastern states including Chhattisgarh of India.

A large number of local genotypes are grown in different parts of Chhattisgarh. Bastar is rich in biodiversity of aroids and tribals grow these tubers in their *badi* or kitchen garden as a source of carbohydrate. However, the available colocasia genotypes were not evaluated in Chhattisgarh for corm yield and anti-nutritional properties. Further, summer colocasia is a relatively new crop in Chhattisgarh plains and superior genotypes can be introduced into different horticultural cropping systems of the region.

Genetic diversity in a population is a pre-requisite for an effective plant breeding programme.

The importance of genetic divergence in the improvement of crops has been stressed in both self and cross-pollinated crops. The major objective of colocasia reproduction is to improved potential cultivars so as to make sure maximum and stable yield in a range of climates. Genetic divergence is critical to gather the diversified aim of plant breeding such as breeding for crop growing for improving production, wider adaptation, excellence quality, pest and disease resistance. Therefore, the specific information on the nature and amount of genetic diversity helps the plant breeders before finalizing the parents for hybridization.

Materials and Methods

The field experiments consisting of 24 locally collected genotypes including check (White Gauriya) evaluated in RBD with 3 replications in a plot of 3 x 3 m^2 at spacing of 60 x 30 cm in between rows and plants, respectively. The experiments were conducted at SG, College of Agriculture and Research Station, IGKV, Instructional cum Research Farm, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh (Ll), Krishi Vighyan Kendra, IGKV, Kanker (L2) and on Farmer field at Village - Karli, Distt. Dantewada (L3) during the summer season from 1st year February to August 2018 and 2nd year during February to August 2019.

During the cropping season total rainfall received was 94.04 mm, maximum and minimum temperature varied from 35.4 and 8.1°C respectively, as well as relative humidity varied from 26 to 94%. The standard package of the practices prescribed by the AICRP on Tuber crops, SG, CARS, was followed.

Experimental materials

The experimental materials consisted of 24 genotypes including check indigenous genotypes of colocasia (*Colocasia esculenta* var. *antiquorum* (L.) Schott) collected from 24 districts of Chhattisgarh (latitude 21.2787 °N and longitude 81.8661° E) *viz*., Dantwada, Bastar, Kondagaon, Naryanpur, Kanker, Gariyaband, Mahasmund, Bilashpur, Korba, Dhamtari, Rajnandgaon, Surguja, Jashpur, Korea and Balod during March 2017 to January 2018.

Results and Discussion

Intra and inter cluster distance

At location -1, 24 genotypes were grouped in to 6 different clusters. The inter and intra cluster D^2 Values are presented in Fig 1**.**

Data revealed that Clusters IV had the highest intra cluster distance of 663.44 followed by cluster III (310.37), cluster II (290.48) and cluster I (251.41) whereas, the zero intra cluster distance observed in clusters V and VI (0.0).

The inter cluster distance was observed to be the highest in between cluster I and VI (5240.01). The inter cluster D^2 values were also high in between clusters IV and VI (4077.84), clusters I and V (2539.19), clusters I and II (2433.82), Clusters IV and V (2164.09), Clusters III and VI (1969.76), clusters II and IV (1524.69), V and VI (1474.48), clusters III and IV (1408.04), Clusters I and III (1225.38), clusters III and IV (1205.78), I and IV (989.71), clusters II and V (927.12), Clusters II and VI (917.14), clusters II and III (832.59). The lowest inter cluster D^2 value was found in between clusters I and I (251.41).

In the location-2, 24 genotypes were grouped in to three distinct clusters. The inter and intra cluster D^2 value are showed in Fig 2**.**

Cluster III had the highest intra cluster distance of 595.89 followed by clusters II (379.66) and clusters I (223.11).

The inter cluster distance was observed highest between clusters I and II (1197.83) followed by clusters II and III (953.74) and clusters I and III (898.48).

At location–3, 24 genotypes were grouped into six different clusters. The intra and inter cluster D^2 values are given in Fig 3.

Cluster III had the highest intra cluster distance of 220.79 followed by cluster II (117.45), cluster I (124.28) and the lowest *i.e.* intra cluster distance was observed in clusters IV, V and VI (0.0).

The highest inter clusters distance was observed between clusters V and VI (1079.35) followed by clusters I and VI (1016.53), clusters II and V (820.74), clusters I and II (804.76), clusters IV and VI (707.58), clusters III and VI (687.05), clusters IV and V (604.37), clusters II and IV (537.32), clusters III and V (489.48), clusters I and V (474.34), clusters III and IV (376.82), clusters II and III (363.22), clusters I and III (347.55) and clusters II and VI (327.69). The lowest inter clusters distance was observed in between clusters I and IV (285.50).

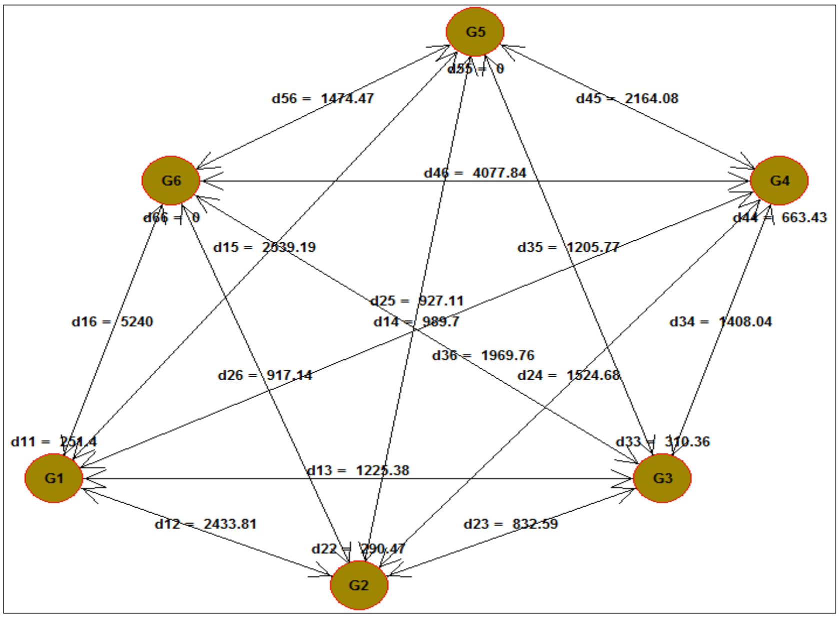

Fig 1: Cluster distance (inter and intra) values in colocasia genotypes, at location 1

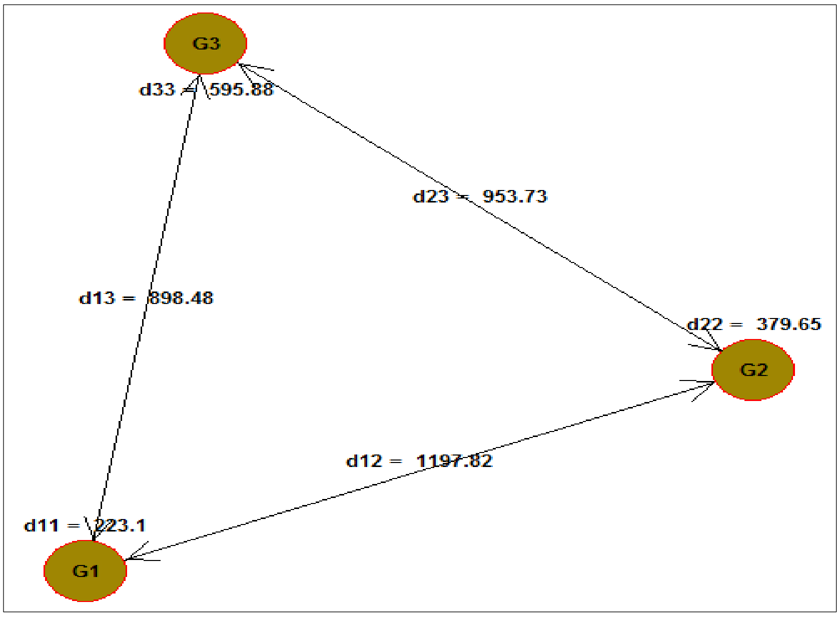

Fig 2: Cluster distance (inter and intra) values in colocasia genotypes, at location 2

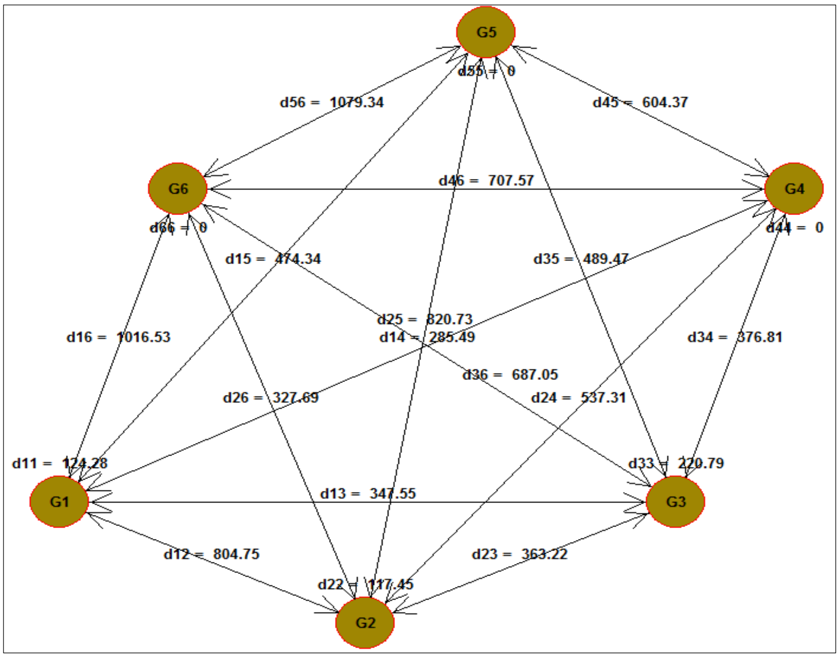

Fig 3: Cluster distance (inter and intra) values in colocasia genotypes at location 3

Grouping of genotypes in to various clusters

On the basis of D^2 analysis, twenty four genotypes were grouped into six different clusters and presented in Fig. 4. At location-1, maximum number of genotypes was grouped into cluster I (IGCOL-KS-10-1, IGCOL-DK-17-1, IGCOL-BNR-17-1, IGCOL-KS-13-1, IGCOL-PTD- 17-1, IGCOL-BDL-17-1, IGCOL-MNDG-17-1, IGCOL-SPL-17-1, IGCOL-CHHTD-18-1, IGCOL-JS-12-1, IGCOL-NGR-17-1, IGCOL-BL-12-1, IGCOL-KOTA-17-1 and IGCOL-PITH-17-1) included 14 genotypes followed by cluster II (IGCOL-PWD-17-1, IGCOL-PKJ-17-1 and IGCOL-CHLN-17-1) 3 genotypes, cluster number III (IGCOL-PWND-17-1, IGCOL-CHMD-18-1 and IGCOL-LHDD-18-1) 3 genotypes, cluster number IV (IGCOL-KDKN-17-1 and White Gauriya (S.C.) 2 genotypes and was lowest in clusters V (IGCOL-MUNG-17-1) and VI (IGCOL-GB-17-1) 1 genotype each in the material studied.

At location-2, (Fig. 5) 17 genotypes were grouped into cluster I (IGCOL-PTD-17-1, IGCOL-BNR-17-1, IGCOL-DK-17-1, IGCOL-KS-13-2, IGCOL-KS-10-1, IGCOL-BDL-17-1, IGCOL-MNDG-17-1, IGCOL-CHHTD-18-1, IGCOL-NGR-17-1, IGCOL-SPL-17-1, IGCOL-JS-12-1, IGCOL-KOTA-17-1, IGCOL-BL-12-1, IGCOL-PWND-17-1, IGCOL-CHMD-18-1, IGCOL-LHDD-18-1, IGCOL-PITH-17-1), 5 genotypes in cluster II (IGCOL-PWD-17-1, IGCOL-GB-17-1, IGCOL-CHLN-17-1, IGCOL-MUNG17-1, IGCOL-PKJ-17-1) and remaining 02 genotypes (IGCOL-KDKN17-1 and White Gauriya S. C.) in cluster III.

At location-3, grouping of 24 colocasia genotypes in to various clusters are presented in Fig. 6. Cluster I consisted of the highest number of 18 genotypes (IGCOL-KS-10-1, IGCOL-DK-17-1, IGCOL-BNR-17-1, IGCOL-KS-13-2, IGCOL-PTD-17-1, IGCOL-MNDG-17-1, IGCOL-BL-12-1, IGCOL-BDL-17-1, IGCOL-CHHTD-18-1, IGCOL-SPL-17-1, IGCOL-NGR17-1, IGCOL-KOTA-17-1, IGCOL-JS-12-1, IGCOL-PITH-17-1 and IGCOL-PWND-17-1) followed by cluster II (IGCOL-PWD-17-1, IGCOL-CHLN-17-1 and IGCOL-GB-17-1) 3 genotypes, cluster III (IGCOL-CHMD-18-1, IGCOL-LHDD-18-1 and White Gauriya S. C) 3 genotypes and the lowest in clusters IV (IGCOL-PKJ-17-1), cluster V (IGCOL-KDKN-17-1) and cluster VI (IGCOL-MUNG-17-1) with one genotype.

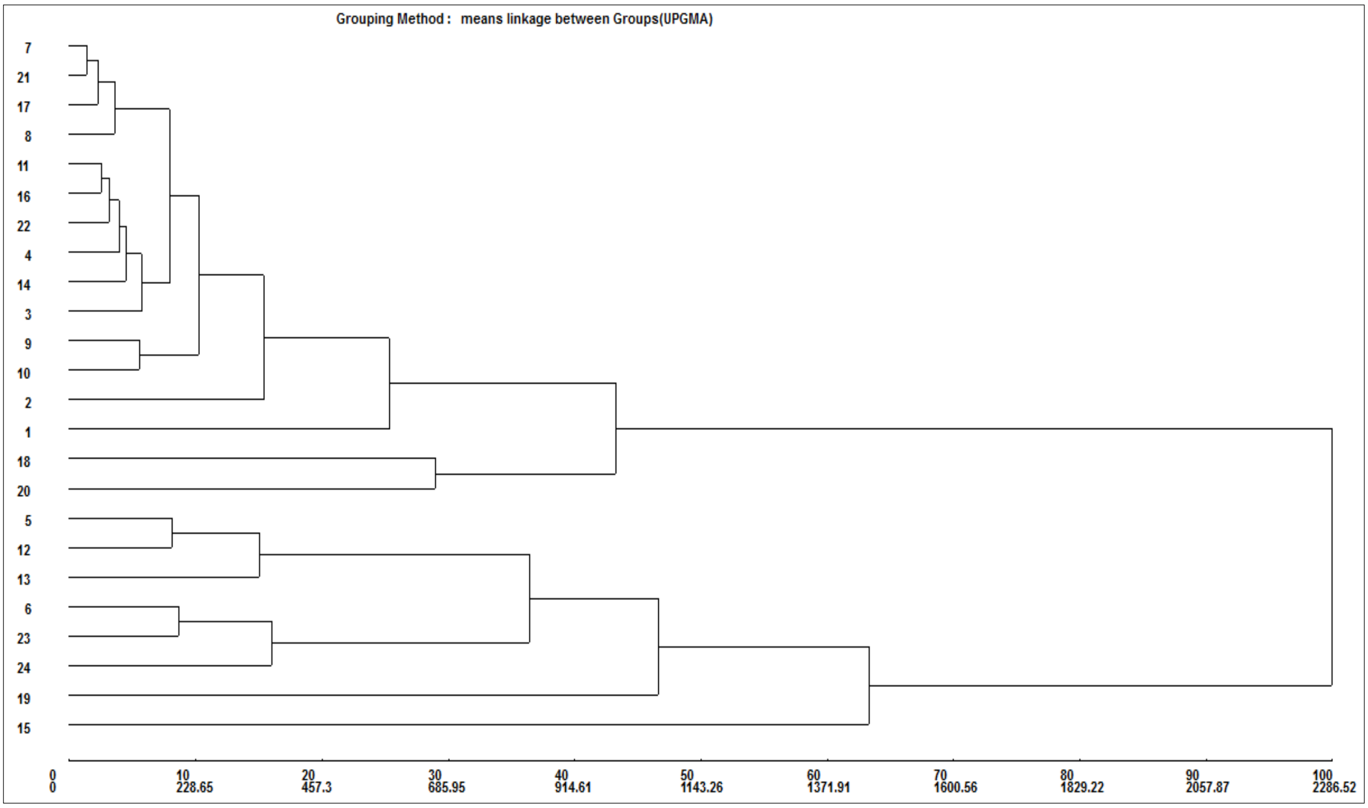

Fig 4: Genotypes of colocasia included in different clusters/ grouping at location 1

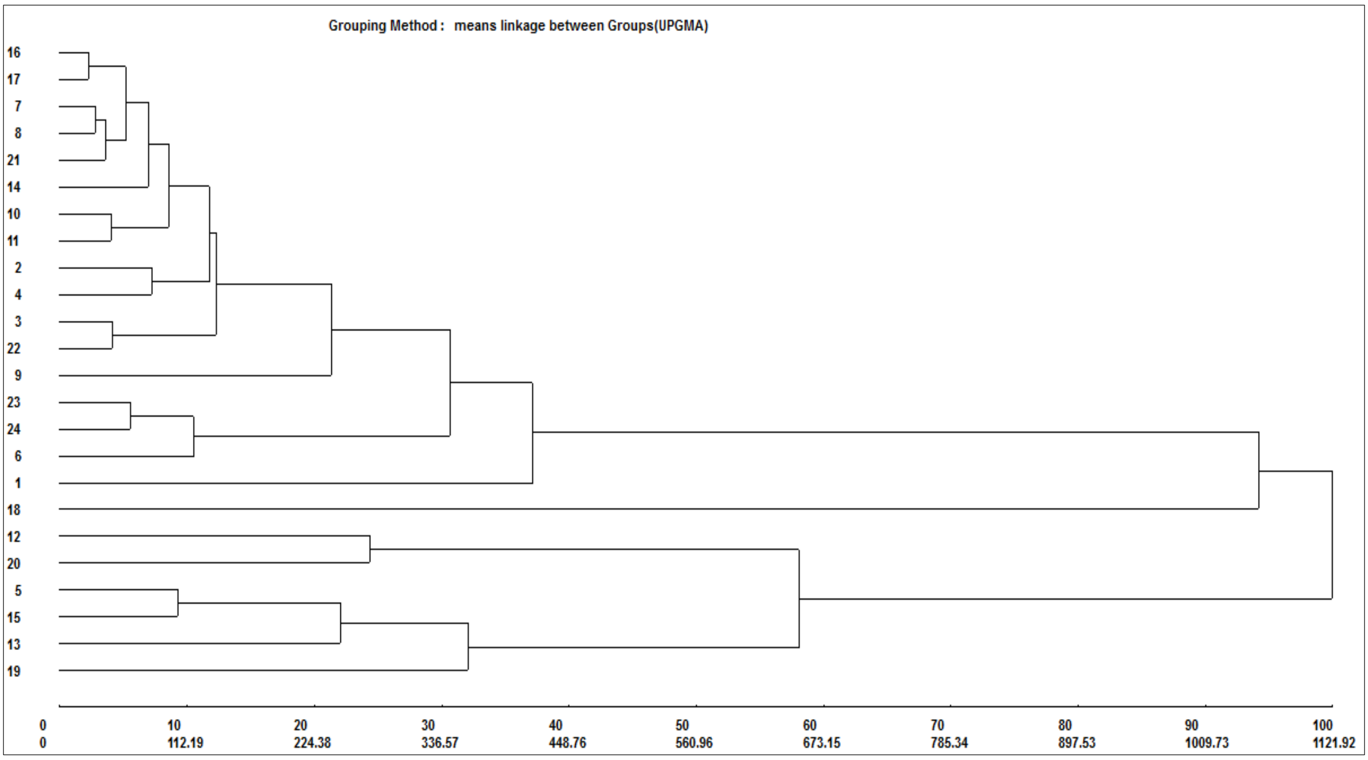

Fig 5: Genotypes of colocasia included in different clusters/ grouping, at location 2

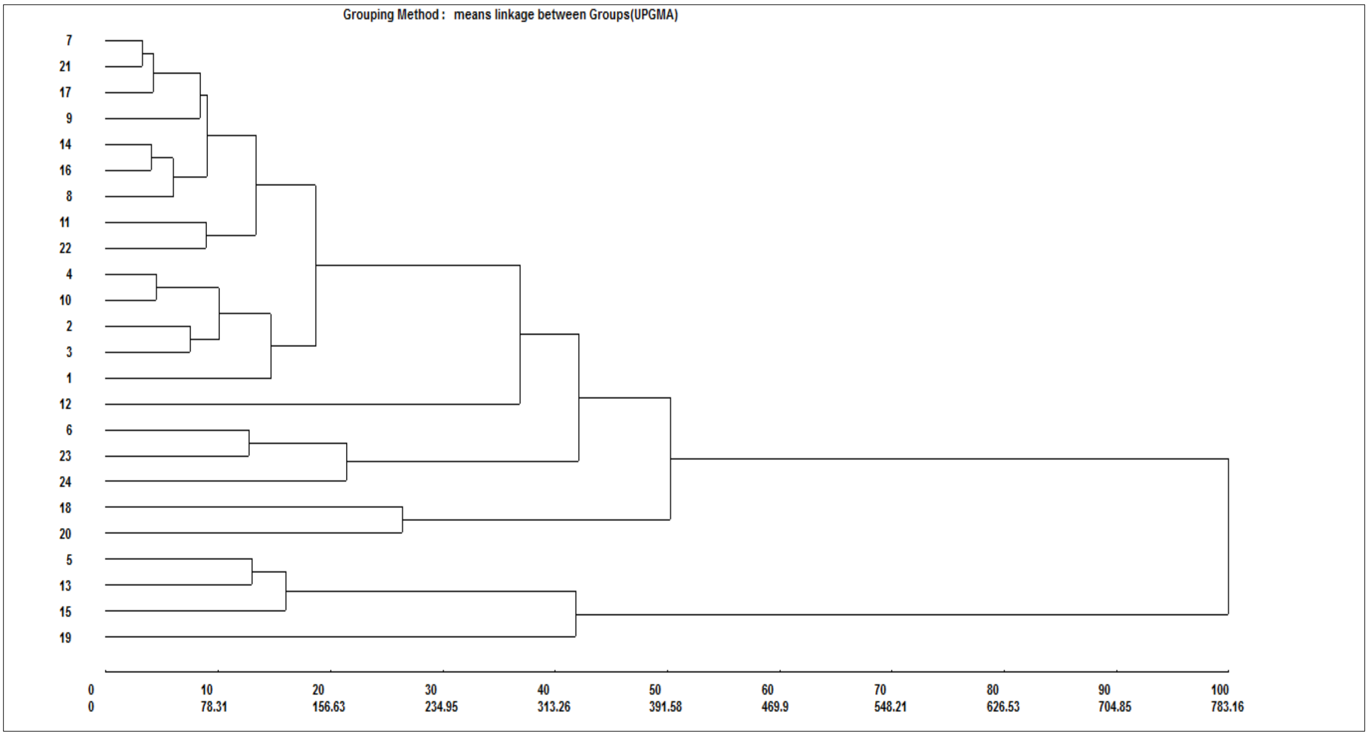

Fig 6: Genotypes of colocasia included in different clusters/ grouping at location 3

Components of intra cluster mean in colocasia

The component of intra cluster means for different clusters of genotypes for corm and cormels yield and its attributing traits are presented in Table 1 to 3. The data on cluster means performance for all the characters studied showed appreciable differences based on different traits. The location wise components are described below:

At location-1 intra cluster means for sixteen characters are presented in Table 1 revealed remarkable differences between the six clusters in respect of cluster means for different characters. Based on top performance that the highest treatment mean cormel yield plant^{-1} for cluster VI (301.58) followed by corms & cormels yield ha^{-1} for cluster VI (278.86), corms & cormels yield ha^{-1} for clusters II (220.43), cormels yield plant^{-1} for clusters II (217.19), corms & cormels yield ha^{-1} for clusters V (208.91) and cormels yield plant^{-1} for clusters III (195.50).

The cluster mean for plant height was the highest for cluster VI (102.31 cm) followed by cluster V (95.44 cm), cluster III (94.27 cm), cluster II (74.83 cm) and cluster I (66.48 cm). Whereas, it was noted the lowest cluster mean for plant height in cluster IV (64.35 cm).

In case, the number of suckers plant^{-1}, the highest mean performance was obtained for cluster V (3.50) followed by cluster VI (2.73), cluster II (1.74), cluster III (1.60), cluster I (1.26) and cluster IV (0.71) showed the lowest cluster mean value.

The highest mean performance for petiole length (cm) was observed for cluster III (63.15 cm) followed by cluster VI (62.97 cm), cluster V (58.77 cm), cluster II (52.00 cm) and cluster I (43.89 cm). The lowest cluster mean for petiole length (cm) was observed in cluster IV (43.36 cm).

Cluster III (4.68 cm) showed the highest mean performance for girth of pseudo-stem followed by, cluster VI (4.58 cm), cluster II (4.07 cm), cluster V (3.81 cm) and cluster I (3.25 cm). The lowest cluster mean was observed in cluster IV (3.19).

The highest mean performance values for leaf area index was observed for cluster VI (2.18) followed by cluster III (1.50), cluster II (1.30), cluster V (1.21) and cluster I (0.75). The lowest cluster mean was observed for cluster IV (0.69).

Table 1: Mean performance of different clusters for corm and cormels yield and its components at Location 1

Clusters	Traits code																Remark based on top performance
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
I	66.48	1.26	43.89	3.25	0.75	7.67	4.92	2.81	22.62	123.61	26.31	5.15	5.11	74.47	25.13	110.04	VI
II	74.83	1.74	52.00	4.07	1.30	10.94	6.51	2.68	28.22	217.19	26.56	8.37	6.26	179.59	25.00	220.43	II
III	94.27	1.60	63.15	4.68	1.50	9.09	5.33	2.96	29.83	195.50	27.04	6.13	6.22	124.84	24.96	177.97	IV
IV	64.35	0.71	43.36	3.19	0.69	5.77	6.04	2.52	23.33	99.07	27.22	7.83	5.62	136.03	26.62	130.61	V
V	95.44	3.50	58.77	3.81	1.21	9.34	7.48	2.65	30.10	187.45	26.79	9.63	6.01	188.60	26.22	208.91	III
VI	102.31	2.73	62.97	4.58	2.18	12.67	7.01	2.90	35.80	301.58	26.92	9.42	6.43	200.37	24.38	278.86	1

Table 2: Mean performance of different clusters for corm and cormels yield and its components at location 2

clusters	Traits																Remark based on top performance
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
I	69.77	1.35	44.75	3.55	0.88	8.62	5.03	2.88	24.41	134.25	27.14	5.31	5.35	83.61	25.51	121.03	III
II	86.80	2.45	55.73	4.44	1.58	11.65	6.87	2.83	32.10	257.07	27.80	9.14	6.34	197.30	25.50	252.43	I
III	61.58	0.97	39.95	3.20	0.76	6.55	6.42	2.61	26.68	130.77	26.71	8.50	6.04	164.58	26.22	164.08	II

Table 3: Mean performance of different clusters for corms and cormels yield and its components at Location 3

clusters	Traits																Remark based on top performance
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
I	64.31	1.12	42.09	3.41	0.81	7.71	4.89	2.78	22.60	122.68	27.16	5.30	5.20	77.84	25.31	111.40	V
II	80.48	1.91	51.68	4.53	1.52	10.31	6.68	2.88	30.45	232.69	28.68	8.88	6.38	193.07	25.51	236.53	I
III	80.56	1.30	53.38	4.31	1.35	7.85	5.56	2.81	27.83	167.06	27.54	6.49	6.29	138.41	25.91	169.70	IV
IV	62.81	1.13	42.56	4.18	1.01	11.07	6.50	2.34	22.50	170.17	27.10	7.42	6.10	138.63	24.31	171.55	III
V	57.55	0.71	37.70	2.72	0.64	4.48	5.75	2.44	23.00	78.73	25.24	9.07	5.39	137.77	27.75	120.27	VI
VI	81.55	3.33	52.64	3.82	1.19	9.89	7.50	2.59	28.95	177.00	27.03	9.76	6.19	193.71	25.88	205.95	II

Traits code					
1. Plant height (cm)	2.No. of suckers plant $^{-1}$	3.Petiole length (cm)	4. Girth of pseudo-stem (cm)	5. Leaf area index	6. No. of cormels plant^{-1}
7.Cormel length (cm)	8. Cormel girth (cm)	9. Cormel weight (g)	10. Cormels yield plant^{-1} (g	11. Dry matter % of cormel	12. Corm length (cm)
13. Corm girth (cm)	14. Corm yield plant^{-1}	15. Dry matter % of corm		16. Corms & cormels yield ha^{-1}	

Cluster VI had the highest mean for number of cormels plant^{-1} (12.67) followed by, clusters I1 (10.94), cluster V (9.34), cluster III (9.09) and cluster I (7.67). The lowest cluster mean was observed for cluster IV (5.77).

Cluster V had the highest treatment mean for cormel length for cluster V (7.48) followed by clusters VI (7.01), cluster II (6.51), cluster IV (6.04) and cluster III (5.33). The lowest cluster mean was observed for cluster I (4.92).

The highest cluster mean for cormel girth (cm) was observed for cluster III (2.96cm) followed by cluster VI (2.90cm), Cluster I (2.81cm), Cluster II (2.68cm) and cluster V (2.65cm). The lowest cluster mean was observed the cluster IV (2.52).

Cluster VI had the highest mean for cormel weight for cluster VI (35.80g) followed by cluster V (30.10 g), cluster III (29.83 g), Cluster II (28.22 g) and cluster IV (23.33 g). The lowest cluster mean was recorded by the cluster I (22.62).

Cluster VI had the highest treatment mean for cormel yield plant^{-1} for cluster VI (301.58 g) followed by cluster II (217.19 g), cluster III (195.50 g), Cluster V (187.45 g) and cluster I (123.61 g). The lowest cluster treatment mean was recorded by the cluster IV (99.07 g).

Cluster IV had the highest mean for dry matter per cent of cormel for cluster IV (27.22) followed by cluster III (27.04), cluster VI (26.92), Cluster V (26.79) and cluster II (26.56). The lowest cluster mean was recorded by the cluster I (26.31).

The highest mean performance for corm length (cm) was observed for cluster V (9.63cm) followed by, cluster VI (9.42 cm), cluster II (8.3 cm 7), cluster IV (7.83 cm) and cluster III (6.13 cm). The lowest cluster mean was observed in cluster I (5.15).

The highest cluster mean for corm girth was recorded for cluster VI (6.43) followed by, cluster II (6.26 cm), cluster III (6.22 cm), cluster V (6.01 cm) and cluster IV (5.6 cm 2). The lowest cluster mean was recorded in cluster I (5.11 cm).

The highest cluster means for corm yield plant^{-1} (g) was observed for cluster VI (200.37 g) followed by, cluster V (188.60 g), cluster II (179.59 g), cluster IV (136.03 g) and cluster III (124.84 g). The lowest cluster mean was noted by cluster I (74.47 g).

The highest cluster mean for dry matter per cent corm was observed for cluster IV (26.26) followed by cluster V (26.22), cluster I (25.13), cluster II (25.00) and cluster III (24.96). The lowest cluster mean was recorded by the cluster VI (24.38).

Cluster V had the highest treatment means for corms and cormels yield ha^{-1} for cluster VI (278.86 qha^{-1}) followed by cluster II (220.43 qha^{-1}), cluster V (208.91 qha^{-1}), cluster III (177.97 qha^{-1}) and cluster IV (130.61 qha^{-1}). The lowest cluster mean was noted in cluster I (110.04 qha^{-1}).

Based on top performance the that the highest treatment mean cormel yield plant^{-1} for cluster VI (301.58) followed by corms & cormels yield ha^{-1} for cluster VI (278.86), corms & cormels yield ha^{-1} for clusters II (220.43), cormels yield plant^{-1} for clusters II (217.19), corms & cormels yield ha^{-1} for clusters V (208.91) and cormels yield plant^{-1} for clusters III (195.50).

At location-2 intra- cluster means are presented in Table 2. Cluster means performance for the sixteen characters are presented in Table 4.6.8. Cluster II had the highest treatment means for plant height (86.80cm) followed by cluster I (69.77 cm) and cluster III with the lowest treatment mean (61.58 cm) for plant height.

Cluster II had the highest treatment means for number of suckers plant^{-1} (2.45) followed by cluster I (1.35) and cluster III with the lowest treatment means (0.97).

Cluster II had the highest treatment means for petiole length (55.73 cm) followed by cluster I (44.75 cm) and cluster III with the lowest treatment mean (39.95 cm).

Again cluster II had the highest treatment mean for girth of pseudo-stem (4.44 cm) followed by cluster I (3.55 cm) with the lowest treatment mean in cluster III (3.20 cm).

Cluster II had the highest treatment mean for leaf area index (1.58) followed by cluster I (0.88) and cluster III recorded with the lowest treatment mean (0.76).

Again cluster II had the highest treatment mean for number of cormels plant^{-1} (11.65) followed by cluster I (8.62) and cluster III observed with the lowest treatment mean (6.55).

Cluster II had the highest treatment mean for cormel length (6.87 cm) followed by cluster III (6.42cm) and cluster I recorded with the lowest treatment mean (5.03 cm).

The highest cluster mean for cormel girth was observed for cluster I (2.88 cm) followed by cluster II (2.83 cm). The lowest cluster mean was observed in cluster III (2.61 cm).

The highest cluster mean for cormel weight was observed for cluster II (32.10g) followed by cluster III (26.68g). The lowest cluster mean was recorded cluster I (24.41g).

Cluster has the highest treatment mean for cormel yield plant^{-1} was observed for cluster II (257.07g) followed by cluster I (134.25g). The lowest cluster mean was recorded III cluster (25.34g).

Cluster II had the highest treatment mean for dry matter percentage of cormel (27.80) followed by cluster I (27.14) and cluster III observed with the lowest treatment mean (26.71).

Cluster II had the higher treatment mean for corm length (9.14 cm) followed by cluster III (8.50 cm) whereas, the lowest cluster mean recorded in cluster I (5.31 cm) mean.

Cluster II had the highest treatment mean for corm girth (6.33 cm) followed by cluster III (6.04 cm) and cluster I recorded with the lowest treatment mean (5.35 cm).

Cluster II had the highest treatment mean for corm yield plant^{-}

^{1} (197.30g) followed by cluster III (164.58g) and cluster I had lowest treatment mean (83.61g).

Cluster III had the highest treatment mean for dry matter percentage of corm (26.22) followed by cluster I (25.51) and cluster II recorded with the lowest treatment mean (25.50).

Cluster II (252.43 q ha^{-1}) showed the highest cluster mean for corms and cormels yield ha^{-1} followed by cluster III (164.08 q ha^{-1}). The lowest cluster mean was showed by cluster I (121.03 q ha^{-1}).

Based on top performance the highest treatment mean cormel yield plant^{-1} for cluster II (257.07) followed by corms & cormels yield ha^{-1} for cluster II (252.43), corms yield plant^{-1} for clusters II (197.30), corms yield plant^{-1} for clusters III (164.58), corms & cormels yield ha^{-1} for clusters III (164.08) and cormels yield plant^{-1} for clusters I (134.25).

In the location-3, intra cluster mean for the 16 characters are presented in Table 3. Cluster VI had the highest cluster mean performance for plant height (81.55 cm) followed by cluster III (80.56 cm), cluster II (80.48 cm), cluster I (64.31 cm), cluster IV and (62.81 cm) whereas, cluster V with the lowest treatment mean (57.55 cm).

Cluster VI had the highest treatment means for number of suckers plant^{-1} (3.33) followed by cluster II (1.91), cluster III (1.30), cluster IV (1.13), cluster I (1.12) and cluster V with the lowest treatment mean (0.71).

Cluster VI had the highest treatment mean for petiole length (52.64 cm) followed by cluster III (53.38 cm), cluster II (51.68 cm), cluster IV (42.56 cm), cluster I (42.09) and cluster V with the lowest treatment mean (37.70 cm).

Cluster II had the highest treatment mean for girth of pseudo-stem (4.53 cm) followed by cluster III (4.31 cm), cluster IV (4.18 cm), cluster VI (3.82 cm), cluster I (3.41 cm) and cluster V with the lowest cluster mean (2.72 cm).

The highest cluster II mean for leaf area index (1.52) followed by cluster III (1.35), cluster VI (1.19), cluster IV (1.01), cluster I (0.81). The lowest cluster mean was showed by cluster V (0.64).

The highest cluster mean for number of cormels plant^{-1} was observed for cluster IV (11.07) followed by cluster II (10.31), cluster VI (9.89), cluster III (7.85), cluster I (7.71) and cluster V with the lowest cluster mean (4.48).

Cluster VI had the highest treatment mean for cormel length (7.50) followed by cluster II (6.68 cm), cluster IV (6.50 cm), cluster V (5.75 cm), cluster III (5.56 cm) and cluster I with the lowest treatment mean (4.89 cm).

Cluster II had the highest treatment mean for cormel girth (2.88) followed by cluster III (2.81 cm), cluster I (2.78 cm), cluster VI (2.59 cm), cluster V (2.44 cm) and cluster IV with the lowest treatment mean (2.34 cm).

Again cluster II had the highest treatment mean for cormel weight (30.45g) followed by cluster VI (28.95 g), cluster III (27.83 g), cluster V (23.00 g), cluster I (22.60 g)and cluster IV with the lowest treatment mean (22.50 g).

The highest cluster means for cormels yield plant^{-1} in cluster II (232.69 g) followed by cluster VI (177.00 g), cluster IV (170.17), cluster III (167.06 g) and cluster I (122.68). The lowest cluster mean was showed by cluster V (78.73 g).

The highest cluster means for dry matter per cent of cormel in cluster II (28.68) followed by cluster III (27.54), cluster I (27.16), cluster IV (27.10) and cluster VI (27.03). The lowest cluster mean was showed by cluster V (25.24).

Cluster VI had the highest treatment mean for corm length (9.76) followed by cluster V (9.07 cm), cluster II (8.88 cm), cluster IV (7.42 cm), cluster III (6.49 cm) and cluster I with the lowest treatment mean (5.30 cm).

Cluster II had the highest treatment mean for corm girth (6.38) followed by cluster III (6.29 cm), cluster VI (6.19 cm), cluster IV (6.10 cm), cluster V (5.39 cm) and cluster I with the lowest treatment mean (5.20 cm).

Cluster VI had the highest treatment mean for corm yield plant^{-1} (193.71) followed by cluster II (193.07 g), cluster IV (138.63 g), cluster III (138.41 g), cluster V (137.77 g), and cluster I with the lowest treatment mean (77.84 g).

Cluster V had the highest treatment mean for dry matter percentage of corm (27.75) followed by cluster III (25.91), cluster VI (25.88), cluster II (25.51), cluster I (25.31) and cluster IV with the lowest treatment mean (24.31).

The highest treatment mean for corms and cormels yield ha^{-1} was observed for cluster II (236.53 qha^{-1}) followed by cluster VI (205.95 qha^{-1}), cluster IV (171.55 qha^{-1}), cluster III (169.70 qha^{-1}) and cluster V (120.27 qha^{-1}). The lowest treatment mean of cluster was showed by cluster I (111.40 qha^{-1}).

Based on top performance the highest treatment mean corms & cormels yield ha^{-1} for cluster II (336.53) followed by cormels yield plant^{-1} for cluster II (232.69), corms & cormels yield ha^{-1} for clusters VI (205.95), corms yield plant^{-1} for clusters VI (193.71), corms yield plant^{-1} for clusters II (193.07) and cormels yield plant^{-1} for clusters VI (177).

In this study an attempt was made to know the genetic diversity of 24 genotypes for 16 characters. Such an assumption will be helpful for the breeder to plan hybridizations programme selecting diverse parents involving minimum risk from the point of heterosis. Inclusion of diverse parents in hybridization programme will serve the purpose of combining desirable genes or to obtain superior recombinants. Among the various methods of multivariate analysis available for classification of germplasm collections, D^{2} analysis was found to be quite better in quantification of genetic diversity available in the population. Therefore, an attempt has been made to quantity the genetic diversity in the available germplasm collection of colocasia. The genetic diversity estimate is of tenly influenced by the environmental conditions. Hence, germplasm/ genotypes/ lines collected from different districts of Chhattisgarh were evaluated in three locations (L1, L2 and L3). The experimental finding of this study with respect to genetic diversity has been discussed in the following paragraphs. To avoid unnecessary reception, only pooled data of three locations with regard to D^{2} analysis have been discussed.

On the basis of graphical presentation 24 genotypes were grouped in to six different clusters of location-1. The highest intra cluster distance was observed between cluster IV and IV and lowest intra cluster distance was observed between V and V, VI and VI. Cluster I and VI had the highest inter cluster distance and cluster II and III had lowest. Cluster number I had the maximum number of genotypes whereas cluster number V and VI had lowest. At location- 2, cluster III and III had the maximum intra cluster distance while cluster I and I had lowest. The inter cluster distance was observed highest between cluster I and II and lowest was between I and III. Cluster number I had the maximum number of genotypes (17) and cluster number III had lowest (2). In the location - 3, highest cluster distance was observed in cluster III and lowest was in cluster IV, V and VI. The highest inter cluster distance was observed between cluster V and VI and lowest between cluster I and IV. Cluster I had the highest number of genotypes (18) and lowest was in cluster IV, V and VI (1 genotypes each clusters).

The intra cluster means for 16 characters for the pooled data of location-1, 2 and 3 are discussed below. In the location-1 cluster VI had the highest mean value for plant height, leaf area index, number of cormels plant^{-1}, cormel weight, cormels yield plant^{-1} corm girth, corm yield plant^{-1} and corms and cormels yield ha^{-1}, whereas, cluster V had the highest mean value for number of suckers plant^{-1}, cormel length and corm length although cluster III had highest mean value for petiole length, girth of pseudo-stem and cormel girth and cluster IV had dry matter percentage of cormel and dry matter percentage of corm for maximum mean values. At the location - 2 cluster II had the highest mean values of plant height, number of suckers plant^{-1}, petiole length, girth of pseudo-stem, leaf area index, number of cormels plant^{-1}, cormel length, cormel weight, cormels yield plant^{-1}, dry matter percentage of cormel, corm length, corm girth, corm yield plant^{-1} and corms and cormels yield q ha^{-1} while cluster I had the highest mean values for corm girth and cluster III was showed high mean value for dry matter percentage of corm. In the location of L3, cluster II had the highest mean values for girth of pseudo-stem, leaf area index, cormel girth, cormel weight, cormels yield plant^{-1} dry matter percentage of cormel, corm girth and corms & cormels yield ha^{-1} whereas cluster VI had maximum mean values for plant height, number of suckers plant^{-1}, petiole length, cormel length, corm length and corm yield plant^{-1}. However cluster IV had highest mean value for number of cormels plant^{-1} and cluster V had maximum mean values for dry matter percentage of corm.

Based on inter cluster distance and cluster means, it can be concluded that genotypes of the cluster VI and II could be select for hybridization programme as they are expected to produce highly heterogenic crosses.

Based on D^2 studies genotypes IGCOL-GB-17-1, IGCOL-MUNG-17-1, IGCOL-KDKN-17-1, IGCOL-PWND-17-1, IGCOL-CHMD-18-1, IGCOL-LHDD-18-1, IGCOL-PWD-17-1, IGCOL-PKJ-17-1 and IGCOL-CHLN-17-1 could be selected for hybridization and colocasia improvement programme. For hybridization programme parents of colocasia should not be selected from the same cluster. On the basis of the above analysis, genotypes IGCOL-GB-17-1, IGCOL-CHMD-18-1 and IGCOL-LHDD-18-1 is recommended to be used as parents for corms and cormels yield.

Genetic diversity is the most important tool to select prospective parents in crop improvement programme. The genotypes from the clusters which were separated by high estimated distance could be utilized in hybridization programme for obtaining wide variation among segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters *i.e.* clusters IGCOL-GB-17-1, IGCOL-CHMD-18-1 and IGCOL-LHDD-18-1 at all the locations. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters were measured. Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield wide range of segregants on which selection could be practiced. Similar results have been reported for corms & cormels yield ha^{-1} by Jianchu *et al.* (2001) [15], Amsalu and Nebiyu (2003) [2], Teshome *et al.* (2002) [29], Mondal (2003) [21], Haydar *et al.* (2007) [13], Naskar and Sreekumar (2011) [23], Choudhary *et al.* (2011) [6], Devi *et al.* (2013) [7], Laurie *et al.* (2013) [16], Getachew *et al*., (2013) [11], Tewodros (2013) [11], Mandal *et al.* (2013) [19], Fantaw *et al.* (2014) [8], Bhattacharjee *et al.* (2014) [4], Poddar *et al.* (2015) [24], Agre *et al*., (2017) [1], Silva *et al.* (2017) [27], Narayan *et al.* (2018) [22] and Bhanu Prakash *et al.* (2019) [3].

Conclusion

From the present study, it is concluded that wider variability was observed among most of the accession. The accession 23 and 24 were found to be superior in cormels production, corm and cormels weight and yield plant^{-1} based on evaluation. Hence, these accessions may be finalized for further breeding programme.

Novelty statement

Present investigation comprised the genetic diversity of colocasia germplasms. All evaluated genotypes are available locally in state which were collected through extensive survey and submitted to National Bureau of Plant Genetic Resources (NBPGR) sub-station Hyderabad. Accessions will serve as parent material and can be used for further breeding program as well as releasing of potential variety.

Competing interest

The authors declare that they have no competing interest.

References

1. Agre AP, Bhattacharjee R, Dansi A, Becerra LA, Lavalle L, Dansi M, *et al*. Assessment of cassava (*Manihot esculenta* Crantz) diversity, loss of landraces and farmers preference criteria in southern Benin using farmers' participatory approach. Genetic Resources and Crop Evolution 2017;64:307–20.
2. Amsalu, Nebiyu. Characterization and divergence analysis in cassava (*Manihot esculenta* Cranz) genotypes at Jimma. *M.Sc. thesis*. Alemaya University, Ethiopia 2003.
3. Bhanu Prakash GC, Ramesh Babu B, Mamatha K, Snehalatha Rani A, Umayjothi K. Genetic divergence studies in colocasia [*Colocasia esculenta* (L.) Schott] germplasm. International Journal of Chemical studies 2019;7(1):998-1002.
4. Bhattacharjee M, Tarafdar J, Sadhukhan R. Assessment of Genetic Diversity of Some Indigenous Collections of Upland Taro [*Colocassia esculenta* var. *antiquorium* (L.) Schott] for Selection of Genotypes Aiming at Improvement in Breeding Programme. IOSR Journal of Agriculture and Veterinary Science 2014;7(7):31-43.
5. Bradburry JH, Holloway WD. Chemistry of tropical root crops: Significance for nutrition and agriculture in the Pacific. ACIAR, Canberra, ACIAR Monograph 1998;6:201-204.
6. Choudhary VK, Kumar SP, George J, Kanwat M, Saravanan R. Genetic variability and character association in taro (*Colocasia esculenta* (L.) Schott.) under Mid-Hills of Arunachal Pradesh. Journal of Root Crops 2011;37(2):155-161.
7. Devi HS, Singh V, Duwey RK, Chauhan VBS. Assessment of genetic diversity in taro (*Colocasia esculent* L.) National conference on: Tuber crops (other than potato) for sustainable agriculture and livelihood security in climate change scenario AAU, Jorhat on 2013;29:53-54.
8. Fantaw S, Nebiyu A, Tewodros M. Genetic diversity of

tannia (*Xanthosoma sagittifolium* (L.) Schott) genotypes using multivariate analysis in Jimma, South West Ethiopia. International journal of plant breeding and genetics 2014;8(4):194-204.
9. FAO. Taro: A south Pacific specialty. Leaflet – revised 1992. Community Health Services, South Pacific Commission, B.P. D 5, Noumea, Cedex, New Caledonia 1992.
10. FAOSTAT. FAO org. Retrieved 6 December 2019.
11. Getachew W, Kifle B, Tewodros M. Genetic diversity of taro (*Colocasia esculenta* (L.) Schott) genotypes in Ethiopia based on agronomic traits. Time Journals of Agriculture and Veterinary Sciences 2013;1(2):23-30.
12. Grubben GJH, Denton OA. Vegetables. Plant Resources of Tropical Africa. Prota 2004.
13. Haydar A, Ahmed MB, Hannan MM, Razvy MA, Mondal MA, Salahin M, *et al*. Analysis of genetic diversity in some potato varieties grown in Bangladesh. Middle- East Journal of Science Research 2007;2(2-3):143-54.
14. Henry RJ. Plant genotyping: The DNA fingerprinting of plants. CAB Publishing, Southern Cross University, Australia 2001.
15. Jianchu X, Yang, Yong Y, Yingdong P, Ayad WG, Eyzaguirre PB. Genetic diversity in taro (*Colocasia esculenta* schott, araceae) in china: an ethnobotanical and genetic approach. Economic Botany 2001;55(1):14-31.
16. Laurie SM, Calitz FJ, Adebola PO, Lezar A. Characterization and evaluation of South African sweet potato (*Ipomoea batatas* (L.) LAM) land races. South African Journal of Botany 2013;85:10–16.
17. Lebot V. Tropical Root and Tuber Crops: Cassava, Sweet Potato, Yam and Aroids. CABI, Wallngford, U K 2009, 413-416.
18. Mahalanobis PC. A statistical study of Chinese head measurement. Man in India 1928;8:32-64.
19. Mandal R, Mukherjee A, Mandal N, Tarafdar J, Mukherjee A. Assessment of Genetic Diversity in Taro using morphometrics. Curr. Agri. Res. 2013, 1(2).
20. Matthews P. Genetic diversity in taro, and the preservation of culinary knowledge. Ethnobotany J 2004;2:55-77.
21. Mondal MAA. Improvement of potato (*Solanum tuberosum* L.) through hybridization and *in-vitro* culture technique. Ph.D. Thesis. Rasshahi University, Rasshahi, Bangladesh 2003.
22. Narayan A, Prasad R, Singh PP, Kumar A, Singh RS. Genetic divergence and correlation of tuber characteristics in bunda germplasm (*Colocasia esculenta* var. *esculenta*) of Bihar. Int. J Curr. Microbiol. App. Sci 2018;7:1022-30.
23. Naskar SK, Sreekumar J. Evaluation of taro (*Colocasia esculenta* (L.) Schott.) germplasm using multivariate analysis. Journal of Root Crops 2011;37(2):150-54.
24. Poddar A, Mukherjee A, Sreekumar J, Abraham K, Naskar SK, Unnikrishnan M, *et al*. Phenotypic variability of among germplasm lines of elephant foot yam (*Amorphophallus paeoniifolius*) and taro (*Colocasia esculenta*). Int. J of Tropical Agric 2015;33(2):377-80.
25. Rao CR. Advance Statistical Methods in Biometrics Research. Hofaer Pub. Darion. 1952, pp. 371-378.
26. Rao RV, Matthews P, Eyzaguirre PB, Hunter D. The global diversity of *C. esculenta*: ethnobotany and conservation. Biodiversity International, Rome 2010.
27. Silva LRG, Mezette TF, Nascimento WF, Silva EF, Veasey EA. Spatially structured morphological and molecular diversity among *Dioscorea cayenensis* and *D. rotundata* yam accessions. Plant Genetic Resources: Characterization and Utilization 2017;15(4):296–309.
28. Singh S, Singh DR, Faseela F, Kumar N, Damodaran V, Srivastava RC. Diversity of 21 taro (*Colocasia esculenta* (L.) Schott.) Accessions of Andaman Islands. Genet. Resour. Crop Evol 2012;59:821-829.
29. Teshome A, Veeraragarathatham D, Kannan M. Genetic divergence for yield and yield contributing characters in potato. Proceedings of African potato association 5th to10th April held at Agidir, Morocco 2002.
30. Tewodros MB. Morpho-agronomical characterization of taro (*Colocasia esculenta*) accessions in Ethiopia. Plant 2013;1(1):1-9.