International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
IJCS 2019; 7(1): 998-1002

Received: 13-11-2018
Accepted: 16-12-2018

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Genetic divergence studies in colocasia [*Colocasia esculenta* (L.) Schott] germplasm

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Abstract
The present investigation entitled "Genetic divergence studies in colocasia [*Colocasia esculenta* (L.) Schott] germplasm" was conducted at Horticultural Research Station, Kovvur, Andhra Pradesh during the period 2017 to 2018 with twenty eight taro genotypes along with two check varieties to assess the extent of genetic diversity by D2 analysis in an Augmented Block Design during the period 2017 to 2018. Observations were recorded on 19 quantitative characters which included leaf, petiole, corm, cormel and corm biochemical characters. The analysis was conducted for D2 analysis and was concluded from D2 analysis that, the characters leaf area, corm weight/plant, cormel weight/plant and yield/plant contributed the maximum towards diversity. The 30 genotypes were grouped into six clusters based on Ward's minimum variance method where eight genotypes grouped in cluster I and III while, cluster II, IV, V and VI had three, two, five and four genotypes, respectively. The intra cluster distance was more in cluster VI and the inter cluster distance was maximum between cluster II and cluster VI.

Keywords: Genetic diveregence, taro, cluster mean, cluster distance, grouping

Introduction
Tropical tuber crop Taro [*Colocasia esculenta* (L.) Schott] known as Colocasia or eddoe or arvi, belongs to the family araceae and order arales (Vinning, 2003) [15]. Cultivated *Colocasia* are mostly diploid (2n=2x=28) although some triploids (2n=2x=32) are found. Taro originated from the tropical region between India and Indonesia (Matthews, 2004) and been in cultivation in the South Pacific for hundreds of years (FAO, 1992) [3]. *Colocasia esculenta* var. *antiquorum* (eddoe type) a small or medium sized corm with a large number of edible cormels which is widely cultivated in India (Rao *et al.* 2010) [13]. Taro is cultivated in an area of around 1.30 m ha with an annual production of 9.98 mt and average yield of 7.68 t/ha (FAOSTAT, 2016) [4]. In India, cultivated in Manipur, Assam, Nagaland, Orissa, Meghalaya, Gujarat, Maharashtra, Kerala, Andhra Pradesh, Tamil Nadu, West Bengal, Uttar Pradesh and Bihar. In Andhra Pradesh, taro is cultivated in an area of 510 ha with an annual production of 6630 tonnes (Anon., 2016) [1]. It is grown as pure crop or as an intercrop in different farming systems and can tolerate salinity (Grubben and Denton, 2004) [6].
For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence are more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents based on information on genetic diversity present in the available germplasm. Assessment of divergence in the germplasm is essential to know the spectrum of diversity, so that improvement in yield can be normally attained through involvement of the genetically diverse parents in breeding programmes. In view of this, the present investigation was under taken to elicit the above information with the objective to study the genetic divergence existing in the Colocasia germplasm.

Materials and Methods
The present investigation consisting of 28 taro accessions along with two checks namely, KCS-2 and Sree Reshmi was conducted at Horticultural Research Station, Kovvur, West Godavari district, Andhra Pradesh, India, during 2017-18. The experiment was laid out in Augmented Block Design consisting of four augmented blocks and in each block two checks (KCS-2 and Sree Reshmi) and seven entries were planted at spacing of 45 x 45 cm. Data was collected from five randomly selected plants tagged from each accession.

Harvesting was done as soon as leaves begin to turn yellow colour. Before harvesting, all the leaves were cut back to 10 cm above the ground level using sickles, soil around the corm was loosened without causing any damage to corms and cormels and then, the corm was harvested by grabbing the base of the petioles.

The data was analyzed statistically and Analysis of Variance (ANOVA) was carried out based on augmented complete block design accounting for both inter and intra – block differences. Means were adjusted for inter and intra – block variations and were compared based on the two means with checks and with germplasm entries. The statistical analysis was carried out as per the method suggested by Gomez and Gomez (1984) [5]. The data collected on different characters was also analyzed using Mahalanobis' (1928) D^2 analysis to classify the genotypes into different clusters based on their relative distances to determine the genetic divergence among the genotypes and Ward's minimum variance method suggested by Ward (1963) was used for cluster formation.

Results and Discussion

The data collected on quantitative characters viz., days to sprouting, plant height (cm), number of suckers/plant, leaf length (cm), leaf width (cm), leaf area (cm^2), number of leaves/plant, corm length (cm), corm width (cm), corm weight/plant (gm), number of cormels/plant, length of cormels (cm), width of cormels (cm), weight of cormels/plant (gm), corm dry matter content (%), starch content (%), calcium oxalate content (%), yield/plant (kg) and yield (t/ha) for 30 genotypes of taro were subjected to multivariate analysis by using Mahalanobis D^2 statistic for quantitative assessment of genetic divergence in contributing characters.

Relative contribution of different characters towards genetic divergence

The correlated unstandardized means of 16 characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis' D^2 value) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered at a time and these were used for final grouping of genotypes. The parameter leaf area ranked first for 220 times with a maximum contribution of 50.57 per cent followed by yield/plant (46.44%) and weight of cormels/plant (2.30%) suggesting that these tuber characteristics might be considered in genetic diversity evaluation programmes. Number of days taken to sprouting, plant height (cm), leaf length (cm), leaf width (cm), number of suckers/plant, number of leaves/plant, corm length (cm), corm width (cm), corm weight/plant (gm), number of cormels/plant, length and width of cormels (cm) and yield (t/ha) contributed very less (0.00) towards genetic divergence in the taro genotypes under the study. Similar studies by Narayan *et al.*, (2018) [11] revealed that maximum contribution for genetic divergence was found through tuber yield (38.10%) followed by tuber length (28.84%) and tuber girth (14.55%). Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion for improvement in taro. Several workers have reported morphological characterization to determine the genetic diversity in taro genotypes (Bhattacharjee *et al*., 2014; Mandal *et al*., 2013; Getachew *et al*., 2013; and Tewodros *et al*., 2013) [2, 8, 14].

Grouping of genotypes into various clusters

Thirty genotypes were grouped into six clusters based on D^2 values using the Ward's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters (Table 1 and Fig. 1). Out of six clusters, cluster I (CA-1,NO.44, CA-15, NO.49, CA-13, CA-135, CA-17 and NO.18) and cluster III (CA-3, CA-12, CA-56, N0.54, CA-16, Muktakesi, B.Col-2 and Sree Reshmi) were largest comprising of 8 genotypes each followed by cluster V with 5 genotypes (CA-461, N0.55, B.Col-1, Kasibugga and C-497) and cluster VI with 4 genotypes (No.52, C-149, C-266 and Bhavapuri). Cluster II contain 3 genotypes (CA-2, NO.48 and CA-11) and among all the six clusters, cluster IV was recorded as the smallest consisting of two genotypes (Panchmukhi and Sonajuli). 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. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Wider genetic diversity between the cluster II (CA-2, NO.48 and CA-11) and VI (No.52, C-149, C-266 and Bhavapuri) followed by cluster II (CA-2, NO.48 and CA-11) and IV (Panchmukhi and Sonajuli) and cluster III (CA-3, CA-12, CA-56, N0.54, CA-16, Muktakesi, B.Col-2 and Sree Reshmi) and VI (No.52, C-149, C-266 and Bhavapuri) was recorded. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity. This indicated that different clusters have different breeding values that enable breeders to improve different traits and parental selection should be made based on the relative merits of each cluster for each trait depending on the objective of the breeding program and while selecting genotypes from a particular cluster, the inter cluster distance; cluster mean performance should be taken into consideration. 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 cultivars belonging to distant clusters for getting highly heterotic crosses which are likely to yield wide range of segregants on which selection could be practiced (Tewodros *et al.* 2013) [14].

Average intra and inter cluster distances

The mean intra and inter cluster D^2 values among the six clusters are given in the Table 2 and Fig.2. The intra cluster distance ranged from 14.28 (cluster IV) to 36.87 (cluster VI). Maximum intra cluster distance was observed in cluster VI (36.87) followed by cluster III (22.60), cluster I (20.29), cluster II (18.23) and cluster V (15.50) indicating that some divergence still existed among the genotypes. Promising genotypes included in cluster VI showed maximum intra cluster distance are No.52, C-149, C-266 and Bhavapuri which are highly divergent among themselves. This could be made use in the yield improvement through recombination breeding. The inter cluster D^2 values varied from 30.07 to 86.81 and maximum genetic divergence existed between clusters II and VI (86.81) followed by cluster II and IV (72.85) and cluster III and VI (67.81) suggesting the

crosses involving genotypes from these clusters would give desirable recombination. While, the minimum inter cluster distance of 29.96 was recorded between cluster III and V followed by, cluster IV and V (30.07) and cluster I and III (30.34) indicating that genotypes of these clusters had maximum number of gene complexes and their relative closeness. The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. These results are in accordance with Mandal *et al* (2013) [8]. The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. Statistical distance represents the extent of genetic diversity among clusters. Cluster IV displayed minimum intra cluster distance, while the maximum intra cluster distance was recorded in cluster IV which may be due to limited gene exchange or selection practices among the genotypes for diverse characters. In this experiment, inter cluster distance was always higher than intra-cluster distance.

Maximum inter cluster distance was observed between cluster II and cluster VI followed by cluster II and cluster IV indicating wider genetic diversity among the genotypes included in these groups. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants. Highly divergent genotypes may produce a wide range of variability enabling further selection (Naskar and Sreekumar, 2011) [12]. So, the genotypes of these clusters may be considered for selection of parents in hybridization programme in taro.

Mean performance of characters in clusters

Cluster means indicate average performance of all varieties clubbed in a cluster. The clusters mean values for all the characters under study are presented in Table 3. From the data, it was observed that considerable differences existed among the characters studied.

The cluster I was recorded for maximum mean values for plant height (142.58 cm) and minimum mean values for days to sprouting (7.38), and length of cormels (4.25 cm). Cluster II was recorded for highest mean values for leaf length (50.12 cm), leaf width (43.77 cm), leaf area (2194.26 cm^2) and no of leaves /plant (6.09) while, minimum mean values for corm length (7.63 cm), corm width (22.59 cm), corm weight (230.54 gm), no of cormels (17.18), weight of cormels (238.94 gm), corm dry matter (19.46%), starch content (25.73%) and yield/plant and yield/ha (469.48kg and 23.18t/ha). Similarly, cluster IV was recorded for maximum mean values for days to sprouting (15), corm length (13.20 cm), cormel length (4.80 cm) and calcium oxalate content (0.27%) while, minimum mean values for plant height (111.05 cm) and no of suckers/plant (2.7). Further, cluster V was recorded maximum mean values for dry matter content (24.25%) while minimum mean values for leaf length (43.67 cm), leaf width (37.68 cm), leaf area (1646.43 cm^2), no of leaves /plant (5.17), width of cormels (8.93 cm) and calcium oxalate content(0.10%). Cluster VI was recorded for maximum mean values for no of suckers/plant (4.93), corm width (39.19 cm), corm weight (535.47 gm), no of cormels (35.77), width of cormels (10.68 cm), weight of cormels (573.34 gm), starch content (28.67%) and yeild/plant (1108.81kg) as well as yield/ha (54.75t/ha). These results indicated that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character (Vinutha *et al*., 2015). [16]

Table 1: Clustering pattern of taro genotypes by Wards's method

Cluster Number	Number of genotypes	Name of genotypes
I	8	CA-1,NO.44, CA-15, NO.49, CA-13, CA-135, CA-17, NO.18
II	3	CA-2, NO.48, CA-11
III	8	CA-3, CA-12, CA-56, N0.54, CE-16, Muktakesi, B.Col-2, SreeReshmi
IV	2	Panchmukhi, Sonajuli
V	5	CA-461, N0.55, B.Col-1, Kasibugga, C-497
VI	4	No.52, C-149, C-266, Bhavapuri

Table 2: Mean intra (bold) and inter cluster distance among six clusters formed by Ward's minimum variance method in taro genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	20.29	35.53	30.34	44.32	30.46	42.88
Cluster II		18.23	31.00	72.85	52.00	86.80
Cluster III			22.60	38.00	29.96	67.81
Cluster IV				14.28	30.07	48.87
Cluster V					15.50	55.91
Cluster VI						36.87

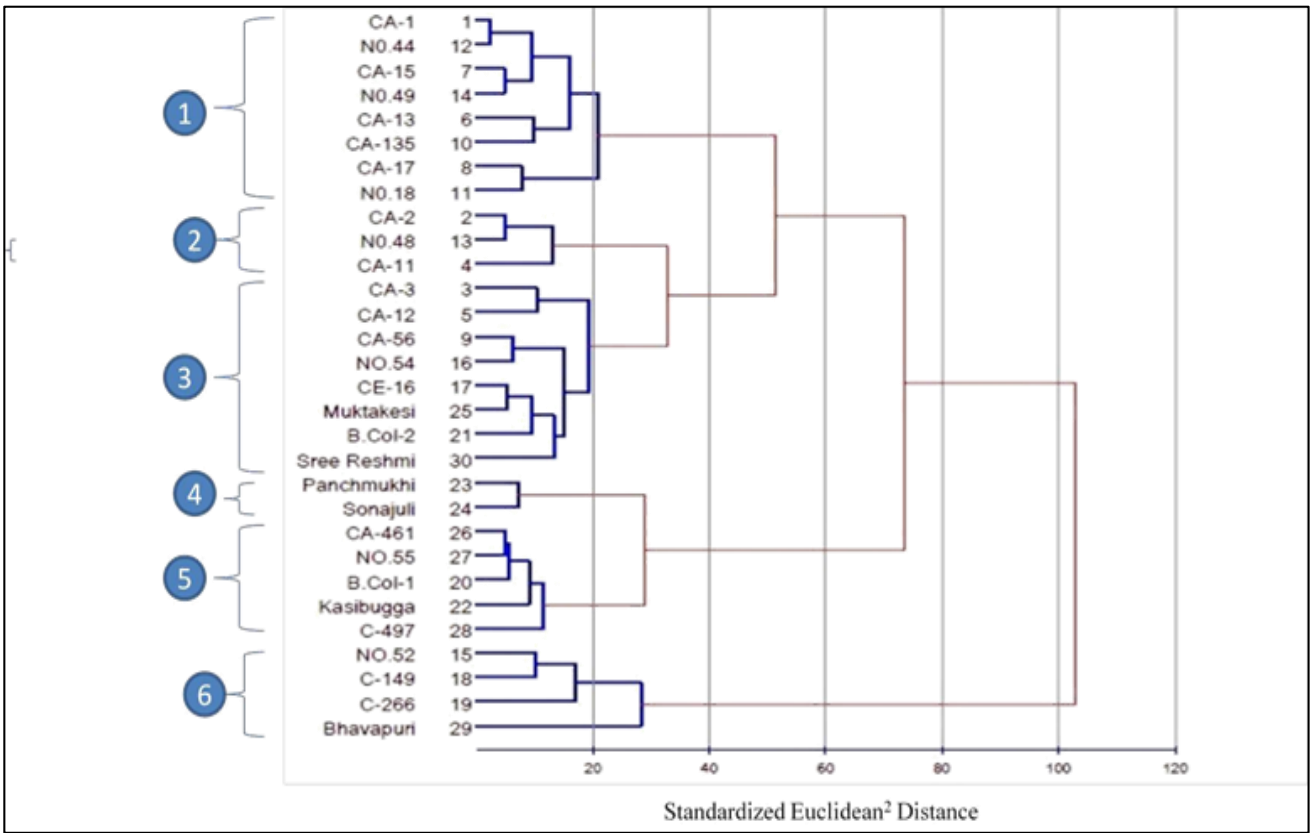

Fig 1: Dendrogram showing clustering pattern of 30 taro genotypes by Ward's minimum variance method

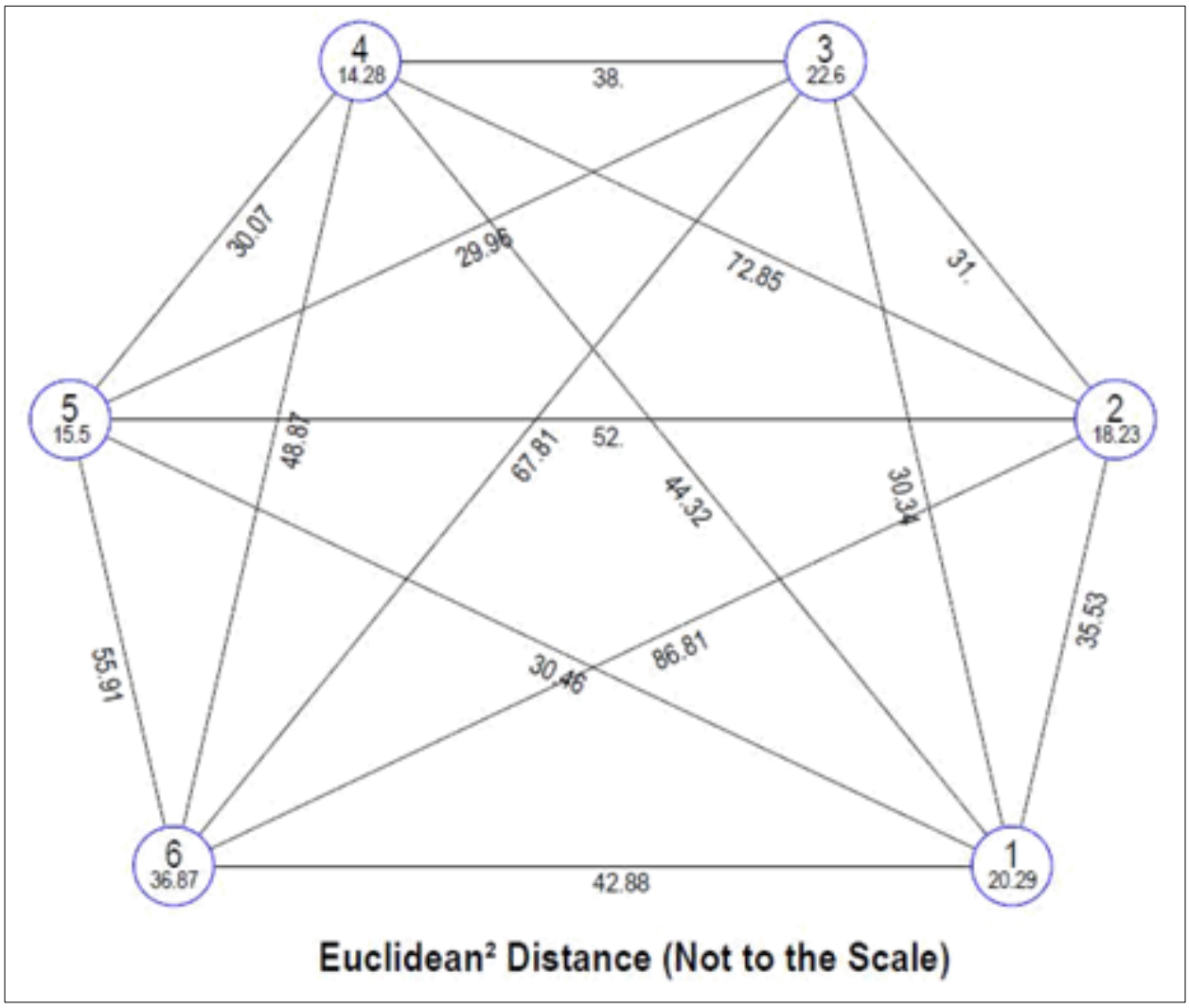

Fig 2: Inter and Intra cluster distances for quantitative characters of taro genotypes by Ward's minimum variance method

Table 3: Mean values of six clusters for nineteen characters in taro genotypes by using Ward's minimum variance method

S. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1.	Days to sprouting	7.34	7.67	10.75	15.00	7.60	7.75
2.	Plant height (cm)	142.58	138.01	130.25	111.05	125.50	127.01
3.	Number of suckers/plant	4.54	4.00	3.42	2.70	3.66	4.93
4.	Leaf length (cm)	47.21	50.12	45.49	43.76	43.67	47.83
5.	Leaf width (cm)	42.32	43.77	40.92	38.49	37.68	43.50
6.	Leaf area (cm^2)	2001.33	2194.26	1865.75	1684.39	1646.43	2084.24
7.	Number of leaves/plant	5.70	6.09	5.54	5.25	5.17	5.45
8.	Corm length (cm)	10.52	7.63	9.18	11.72	10.36	13.20
9.	Corm width (cm)	31.64	22.59	27.64	32.62	29.96	39.19
10.	Corm weight/plant	386.00	230.54	303.14	470.38	369.08	535.47
11.	Number of cormels/plant	25.75	17.18	19.26	27.85	27.50	35.77
12.	Length of cormels (cm)	4.25	4.50	4.39	4.80	4.42	4.78
13.	Width of cormels (cm)	9.23	9.05	9.52	9.61	8.93	10.68
14.	Weight of cormels/plant	419.00	238.94	256.45	452.88	371.08	573.34
15.	Corm dry matter content (%)	21.55	19.46	20.33	21.90	24.25	22.98
16.	Starch content (%)	28.63	25.73	28.50	27.23	25.98	28.67
17.	Calcium oxalate content (%)	0.15	0.17	0.17	0.27	0.11	0.18
18.	Yield/plant (Kg)	805.00	469.48	559.59	923.25	740.15	1108.81
19.	Yield (t/ha)	39.75	23.18	27.63	45.59	36.55	54.75

Conclusion

It was concluded from D^2 analysis that, the characters leaf area, corm weight/plant, cormel weight/plant and yield/plant contributed the maximum towards diversity. The 30 genotypes were grouped into six clusters based on Ward's minimum variance method where eight genotypes grouped in cluster I and III while, cluster II, IV, V and VI had three, two, five and four genotypes, respectively. The intra cluster distance was more in cluster VI and the inter cluster distance was maximum between cluster II and cluster VI.

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