Content list available at http://epubs.icar.org.in, www.kiran.nic.in; ISSN: 0970-6429

Indian Journal of Hill Farming

June 2019, Special Issue, Page 1-4

Multivariate Analysis in Taro [*Colocasia esculenta* (L.) Schott]

H. Supriya Devi[1] . Vikas Singh[2] . L Hemochandra[1]

[1]College of Post-Graduate Studies, Umiam, CAU, Imphal

[2]IIVR, RRS, Kussinagar, UP

ARTICLE INFO

Article history:
Received 27 October 2017
Revision Received 15 April 2018
Accepted 24 June 2018

Key words:
Colocasia esculenta, multivariate analysis, genetic divergence, Pseudostem girth

ABSTRACT

The genetic divergence of 40 accessions of taro (*Colocasia esculenta* (L.) Schott) collected from North East states were studied. Multivariate analysis of divergence among the accessions for 17characters led to their grouping into 07 clusters. No relationship was found between genetic divergence and geographic distribution of accessions and so geographic diversity is not adequate as index of genetic diversity. The values of intra cluster distance ranged from 0.00 (clusters II, VI and VII) to 64.90 (cluster V).The maximum inter cluster D^2 value was observed between cluster II and VII (218.30), while lowest inter cluster distance was observed between cluster II and V (46.94). Breeding programme involving accessions under these clusters may produce desirable segregants. Cluster means revealed appreciable variation for different characters and the cluster V had maximum mean for number of cormels per plant. The entries under these clusters viz., o CHFCOL-2, CHFCOL-28, CHFCOL-25 and CHFCOL-11 are found to be high yielders and may be subjected to advance evaluation to validate their superiority.

1. Introduction

Taro [*Colocasia esculenta* (L.) Schott] is an ancient crop belonging to the monocotyledonous family Araceae whose members are known as aroids (Henry, 2001 and Van Wyk, 2005). It is thought to have originated in North Eastern India and Asia (Kuruvilla and Singh, 1981; Hanson and Imamuddin, 1983 and Ivancic, 1992). Taro is a highly polymorphic, vegetatively propagated and predominantly allogamous species characterized by protogyny (Purseglove, 1972). There are eight recognized variants within *Colocasia esculenta*, of which two are commonly cultivated i) *Colocasia esculenta* (L.) Schott var. *esculenta* which possesses a large cylindrical central corm and only fewcormels; agronomically it is referred to as the dasheen type of taro and (ii) *Colocasia esculenta* (L.) Schott var. antiquorum which has a small globular central corm with several relatively large cormels arising from the corm; agronomically this variety is referred to as the eddoe type of taro (O'Sullivan *et al.*, 1996; Purseglove, 1972 and Lebot and Aradhya, 1991). Chromosome numbers reported for taro from various regions include 2n = 22, 26, 28, 38 and 42 (Onwueme, 1978). The most commonly reported chromosome numbers are: diploids 2n = 28 and triploids 3n = 42 (Kuruvilla and Singh, 1981; Wang, 1983; Lebot and Aradhya, 1991 and Lee, 1999). Considerable variation exists among accessions with respect to an array of plant morphological characters, both qualitative and quantitative. Despite the great intraspecific variation manifested in a multiplicity of character states, limited taxonomic work has been done in the crop aimed at differentiating accessions and clustering them in to viable groups. Breeding of crop plants adopting hybridization as a tool is one of the most important crop improvement methods.

*Corresponding author: supriyahuidrom@rediffmail.com

Studies on genetic diversity are important as the individual plant selection is solely dependent on variability. More the diversity, better are chances of improving the economic characters under consideration in the resulting offspring. Mahalanobis D^2 statistics (Mahalanobis, 1936) is one of the potent techniques of measuring genetic divergence. The generalized distance concept of Mahalanobis is based on multivariate analysis of quantitative traits. These techniques measure the force of differentiation at the intra cluster and inter cluster levels and thus provide a basis for selection of genetically divergent parents in breeding programme. Inter varietal hybridization between more divergent parents is expected to generate a broad spectrum of variability as well as heterotic hybrids. The present study was taken up to analyse the genetic divergence of 40 accessions of taro to select most divergent accession for meaningful breeding programme.

2. Material and Methods

The experiment consisting of 40 taro genotypes was laid out in Randomized Block Design with three replications at Vegetable Farm of College of Horticulture and Forestry, Pasighat under Central Agricultural University, Imphal, Manipur during *rainy* season, 2011. The recommended spacing (60 cm x 45 cm), plot size (2.40 m X 2.25 m) and package of practices were adapted uniformly to all the genotypes. Observations were recorded on five randomly tagged plants in each genotype on days to 50% emergence, pseudostem height (cm), pseudostem girth (cm), number of suckers per plant, number of leaves per plant, leaf length (cm), leaf breadth (cm) were recorded at maximum vegetative growth stage i.e. 120 days after planting and number of days from planting of tuber to emergence of 50 percent sprouts above soil surface was counted in each genotype and expressed as days to 50% plant emergence, number of days to maturity, number of corms per plant, weight of corm per plant of cormels per plant, weight of cormel per plant (g), average weight of cormel (g), dry matter content (%), starch content (%), total tuber yield per plant (g).The mean data for each character ecorded were subjected to multivariate analysis (D^2 statistics) according to Mahalanobis (1936 (g), average weight of corm (g), number). The accessions were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

3. Results and Discussion

Divergence analysis based on the data from seventeen quantitative morphological characters (Table 1) in the present study, grouped the 40 accessions into 07 diverse clusters (Table 1). Cluster I was the largest with 20 genotypes followed by cluster III with 8 genotypes, cluster IV with 5 Mahalanobis, genotypes and cluster V with 4 genotypes. Remaining clusters viz., II, VI and VII were unique included only one genotype in each 129 namely, CHFCOl-34, CHFCOL-36 and CHFCOL-4, respectively. The genotypes originating from the same region did not form a single cluster and local accessions collected from the same district were grouped in different clusters (Table 1). This indicates that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. This suggests that forces other than geographic origin, such as exchange of breeding material, genetic drift, variation, natural and artificial selection are responsible for diversity as reported earlier (Murty and Arunachalam, 1966; Singh et al., 1981; Anand and Rawat, 1984; Das and Gupta, 1984; Patel et al., 1989; Saleh Ahmed et al., 1994; and Mannan et al., 1994). Therefore, the selection of cultivars for hybridization should be based on genetic diversity rather than geographic diversity.

Table.1. Grouping of 40 taro genotypes based on D^2 analysis

Sl. No.	Clusters	Number of genotypes	Name of the genotypes
1.	I	20	CHFCOL-18, CHFCOL-41, CHFCOL-42, CHFCOL-21, CHFCOL-20, CHFCOL-15, CHFCOL-8, CHFCOL-10, CHFCOL-35, CHFCOL-13, CHFCOL-26, CHFCOL-12, CHFCOL-17, CHFCOL-32, CHFCOL-6, CHFCOL-22, CHFCOL-40, CHFCOL-5, CHFCOL-16 and CHFCOL-19
2.	II	1	CHFCOL-34
3.	III	8	CHFCOL-14, CHFCOL-37, CHFCOL-33, CHFCOL-7, CHFCOL-39, CHFCOL-30, CHFCOL-38 and CHFCOL-1
4.	IV	5	CHFCOL-9, CHFCOL-23, CHFCOL-24, CHFCCOL-3 and CHFCCOL-27
5.	V	4	CHFCOL-2, CHFCOL-28, CHFCOL-25 and CHFCOL-11
6.	VI	1	CHFCOL-36
7.	VII	1	CHFCOL-4

Genetic divergence

It was observed that the inter cluster distance is higher than intra cluster distance indicating wide genetic diversity among the genotypes of different groups than those of same cluster. The intra cluster values showed that the genotypes in cluster V had maximum genetic dissimilarity due to having maximum intra cluster distance (64.90) with 4 genotypes followed by cluster IV (41.95) with 5 genotypes and cluster I (37.88) with 20 genotypes. The lowest intra cluster distance was observed in cluster III (29.97) having 8 genotypes. The intra cluster diversity among genotypes could be due to genetic architecture of the populations, past history of selection in developmental traits and degrees of general combing ability (Mahapatra et al., 1993; and Dikshit and Swain, 2000). The highest inter cluster distance was observed between clusters II and VII (218.30) followed by VI and VII (215.65), V and VII (193.94), IV and VI (191.50), II and IV (180.26) and IV and V (148.95) indicating wider genetic variability and diversity among the genotypes within these groups. The least inter cluster distances were observed between II and V (46.94) and I and II (55.93) which showed that the genotypes from these clusters were genetically close.

Inter cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum inter cluster distance are genetically close. Inter cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum inter cluster distance are genetically more divergent and hybridization between divergent clusters is likely to produce desirable segregants for developing high yielding genetic stock/varieties. The average D^2 values of intra and inter cluster distances are presented in Table 2. The values of intra cluster distance were ranged from 0.00 (clusters II, VI and VII) to 64.90 (cluster V). The maximum intra cluster distance was observed in the cluster V (64.90) followed by cluster IV (41.95), cluster I (37.88) and cluster III (29.97) as the clusters II, VI and VII were monogenotypic with 0.00 intra cluster distances value. maximum inter cluster D^2 value was observed between cluster II and VII (218.30) followed by cluster VI and VII (215.65), cluster V and VII (193.94), cluster IV and VI (191.50), cluster II and IV (180.26), cluster IV and V (148.95), while lowest inter cluster distance was observed between cluster II and V (46.94) followed by cluster I and II (55.93).

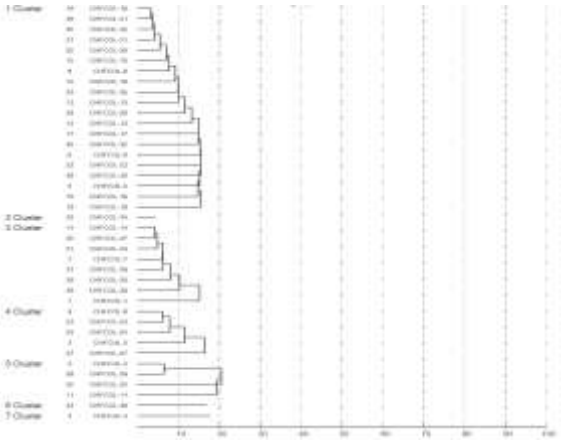

Figure 1. Dendrogram of 40 genotypes of taro

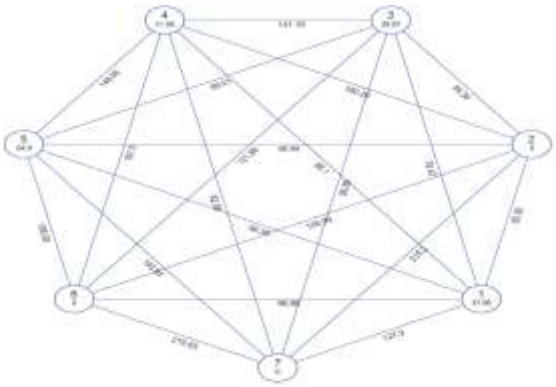

Figure 1. Dendrogram of 40 genotypes of taro

CLUSTER MEAN

Cluster means were computed in all 7 clusters for 17 characters and presented in table 4.9. Results revealed that different clusters exhibited marked differences in respect of all 17 characters. It was observed that cluster I, III and IV did not show the highest mean values for any character but had the lowest mean value for dry matter content (39.65) in cluster I, for days to 50% plant emergence (9.50) in cluster III, and for weight of cormels (67.13) and tuber yield (184.63) per plant in cluster IV. The cluster II exhibited the highest mean for days to 50% plant emergence (14.67), leaf breadth (29.82) and weight of cormels per plant (105.75) with the lowest mean value for pseudostem height (47.73), pseudostem girth (25.04), number of suckers per plant (2.80), number ves per plant (9.07), number of corms per plant (1.33) and starch content (2.78). The cluster V had maximum mean for number of cormels per plant while minimum mean under this cluster was observed for leaf length (18.32), leaf breadth (16.80), number of days to maturity (169), weight of corm per plant (96.04), average weight of corm (58.81) and average weight of cormel (10.02).

Table 2. Intra (Bold) and inter cluster distances of D^2 value of 7 clusters

Sl. No.	Clusters	I	II	III	IV	V	VI	VII
1	I	37.88	55.93	78.47	86.10	56.35	99.88	127.90
2	II		0.00	94.35	180.26	46.94	105.99	218.30
3	III			29.97	141.19	89.01	121.86	89.89
4	IV				41.95	148.95	191.50	82.08
5	V					64.90	106.56	193.94
6	VI						0.00	215.65
7	VII							0.00

The cluster VI exhibited the highest mean value for average weight of cormel (9.58) and the lowest mean for number of cormels per plant (2.40).The last, cluster VII exhibited the highest mean value for remaining 12 characters namely, pseudostem height (83.42), pseudostem girth (44.51), number of suckers per plant (5.92), number of leaves per plant (17.53), leaf length (31.95), number of days to maturity (183.67), number of corms per plant (2.27), weight of corm per plant (312.67), average weight of corm (139.96), dry matter content (45.30), starch content (12.40) and tuber yield per plant (412.22).

Contribution of Individual Characters towards Genetic Divergence

The relative contributions of individual character towards divergence are presented in Table 4.10. It was observed that starch content (38.59) was highest contributor towards divergence followed by weight of corm per plant (28.21), days to 50% plant emergence (7.05), dry matter content (5.51), average weight of cormel (5.26) and weight of cormel per plant (4.36). Number of days to maturity (0.38) was the lowest contributor towards divergence followed by number of leaves per plant (0.51), leaf breadth (0.51) and tuber yield per plant (0.51). Pseudostem girth did not contribute at all towards divergence. From the findings of present investigation, all the 40 genotypes were grouped in to 7 divergent clusters which showed high range of inter and intra cluster distance (D^2 value) and there was no relationship observed between geographic diversity and genetic diversity. Starch content, weight of corm per plant, days to 50% plant emergence, dry matter content, average weight of cormel and weight of cormel per plant may be considered as important parameter in selecting genetically diverse parents for hybridization programme as well as for study on genetic diversity in *Colocasia* as these traits together accounted for 88.98 % to the total divergence. On the basis of maximum inter cluster distances and *per se* performance, there is a scope of varietal improvement through hybridization programme involving the selected genotype(s) under cluster II (CHFCOL-34), cluster VI (CHFCOL-36) and cluster V (CHFCOL-2) with genotype under cluster VII (CHFCOL-4).

References

Ahmed M S Quadir MA, Bhuiyan M K R and Dayal TR (1994). Genetic diversity of sweet potato (*Ipomoea batatas* (L.) Lam.) in Bangladesh. *Journal of Root Crops*, 24(1): 11-15.

Dikshit UN and Swain D (2000). Genetic divergence and heterosis in sesame. *Indian Journal of Genetics* 60: 213-219.

Hanson J and Imamuddin H (1983). Germination of *Colocasia gigantean* Hook. Paper presented at the Proceedings of the 6th Symposium of *the International Society for Tropical Root Crops*, Peru.

Henry R J (2001). Plant genotyping: The DNA fingerprinting of plants. CAB Publishing, Southern Cross University, Australia.

Ivancic A (1992). Breeding and genetics of taro [*Colocasia esculenta* (L.) Schott]. Ministry of Agriculture and Lands, Solomon Islands UNDP, Food and Agriculture. Organizations of the United Nations:1-97.

Kuruvilla KM and Singh A (1981). Karyotypic and electrophoretic studies on taro and its origin. *Euphytica* 30: 405-413.

Lebot V and Aradhya KM (1991). Isozyme variation in taro [*Colocasia esculenta* (L.) Schott] from Asia and Oceania. Euphytica 56: 55-66.

Mahalanobis PC (1936). On the generalized distance in statistics. Proceedings of National Academic Science 2: 55-79.

Mahapatra KC Biswal AK and Satpathy D (1993). Relationship of F_2 segregation pattern with genetic divergence of parents in sesame. *Indian Journal Genetics* 53: 372-380.

Murty BR and Arunachalam V (1966). The nature of genetic divergence in relation to breeding system in crop plants. *Indian Journal of Genetics* 49: 188-198.

O'Sullivan J, Asher CJ and Blamey FPC (1996). Nutritional disorders of taro. Australian Centre for International Research.

Purseglove JW (1972). Tropical crops - Monocotyledons. Longman, London.