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Assessment of Breeding Potential of Taro (*Colocasia esculenta* L.) Genotypes Using D^2 Analysis under Hill Zone of Karnataka

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Authors' contributions

This work was carried out in collaboration among all authors. Authors Devaraju and Sangeeta designed the study and did research work, Author LGK performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors AKB and RCS managed the analysis of the study. Authors MA and HMS managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Using Mahalanobis D^2 statistics, the genetic diversity of 20 genotypes of taro for 21 characteristics was assessed as part of a breeding work to increase production potential. Five clusters were formed from the genotypes, indicating a significant level of genetic variation in the material being studied. With eight genotypes, Cluster I was the largest, followed by Cluster II with seven, and Cluster III with three. Each of the solitary clusters IV and V has a single genotype. The clusters that exhibit the greatest number of genotypes are indicative of limited genetic diversity. The intra-cluster distance was highest in cluster III and lowest in clusters IV and V. Clusters I and V have the highest inter-cluster distance, followed by II and V. These clusters could potentially be used as prospective genotypes for a hybridization programme. Tuber yield/plot (13%) showed the largest contribution to the overall divergence, followed by Corm yield/plant (12.20%) and Tuber yield/plant (11.43%). The finding that clusters V and III showed high cluster means for plant height, number of leaves per plant, leaf breadth, leaf area, leaf area index, tuber yield per plant, tuber yield per plot, and estimated tuber yield is noteworthy. These clusters can be effectively used in hybridization programmes to obtain desired transgressive segregants.

Keywords: Cluster mean; clustering pattern; genetic diversity; transgressive segregants; hybridization; genotypes; farming systems.

1. INTRODUCTION

Taro (*Colocasia esculenta* L.), a tropical tuber crop, it is a member of the order arales and family of araceae. It is sometimes referred to as *Colocasia*, eddoe, or arvi [1]. Although few triploids (2n=3x=42) are observed, most cultivated taro is diploid (2n=2x=28). According to [2], taro originated in the tropical region between India and Indonesia and has been cultivated for hundreds of years in the South Pacific [3]. *Colocasia esculenta* var. *antiquorum*, often known as the "eddoe type," is a small to medium-sized corm that is commonly grown in India and produces a significant number of edible cormels [4]. “With an average productivity of 25.6 mt/ha and an annual production of 1024 mt, taro is grown in an area of around 40 ha” [5]. “In India, it is grown in Gujarat, Maharashtra, Manipur, Assam, Nagaland, Orissa, Meghalaya, Kerala, Andhra Pradesh, Tamil Nadu, West Bengal, Uttar Pradesh, and Bihar” [6]. The districts in Karnataka that produce the most taro are Chikamagalur, Dakshina Kannada, Uttar Kannada, Belgaum, and Kodagu. It can withstand salinity and is cultivated in a wide range of farming systems either as a pure crop or as an intercrop [7]. The diversity of parents is vital for a successful breeding approach because crosses between parents with the highest genetic divergence are more likely to produce progenies with desired recombinants. “However, it is preferable to choose suitable genetically divergent parents based on genetic diversity information gathered from available germplasm. The assessment of breeding potential in germplasm is necessary to understand the spectrum of diversity, so that yield improvement may generally be achieved by the inclusion of genetically varied parents in breeding tasks” [7]. In light of this, the current investigation was undertaken to elicit the above-mentioned data with the objective of studying the genetic divergence present in the taro germplasm.

2. MATERIALS AND METHODS

The present study used 20 taro genotypes, including one control i.e., mudigere local, and was conducted during *Rabi* season 2020-21 in an open field condition at the Department of Vegetable Science, College of Horticulture, Mudigere, which is located in the Western Ghats and represents a typical hill zone (Zone 9 and Region V) of Karnataka and lies at 13°25' North latitude and 75°25' East longitude, with an altitude of 980 m above mean sea level. The experiment followed a Randomised Complete Block Design with three replications. Five plants were selected at random from each treatment in each replication, and observations were made on these plants for 21 quantitative characters those are plant height (cm), number of leaves/plant, leaf length (cm), leaf breadth (cm), leaf area (cm^2), leaf area index(LAI), days to sprouting, herbage yield/plant(g), corm length(cm), corm width(cm), cormels length(cm), cormels width(cm), corms weight (kg), cormels weight (kg), number of corms/plant, number of cormels/plant, corm yield/ plant (g), tuber yield/ plant (g), tuber yield/plot(kg), cormels yield/ plant (g) and estimated tuber yield(t/ha). D^2 statistical

analysis was used to assess the genetic divergence among the test entries [8,9]. Described a method for obtaining D^2 values as the corresponding uncorrelated (Ys) values of any two genotypes. Tocher's method, as described by [8], was used to cluster all of the n (n-1)/2 D^2 values. The intra- and inter-cluster distances were calculated using the equations provided by [10].

3. RESULTS AND DISCUSSION

3.1 Grouping of Genotypes into Various Clusters

Twenty genotypes were grouped into five clusters using Tocher's method, which involved estimating D^2 values using metrics such the square of the generalised distance. Table 1 shows the genotype distribution into different clusters. The genotypes' random clustering structure suggests that genetic divergence and geographic diversity are independent. With eight genotypes, Cluster I was the largest, followed by Cluster II with seven, and Cluster III with three. Clusters IV and V, which are isolated and contain a single genotype each, suggest that genotypes within a cluster probably don't differ much from one another when considering the total number of characters evaluated. As a result, it would be preferable to attempt crossings between cultivars from distant clusters in order to obtain highly heterotic crossovers that are likely to generate a diverse range of segregants for selection [11,12].

3.2 Average Intra and Inter Cluster Distances

Table 2 shows the mean intra and inter cluster D^2 values for the five clusters. Cluster III (40176.5) had the highest intra-cluster distance, followed by Cluster I (38160.7), Cluster II (34835.2), Cluster IV, and Cluster V (0), suggesting that there was still some divergence among the genotypes. The genotypes that exhibit highest intra-cluster distance and are included in cluster III are significantly varied among themselves, indicating their potential. “This could be utilised in recombination breeding to increase yield. The maximum genetic divergence was found between clusters I and V (875909.4), followed by cluster II and V (473539.9) and cluster I and III (408343.5). The inter-cluster D^2 values ranged from 102624.3-875909.4, and these results suggested that crosses involving genotypes from these clusters would result in desirable recombination. While clusters II and IV had the lowest inter-cluster distance of 102624.3 followed by cluster I and II (105029.9) and cluster II and III (150155.2) indicating that genotypes of these clusters had the highest number of gene complexes and were the closest in terms of genotypes” [13,14]. The magnitude of D^2 values confirmed that the experimental material assessed had a high degree of diversity. The statistical distance between clusters shows the level of genetic diversity. As a result, the genotypes of these clusters may be considered for parent selection in taro hybridization programmes.

3.3 Mean Performance of Characters in Clusters

Cluster means are the mean performance of all genotypes in a cluster. Table 3 displays the mean cluster values for all of the characters under study. Statistics revealed that there were significant variances amongst the characters analysed. The characters like plant height, number of leaves per plant, leaf breadth, leaf area, leaf area index, tuber yield per plant, tuber yield per plot and estimated tuber yield had the highest cluster mean in cluster V, followed by cluster III. These clusters could be good places to look for genes for yield component characteristics. These findings suggested that genotypes with high values for a certain characteristic may be selected and utilised in a hybridization programme to improve that trait [15,16].

Table 1. Grouping of twenty taro genotypes into different cluster by Tocher’s method

Clusters	Total number of genotypes in each cluster	Genotypes included in the cluster
I	8	Andhra Pradesh Local, Kushalnagar Local, Sakleshpur Local, Mandya Local, Mudigere Local, Gulbarga Local, DavaMudli, Nymati Local
II	7	Hyderabad Local, Mudli, Kumuta-2, Madikeri Local, KasuMudli, Koppa-2, Sirsi Local
III	3	Piriyapattana Local, Koppa-1, Shiralakoppa Local
IV	1	Kumuta-1
V	1	Balehonnur Local

Table 2. Average intra (bold) and inter cluster D^2 distance for twenty one different characters in twenty genotypes of taro

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**38160.71**	105029.9	408343.5	201058.6	875909.4
Cluster II		**34835.18**	150155.2	102624.3	473539.9
Cluster III			**40176.54**	156177.4	151062.7
Cluster IV				**0**	407128.3
Cluster V					**0**

Table 3. Cluster mean values of twenty one characters in twenty taro genotypes

Characters	Clusters				
	I	II	III	IV	V
Plant height (cm)	145.84	151.68	154.13	135.8	171.8
Number of leaves/plant	6.59	7.07	7.68	7.47	8.07
leaf length (cm)	32.74	39.7	38.97	37.08	46.85
leaf breadth (cm)	33.18	35.16	35.93	35.37	42.8
leaf area (cm^2)	351.1	465.84	549.13	278.03	729
Leaf area index (LAI)	0.84	1.22	1.57	0.77	2.18
Days to sprouting	27.39	31.14	27	24.63	31
Herbage yield/plant (g)	51	56.85	41.99	151	55.53
Corm length (cm)	12.34	13.64	12.04	12.47	10.57
Corm width (cm)	6.6	6.95	6.39	6.89	7.17
Cormels length (cm)	5.32	6.36	5.16	6	4.73
Cormels width (cm)	2.64	2.6	2.76	2.41	2.47
Corms weight (kg)	0.94	1.31	2.54	2.81	4.31
Cormels weight (kg)	1.41	2.28	2.63	1.43	1.28
Number of corms/plant	1.86	2.22	3	2.47	1.2
Number of cormels/plant	23.38	28	33.58	17.9	23.3
Corm yield/ plant (g)	185.13	279.29	519.67	592	891.33
Tuber yield/ plant (g)	474.42	724.57	1051.22	881	1149
Tuber yield/plot(kg)	4.72	7.48	10.32	8.76	10.51
Cormels yield/ plant (g)	289.38	445.38	530.56	289	257
Estimated tuber yield(t/ha)	17.53	27.56	37.33	32.19	38.4

Table 4. Per cent contribution of various characters towards total divergence in taro genotypes

Sl.No.	Characters	Per cent contribution	Number of times ranked first
1	Plant height (cm)	2.00	4
2	Number of leaves/plant	3.00	6
3	leaf length(cm)	5.00	10
4	leaf breadth(cm)	5.00	10
5	leaf area(cm^2)	5.50	11
6	Leaf area index (LAI)	4.50	9
7	Days to sprouting	0.50	1
8	Herbage yield/plant (g)	0.50	1
9	Corm length (cm)	2.20	4.4
10	Corm width (cm)	3.00	6
11	Cormels length (cm)	2.00	4
12	Cormels width (cm)	2.50	5
13	Corms weight(kg)	0.80	1.6
14	Cormels weight(kg)	2.65	5.3
15	Number of corms/plant	4.50	9
16	Number of cormels/plant	2.72	5.44
17	Corm yield/ plant (g)	12.20	24.4
18	Tuber yield/ plant (g)	11.43	22.86
19	Tuber yield/plot(kg)	13.00	26
20	Cormels yield/ plant (g)	10.00	20
21	Estimated tuber yield(t/ha)	7.00	14

3.4 Relative Contribution of Different Characters towards Genetic Divergence

The pivotal condensation method was used to convert the correlated unstandardized means of the 21 characters studied to a standardised uncorrelated set of variables. The statistical distance (Mahalanobis' D^2 value) between two genotypes was calculated as the sum of squares of differences between any two genotypes' corresponding uncorrelated values. These values were considered one at a time and were utilised for final genotypes clustering. These clusters were constructed based on the contribution of several characteristics to divergence (Table 4). Tuber yield/plot was placed first 26 times with a maximum contribution of 13%, followed by Corm yield/plant (12.20%) and Tuber yield/plant (11.43%), implying that these tuber traits should be addressed in genetic diversity evaluation programmes. Days to sprouting and Herbage yield/plant (g) contributed relatively little (0.50) to genetic divergence in the studied taro genotypes. Similar research by [17] discovered that “tuber yield (38.10%) contributed the most to genetic divergence, followed by tuber length (28.84%) and tuber girth (14.55%)”. “Apart from the high divergence, the performance of the genotypes and traits with the highest contribution to divergence should be given significant consideration, as it appears suitable for inclusion in taro improvement. Several researchers have published morphological characterisation of taro genotypes to estimate genetic diversity” [18,19,20].

4. CONCLUSION

The findings of the Mahalanobis D^2 analysis revealed that future breeding programmes can be successfully planned utilizing the taro genotypes used in this study. Because of their high values for inter-cluster distance and cluster means, genotypes from clusters I and V can be hybridized as feasible parents to produce superior offspring in segregating generations and boost taro output.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Vinning G. Select markets for taro, sweet potato and yam. RIRDC Project No.UCQ-13A; 2003.
2. Matthews P. Genetic diversity in taro, and the preservation of culinary knowledge. Ethnobot. Res. Appl. 2004;2:55-77.
3. FAO. Taro: A south Pacific specialty. Leaflet – Revised 1992. Community Health Services, South Pacific Commission, B.P. D5, Noumea, Cedex, New Caledonia; 1992.
4. Rao RV, Matthews P, EyzaguirreP B, Hunter D (eds). The global diversity of *C. esculenta*: ethno botany and conservation. Biodiversity International, Rome; 2010.
5. Horticulture Statistics. Department of Agriculture & Farmers Welfare, Ministry of Agriculture & Farmers Welfare, Government of India; 2022.
6. Bhanuprakash GC, Ramesh Babu B, Mamatha K, Snehalatha Rani A, Umayjothi K. Genetic divergence studies in colocasia *[Colocasia esculenta (L.) Schott]* germplasm. Int. J. of Chemical Studies. 2019;7(1):998-1002.
7. Grubben GJH, Denton OA. Vegetables. Plant Resources of Tropical Africa, Prota; 2004.
8. Mahalanobis PC. On the generalized distance in statistics. Proc. National Institute of Science, India. 1936;2:49-55.
9. Rao CR. Advanced Statistical Methods in Biometrics Research. John Wiley and Sons, New York. 1952;357-369.
10. Singh RK, Choudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi; 1977.
11. Tewodros M, Getachew WM, Tadesse B, Tesfaye W. Genetic diversity of cassava (*Manihot esculenta* crantz) genotypes in Ethiopia. Greener J. Agric. Sci. 2013;9: 636-42.
12. Fufa TW, Oselebe HO, Amadi CO, Menamo TM, Abtew WG. Genetic diversity and association of yield-related traits in taro (*Colocasia esculenta* (L.) Schott) sourced from different agro ecological origins of Nigeria. Int. J. Agron; 2023.

Available:https://doi.org/10.1155/2023/8832165.
13. Mandal R, Mukherjee A, Mandal N, Tarafdar J, Mukharjee A. Assessment of genetic diversity in taro using morphometrics. Curr. Agric. Res. J. 2013; 1:79-85.
14. Thirugnanavel A, Deka BC, Borah TR, Rajesha G, Rangnamei L, Walling N. Ex situ evaluation on genetic diversity of indigenous taro landraces in North East India. Curr. Sci. 2023;124(6):748-753.
15. Vinutha KB, Asha devi A, Sreekumar J. Morphological characterization of above ground characters of taro [*Colocasia esculenta* (L.) Schott.] accessions from North East India. J. Root Crops. 2015; 41:3-11.
16. Koffi JMN, Koffi KK, Bonny SB, Bi AIZ. Genetic diversity of taro landraces from côte d'ivoire based on qualitative traits of leaves. Agric. Sci. 2021;12:1433-1446.
17. 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. Appl. Sci. 2018;1022-1030.
18. Bhattacharjee M, Tarafdar J, Sadhukhan R. Assessment of genetic diversity of some indigenous collections of upland taro [*Colocasia esculenta* var. *antiquorum* (L.) Schott] for selection of genotypes aiming at improvement in breeding programme. J. Agric. Vet. Sci. 2014;7:31-43.
19. Oktavianingsih l, Suharyanto E, Daryono BS, Purnomo. Genetic diversity of taro (Colocasia spp.) from Kalimantan Island, Borneo, Indonesia, based on RAPD markers. SABRAO J. Breed. Genet. 2021; 53(3):447-458.
20. Khushboo K, Kushwaha ML, Monisha R. Genetic diversity among taro (*Colocasia esculenta* (L.) Schott var. antiquorum) germplasm- A review. Agricultural Reviews. 2018;39(3):255-258. DOI:10.18805/ag.R-1762.

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