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MULTIVARIATE ANALYSIS IN TARO (*COLOCASIA ESCULENTA* L.)

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ABSTRACT

Thirty one genotypes of taro (*Colocasia esculenta* L.) were studied for genetic divergence for eight characters. The genotypes were grouped into eleven clusters. The genotypes IC-87168(M), IC-87042(M) and IC-89548(A) were quite different and formed separate cluster IX, X and XI, respectively. The genotypes in clusters XI, X and XIII exhibited highest yield per plant and higher values for plant height, weight of mother cormels and number of suckers per plant. These genotypes can be utilized in breeding programmes.

Key Words: Genetic diversity, taro, multivariate analysis.

Taro has a large varietal diversity in North eastern India for various yield contributing traits. Genetic diversity is one of the most important criteria which helps a breeder to choose parents for hybridization either to exploit heterosis or select desirable segregants. The importance of cluster analysis to determine the extent of variability was reported by earlier workers [1–4]. The present investigation attempts to access and analyse the nature and extent of genetic diversity in a set of thirty one genotypes of taro in respect of eight economic characters influencing yield using Mahalanobis D^2 statistics.

MATERIAL AND METHODS

The material used in this study comprised of 31 diverse genotypes of taro viz; IC-87156(1), IC-87149(2), IC-87159(3), IC-87140(4), IC-87161(5), IC-89544(6), IC-87168(7), IC-87038(8), IC-87152(9), IC-89545(10), IC-87145(11), IC-87139(12), IC-87170(13), IC-89546(14), IC-87171(15), IC-87132(16), IC-89547(17), IC- 87042(18), IC-89548(19), IC-89549(20), IC-87137(21), IC- 87141(22), IC-87133(23), IC-87167(24), IC-89550(25), IC-87131(26), IC-87046(27), IC-87153(28), IC-87040(29), IC-89551(30) and IC-87162(31) collected

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from Assam, Meghalaya and Nagaland were grown during kharif of 1991 in RBD with 2 replications. The spacing was maintained as 75 x 60 cm. Recommended package of practices were followed to raise the crop. Five randomly selected competitive plants were scored for eight characters (Table 1). Treating D^2 values as generalized distance [2], the genotypes were grouped into different clusters following the method of Rao [3].

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters. The genotypes IC-89548(A) exhibited highest mean values for yield/plant (933.8g) and weight of mother cormels (640.5g). The genotypes IC-87132(A) and IC-87163(M) in cluster VIII also exhibited highest mean values for yield/plant (875.2g) and weight of cormels (449.8g) alongwith higher values for plant height, leaf length and leaf width. Highest mean values for suckers/plant was observed in cluster X (7.4), followed by in cluster II (6.3) and cluster VII (5.3). These genotypes of these clusters may be utilized for the genetic amelioration of taro as these characters are known to influence yield [3, 4]. Clusters I, II and III comprising 18 genotypes exhibited relative closeness to each other compared to the remaining clusters (Table 1). In general, the clusters VIII, IX, X and XI were

Table 1. Cluster means for eight characters in 31 genotypes of taro

Cluster	No. of genotypes	Genotypes and their origin*	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	No. of suckers per plant	Wt. of mother cormels (g)	No. of cormels per plant	Wt. of cormels (g)	Yield per plant
I	5	IC-89544(M), IC-87038(A), IC-87145(M), IC-87133(N), IC-87131(N)	46.3	27.0	18.2	4.3	133.3	11.9	241.4	381.2
II	8	IC-87149(A), IC-87159(A), IC-87149(A), IC-87170(N), IC-89546(A), IC-87137(N), IC-89550(A), IC-87046(M)	52.1	28.3	18.6	6.3	203.8	14.1	400.3	614.0
III	2	IC-89545(M), IC-89549(N)	61.9	40.7	27.5	4.1	237.4	11.0	317.7	560.4
IV	3	IC-87140(N), IC-87161(M), IC-87152(A)	62.4	41.6	30.0	3.6	350.3	13.0	406.4	771.7
V	3	IC-87156(N), IC-89547(N), IC-87141(N)	59.5	40.4	27.9	2.5	131.8	9.8	243.2	418.5
VI	2	IC-87167(N), IC-87040(A)	52.1	42.0	29.5	4.0	309.6	9.6	211.8	517.3
VII	3	IC-87171(A), IC-87153(M), IC-89551(M)	58.3	26.4	18.9	5.3	293.7	9.6	197.6	484.6
VIII	2	IC-87132(A), IC-87163(M)	87.7	51.3	35.0	4.0	425.4	12.4	449.8	875.2
IX	1	IC-87168(M)	50.9	32.3	24.3	4.8	299.9	11.0	368.6	425.0
X	1	IC-87042(M)	67.6	29.3	19.5	7.4	471.0	9.6	336.0	847.0
XI	1	IC-89548(A)	87.1	41.7	30.3	5.1	640.5	11.8	293.3	933.8

*Origin of genotypes: (A) Arunachal Pradesh, (M) Meghalaya, and (N) Nagaland.

quite divergent from each other as also from the remaining clusters. Hence, the genotypes selected from these clusters in a hybridization programme might yield desired heterosis and release variability in subsequent generations.

The inter- and intracluster genetic divergence (D^2) values among the 11 clusters have been presented in Table 2. Cluster I and III comprising 7 genotypes and clusters II, IV and V comprising 14 genotypes exhibited minimum inter cluster distances indicating more closeness to each other as compared to the remaining clusters. Cluster VI, VII, VIII comprising 7 genotypes and cluster IX, X, XI having one genotype each were quite divergent from each other as also from the each other as also from the remaining clusters. Hence, the genotypes selected from these clusters in hybridization programme might yield desired heterosis and release variability in subsequent generations. However, crossing very diverse genotypes may not yield proportionate heterotic response because a cross between extremely divergent parents might create a situation where in harmonious functioning of alleles is somewhat disturbed and consequently the physiological functions are not so efficient as in a situation where the alleles were exposed to similar selection pressure [6–8]. This suggests that the selection of parents preferably should also be based upon their per se performance, stability and combining ability.

The 31 genotypes collected from different states of NE Region of India, did not show any specific trend in the clustering pattern. The genotypes, in general, belonging to same geographical area fell in different clusters and showed separate genetic identity. This

Table 2. Intra- (in bold) and intercluster divergence (D^2) among 11 clusters in taro

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**9.1**	33.2	57.8	41.8	26.3	58.3	68.7	97.1	38.9	105.9	239.9
II		**11.9**	27.4	24.7	40.9	31.7	47.9	50.5	30.3	73.9	166.0
III			**10.9**	57.0	61.6	50.7	66.7	36.5	45.1	62.7	127.7
IV				**12.0**	69.9	58.7	71.4	77.2	43.1	140.1	199.9
V					**12.6**	77.8	76.5	119.0	49.2	87.2	250.3
VI						**18.7**	64.9	64.2	53.5	73.7	135.1
VII							**27.1**	79.2	47.9	56.5	125.8
VIII								**27.4**	84.0	73.2	80.5
IX									**0.0**	52.4	89.0
X										**0.0**	73.3
XI											**0.0**

indicated no relationship between geographic and genetic diversity. This may be attributed to differential selection pressure applied by farming community for developing varieties suiting to local needs and the genetic drift as vigorous plants are invariably saved by the farmers as seed for the next planting. From the overall picture, it can be concluded that significant improvement in taro can be brought about by selecting parents, having high mean values for the characters, from the divergent clusters and crossing them in a complete or partial diallel fashion to get desired heterotic response and release of variability and exercising selection following suitable breeding methodology.

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REFERENCES

1. P. K. Thankamma Pillai and M. Unnikrishnan. 1991. Heritability studies in taro. CTCRI Annual Report, Kesorgod, Kerala.

2. P. C. Mahalanobis. 1936. On the generalized distance in statistics. Proc. Natl. Inst. Sci. (India): 49–55.

3. C. R. Mohankumar, P. Saraswahty and N. Sadanandan. 1990. Correlation and path coefficient analysis on yield and yield component in taro. J. Root Corp., **16**(2): 140–141.

4. C. R. Rao. 1952. Advanced Statistical Methods in Biometric Research (I edn.). John Wiley & Sons, New York, USA: 357–361.

5. B. Chand, R. C. Jaiswal and N. C. Gautam. 1987. Genetic variability and correlation studies in colocasia (*Colocasia esculenta* L.). Haryana J. Hort. Sci., **16**(1/2): 134–139.

6. V. Arunachalam, A. Bandopadhyaya, S. N. Singh and R. W. Gibbsons. 1983. Heterosis in relation to genetic divergence and sca in groundnut (*Arachis hypogea* L.). Euphytica, **33**: 33–39.

7. V. K. Dobhal, N. S. Murthy, and C. R. N. Rao. 1989. Genetic divergence in hookah and chewing tobacco (*N. rustica* L.). Tobacco Res., **15**(2): 104–107.

8. S. K. Prasad and T. P. Singh. 1986. Heterosis in relation to genetic divergence in maize (*Zea mays* L.). Euphytica, **35**: 919–924.