Phenotypic Variability among the Germplasm lines of Elephant foot yam (*Amorphophallus paeoniifolius*) and Taro (*Colocasia esculenta*)

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ABSTRACT: *Elephant foot yam and taro are important aroids for nutritional management as well as for their medicinal value. The germplasm lines of elephant foot yam and taro maintained at Regional Centre of ICAR-CTCRI, Bhubaneswar was evaluated for their pre-harvest and post-harvest characters using randomized block design. The resources include landraces, primitive cultivars and breeding lines and released varieties. Wide ranges of variations were observed for most of the traits. The majority of the accessions centered on the mean with some accessions as outliers. The frequency of distribution for pre harvest was observed to be symmetrical and unimodal for most of the pre-harvest traits thus indicating a continuous variation among the germplasm lines of both the crops. Similar trend was observed in post harvest characters. Marked difference was observed among the taro genotypes for traits pertaining to disease incidences. Breeding lines, released varieties and some landraces form outliers for yield traits as expected. Correlation matrix and cluster analysis indicated that the evaluated germplasm of both the crops have narrow genetic base.*

Keywords: Phenotypic variability, germplasm, Elephant foot yam, Taro.

INTRODUCTION

Elephant foot yam (*Amorphophallus paeoniifolius* (Dennst.) Nicolson) and taro (*Colocasia esculenta* (L.) Schott.) are cultivated throughout Asia, including India, Srilanka and to some extent in Africa (Beevi *et.al.*, 2010, Stephen *et.al.*, 1986). Yield is largely influenced by a number of component traits that again are governed by definite sub-components. Improvement of yield is a primary objective in crop improvement programmes, thus studies pertaining strength and association of component characters to yield becomes imperative to realize the genetic advancement potential of these crops (Breese & Haywards, 1972). Scope of improvement through conventional breeding is mainly constrained in vegetatively propagated crops like taro and elephant foot yam (Abraham *et.al.*, 2008). Thus, selection of superior lines from the germplasm based on yield attributing parameters will lead to faster screening and yield improvement of these crops. Variability is essential for such a selection and total variability in a population is represented by genotypic, phenotypic and environmental variation. Selection is made by taking character variability and their strength and direction of association into account. The present study attempts to study the morphological characters in germplasm lines of taro and elephant foot yam and the association of yield attributing parameters in determining the variability among the germplasm lines.

METHODOLOGY

38 genotypes of elephant foot yam and 145 genotypes of taro maintained at Regional Centre ICAR-CTCRI farm, Bhubaneswar was evaluated for pre-harvest and post-harvest characters based on standard descriptors. The genotypes include farmer's variety, wild types, landraces and breeding lines. The genotypes were planted in 2 replications with randomized block design. Five plants per accession of elephant foot yam and 10 plants per accession of taro were planted in each replication. Standard package of agrological practices were followed and intercultural operations were done at suitable intervals. The characters were recorded using

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standard descriptors. The mean data was used to estimate phenotypic and genotypic co-efficient of variation. UPGMA method was used for cluster analysis. All the statistical analysis was done using NTSYS 2.02i software (Rolfs, 1999).

RESULTS AND DISCUSSIONS

The pre-harvest morphological characters were found symmetrically distributed and were unimodal. Maximum polymorphism was found in plant height, stem girth and canopy spread in case of elephant foot yam accessions, while plant height and plant span was found to show high polymorphism among taro genotypes. The frequency distribution and significant mean squares showed considerable variability in both taro and elephant foot yam genotypes. The yield attributing characters showed more polymorphism. Similarly, disease susceptibility was found to have more variation among the taro genotypes than the elephant foot yam genotypes.

Among elephant foot yam genotypes, five accessions *viz.,* Pathikanta, Verravada, 64/89, kathagudi and AM-42 were found to be promising with more yield and minimum disease susceptibility (0-5%). Whereas, in case of taro accessions, 42 showed

tolerance to leaf blight (0-5% disease incidence), 77 were moderately susceptible (5-15%) and 26 genotypes were found to be susceptible (15-25%).

The pre-harvest and post-harvest characters with more polymorphism in taro and elephant foot yam germplasm were taken up for variability studies. The extent of variability was estimated in terms of range, mean, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV) and heritability.

Among the elephant foot yam as well as taro genotypes, PCV was found to be higher than the GCV for all the traits, indicating influence of environment on the characters.

ELEPHANT FOOT YAM

Size of cormel, canopy spread, weight of individual corm showed high GCV and PCV indicating that these traits showed greater polymorphism among the evaluated genotypes, which can be due to genotypic differences. These traits subsequently showed higher heritability (Table 1). The results are in coherence with that found by Kumar *et.al.,* 2010. Though Abraham *et.al.,* 2008 found maximum heritability in characters like stem girth, corm diameter along with weight of the corm.

Table 1
Heritability of quantitative characters of elephant foot yam germplasm lines

Morphological traits	Range	General mean	CV%	GCV%	PCV%	Heritability
Plant height (cm)	76.88-123.5	98.63 ± 2.12	6.23	16.54	17.74	0.78
Stem girth (cm)	13.14-22.60	6.36 ± 1.35	10.67	15.81	16.25	0.67
Canopy spread (cm^2)	86.72-146.75	112.54 ± 4.02	7.82	20.20	21.33	0.79
No. of cormels	0.00-15.00	6.47 ± 1.34	12.34	48.52	57.42	0.87
Size of cormels (cm^2)	0.00-58.30	42.18 ± 1.87	14.67	27.64	32.69	0.69
Wight of individual corms (kg)	0.43-2.75	1.86 ± 0.74	12.58	46.17	52.17	0.71
Size of individual corm (cm^2)	786.14-2438.20	1054.24 ± 0.86	9.63	25.55	29.55	0.84
Yield (t/ha)	12.86-25.33	20.73±1.76	8.72	34.68	40.28	0.89

Based on the characters showing high heritability, dendrogram from cluster analysis was generated. All the varieties showed narrow genetic base (Fig.1). The accessions were grouped in two major groups with maximum number of accessions in one group. No association of genotypes based on their geographical collection site was found. Thus, indicating considerable variation among them.

Taro

All the characters selected for variability studies showed higher PCV than GCV, thus indicating the environmental influence over the expression of the

characters (Table.2). Also, high PCV and GCV values indicate the presence of considerable variability among the evaluated genotypes. Maximum heritability was found in yield (0.87), number of cormels (0.85), corm length (0.84) and in plant height (0.75). Choudhary *et.al.,* 2011 found maximum heritability in cormel yield, number of cormels and number of side suckers. Mehta *et.al.,* 2003 found high correlation among the characters showing high heritability in the present study.

Further, PCA derived scatter plot showed narrow genetic base among the taro germplasm collection (Fig. 2). Three major groups are obtained and

Table 2
Heritability of quantitative characters of taro germplasm lines

| Morphological traits	Range	General mean	CV%	GCV%	PCV%	Heritability
Plant height (cm)	12.6-54.50	32.54 ± 2.73	12.48	27.15	32.63	0.75
Plant span (cm)	18.85-42.75	36.20 ± 1.72	14.57	17.11	22.81	0.74
No. of stolons	0.00-6.50	2.15 ± 0.74	11.73	11.28	17.29	0.62
Corm length (cm)	8.54-18.25	12.63 ± 1.63	13.32	22.36	26.44	0.84
Corm branching	0.00-12.33	6.77 ± 0.38	9.68	13.56	18.37	0.72
No. of cormels	0.00-11.50	7.84 ± 0.84	11.54	39.55	44.24	0.85
Yield (t/ha)	4.35-14.76	9.78 ± 1.32	13.64	41.43	45.86	0.87
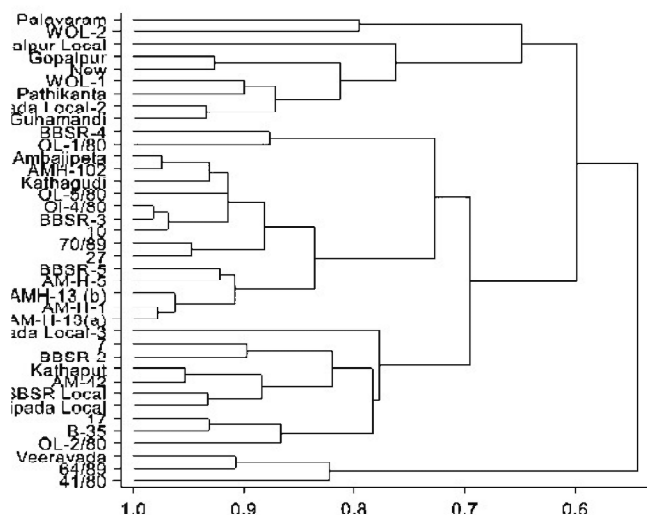
Figure 1: Dendrogram of elephant foot yam genotypes
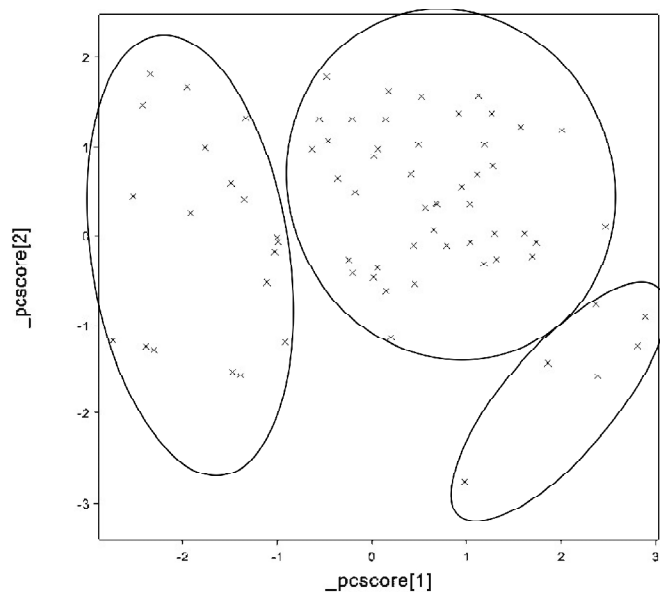

Figure 2: PCA derived scatter plot of 145 taro genotypes

maximum number of genotypes found to be in major group-II. As found in elephant foot yam germplasm collection, there was no association based on the geographical collection of the accessions.

Intra-specific variability in group-I and group-III was found to be more as compared to group-II. This indicates that there is ample scope for selection of genotypes.

The present study revealed that considerable variability is present among elephant foot yam and taro germplasm collections that could be harnessed for varietal improvement for quality attributes. The characters showing high heritability can be selected for screening of superior lines.

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