

# Variability in quantitative traits of elephant foot yam by principal component an...

[Environment](#), [Animals](#)



The genus *Amorphophallus paeoniifolius* (Dennst.), Nicolson syn. *A. campanulatus* (Roxb.) BL. exDence commonly called elephant foot yam, is a tuberous perennial C3 herb belonging to the family Araceae (Ravi et al., 2011). It is a pale-tropical stem-tuber of Africa, Madagascar, India, continental South East Asia, Malesia and North East Australia (Mayo et al., 1997) and cultivated mostly for its underground food reserves (Sahu and Kumar, 2014). It is used as a local staple food in Philippines, Java, Indonesia, Sumatra, Malaysia, Bangladesh, India, China and southeastern Asian countries (Sugiyama and Santosa, 2008). In India, it is cultivated as a summer vegetable especially in South India, North East Region, Bihar, Jharkhand and Eastern Uttar Pradesh.

EFY is known as ‘King of tuber crops’ due to its higher productivity (50–80 t/ha) (Poddar and Mukherjee, 2015) in a short growing season which offers its excellent scope for adaptation as a cash crop (Nedunchezhiyan, 2014; Gao et al., 2017). This crop also offers export opportunities from India as it is not commercially cultivated in other countries (Misra and Shivalingaswamy, 1999; Misra, 2000; Misra et al., 2001). In India, the net economic profit is over 1 lakh rupees/ha from its cultivation (Singh and Wadhwa, 2014).

It is eaten in various manners- as curry, as pickle, as baked, as preserve after cooking in syrup. EFY leaves contain only small amounts of cyanide (Bradbury et al., 1995). Boiling for 10 min is sufficient for reduction of oxalates (71 mg/ 100g) to a reported safer level (Kumoro et al., 2014). Boiling reduces the quantity of both soluble oxalates (35. 39%) and total oxalates (44. 76%) present in the tubers (Kumar et al., 2017). Tubers are

very rich source of starch, carbohydrate, protein, minerals, vitamins (A, B, C), flavanoids, and free from heavy metals (Kay 1987; Shilpi et al. 2005). The leaves are used as a vegetable by local tribes in India because they contain a high concentration of vitamin A (Rajalakshmi et al., 2001). Important medicinal attributes of EFY includes hepatoprotective, antioxidant, uterus stimulating agent (Laderman, 1983; Singh et al. 2011). In ayurveda the tuber is called “ Mahabhaishajyam”, means the superior medicine (Dey et al., 2012). Being a rich source of dietary fiber, omega fatty acids and having low glycemic index, it is used for diabetes treatment and reducing cholesterol level in the body and risks of obesity. It also has laxative properties which helps in curing constipation as well as used in the treatment of piles. One important molecule called Diosgenin which has an anticancerous property is present in the tuber (Vora et al., 2015).

EFY has not gain popularity among the consumer due to palatability problems associated with antinutritional factors like oxalate, trypsin inhibitors, and acidity. The acidity is due to a combination of needle like crystals of oxalate called raphides (Bradbury and Holloway, 1988; Lewu et al., 2010) and a chemical irritant, as yet undetermined, a diglucoside of 3, 4-dihydroxy benzaldehyde (Suzuki, 1980; Saha and Hussain, 1983). Intake of large quantity of oxalate-containing foods leads to chronic effects such as deposition of calcium oxalate crystals in the kidneys (Connor, 1977), occurrence of renal stones (Passmore and Eastwood, 1986).

Based on leaf morphological variations and petiole structure, *A. paeoniifolius* has two morphotypes- rough petiole types (*A. paeoniifolius* var. *sylvestris*)

and smooth – petiole types (*A. paeoniifolius* var. *hortensis*), respectively (Santosa et al., 2002; Sugiyama and Santosa, 2008). Farmers identified these two types based on the petiole roughness as the rough type is associated with acid corms; the smooth type also exhibits acidity but at the immature stage (Santosa et al., 2002; 2003). The plant is assumed to be panmictic (Jansen et al., 1996). Therefore, breeding to enhance palatability to eliminate tuber acidity and reduce oxalic content becomes the main goal of local plant breeders. Principal Component Analysis (PCA) is a multivariate method that analyses a dataset by several inter-correlated quantitative dependent variables. Principal components are linear combinations of non-correlated variables that account for maximum variance within the original dataset to visualize the grouping of accessions based on component loadings (Duntelman 1989). The nature and magnitude of genetic divergence helps in selection of genetically diverse parents (Samsuddin, 1985). Cluster analysis determines the extent of genetic similarity or expanse of one genotype from others (Mellingers, 1972).

The present study was undertaken to determine level of genetic diversity and classification of germplasm by taking into account different yield component characters for identification of suitable parents for future use. In addition, we applied PCA to the entire set of measured elemental data to investigate factors affecting the mineral composition of EFY.

## **Materials and methods**

The experimental materials consisted of 10 genotypes of elephant foot yam collected from different parts of Jharkhand, Chhattisgarh, Odisha and West

Bengal and one popular variety Gajendra developed by Horticultural Research Station, Kovvur, West Godavari district, Andhra Pradesh under Dr Y. S. R.. Horticultural University, Andhra Pradesh. These 11 genotypes were evaluated in Randomized Block Design with three replications. The spacing was maintained at 1.0 m for Row-to-Row and 0.8 m for Plant-to-Plant. Data on different morphological, nutritional and anti-nutritional characters were measured as per the standard protocols. Principal component analysis (PCA) was estimated using IBM-SPSS Statistics version 21.0. The varimax rotation of the PCs redistributes the eigenvalues (without losing any original variance) in order to maximize the relationships among the standardized variables. The PC loading in eigen vectors having values greater than the selection criterion (SC) is considered significant. The SC was calculated as follows:  $SC = 0.50 / (PC \text{ eigenvalues})^{0.5}$  (Ovalles and Collins, 1988; Raghupathi et al., 2004). Paleontological Statistics 3.13 Software Package (PAST 3) (Hammer et al., 2001) was used for dendrogram and GT Biplot construction.

## Results and Discussion

### Principal component analysis

Principal component analysis (PCA), multivariate method, is carried out based on the correlation matrix of the data to understand the most important variables contributing to the total phenotypic variation among the EFY accessions. The PCs with eigenvalues  $> 1$  (Brejda et al., 2000) and those that explained at least 5 % of the variation in the data (Sharma et al., 2005; Gui et al., 2010) were selected and subjected to varimax rotation to

maximize correlation between PCs and the measured attributes (Shukla et al., 2006).

The first seven principal components (PCs) with eigenvalues greater than 1.0 had accounted for 92.81% of the total variation among the eleven genotypes. Other PCs had eigenvalues lower than 0.9 and were not considered. The first PC was the most important component that explained 31.52% of total variability. The PC1 explained largely the characters associated with some morphological traits as well as corm yield and yield attributing traits which were effective in the discrimination of EFY accessions. Eigen vector of the PC1 had high and significant positive loadings for pseudo-stem girth (0.937), canopy spread (0.961) and number of leaflets/plant (0.908), corm length (0.778), corm breadth (0.918), corm volume (0.898) and corm yield/plant (0.885). Whereas, significant negative loadings for K content (0.649) and Zn content (0.749) were also recorded in PC1. The variations in corm dry weight (0.917), Na content (0.846), Mg content (0.490) and Fe content (0.891) were recorded significant positive loadings in PC2 and represented 18.87% of total variation. The traits contributing significant positive loading to PC3 were P content (0.593) and Mn content (0.904) and Cu content (0.937) however, total phenol content (0.699) reflects significant negative loadings. The PC4 was accounted for significant positive variation mainly for starch content (0.936) and significant negative loadings for S content (0.780). Similarly, oxalate content (0.783) and Ca content (0.859) contributed significant positive loadings to the PC5. However, PC6 represented high factor loadings for pseudo-stem height (0.708) and vitamin

C content (0.884) and PC7 had high positive factor loadings for CHO content (0.596) and antioxidant activity (0.804).

Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability and have the tendency to remain together. This may be kept into consideration during utilization of these characters in breeding program. From the first PC1 corm characteristics is the best choice due to largest loading, corm dry weight from PC2, Mn and Cu content from PC3, starch content from PC4, oxalate content from PC5, vitamin C content and antioxidant content from PC6 and PC7, respectively.

The extracted components (PC) were well represented by the communality of the present dataset. Communalities estimate the proportion of variance explained by each factors. In the present study communalities for the plant and corm traits indicated that the seven PCs accounted for 99% of the variance for corm length, 98% for pseudo-stem height, pseudo-stem girth, canopy spread and number of leaflets/plant and 97% for corm yield/plant and starch content.

## **Cluster analysis**

UPGMA cluster analysis was used to understand the relationships among eleven EFYgermplasm. The UPGMA cluster represents three principal clusters which separated all the accessions at a Euclidean distance of 0.84 (Fig. 1). In the first principal cluster released variety Gajendra clustered separately and most distantly placed among all the accessions.

The second principal cluster divided into two groups, the first group had ACC-64 and ACC-85 with ACC-136 standing apart at a Euclidean distance of 0.57. The second group within this principal cluster had two accessions ACC-102 and ACC-134 with ACC-136 placed well apart within this group at a distance of 0.60. The third principal cluster also divided into two groups with five accessions, the first group within this principal cluster had four accessions consisting of accessions ACC-39 and ACC-43 cluster with accessions ACC-58 and ACC-204 placed well apart within this group at a distance of 0.50. In the second group, accession ACC-31 remained apart within this cluster at a Euclidean distance of 0.55. Bootstrap values (1000 replicates) are shown next to the branches represents the percentage of tree in which the associated genotypes clustered together. The cophenetic correlation coefficient of the dendrogram was 0.733 which is very close to 1 depicts that the clustering is good (Chaudhuri and Ambhaikar, 2014) and interpreted as a strong representation of the original centroid dataset.

### **Genotype by trait (GT) biplot**

GT Biplot is an application of the GGE biplot technique. It can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good for certain traits and can be used as a candidature parents in plant breeding program. It graphically displays the genotype by trait biplot and allows the visualization of the associations among traits across the genotypes and of the trait profile of the genotypes.

The GT biplot was plot between PC1 and PC2 to compare accessions on the basis of twenty-five traits to identify superior genotypes in EFY improvement



(Fig 2.). In GT biplot vectors (lines) were drawn from origin and the vector length of the trait decides the magnitude of that particular trait on yield (Yan and Tinker, 2005). The polygon view of GT biplot is best to visualize the interaction pattern between genotypes and traits. The cosine of the angle between two vectors represents the correlation between them (Yan and Rajcan, 2002; Yan and Tinker, 2005). Two traits are positively correlated if the angle between their vectors is an acute angle ( $<90^\circ$ ) while they are negatively correlated if their vectors are an obtuse angle ( $> 90^\circ$ ) whereas, there is no correlation if the angle between their vectors is a right angle ( $90^\circ$ ) (Yan and Kang, 2003; Yan and Tinker, 2005).

The GT biplot axes showed distances among cultivars that reflect diversity among them in terms of variables measured. Among the eleven EFY genotypes corm yield was positively associated with corm volume, corm breadth, corm length and canopy spread and negatively associated with oxalate content. The trait pseudo-stem height was positively associated with carbohydrate and starch content whereas, this character made an 180° angle with oxalate content indicating traits to be opposite in genotype ranking. Oxalate content was positively associated with corm dry weight, vitamin C content and Fe, Mg, Ca, S, P and K content. However, the traits carbohydrate and starch content was positively associated with antioxidant and total phenol content.

GT biplot can provide a quick, visual means to identifying genotypes that have extreme and useful trait profiles. On a GT biplot, the vector length of a genotype, which is the distance between the genotype and the biplot origin,

is a measure of the genotype's distinctiveness. Therefore, genotypes with long vectors are those that have extreme levels for one or more traits. Such genotypes may or may not be a superior variety but they may be useful as parents. The distance between genotype and the biplot origin is a unique measure of the hypothetical genotype that has an average level for all traits and is represented by the biplot origin (Yan and Fregeau-Reid, 2008). In the GT-biplot, genotypes placed farther away from the biplot origin has more extreme trait profiles than the more balanced profiles of genotypes that are located near the biplot origin. The genotypes Gajendra, ACC-85, ACC-43, ACC-31, ACC-204 and ACC-134 have long vectors and extreme values for one or more traits. Whereas, the genotypes ACC-64, ACC-136, ACC-39 and ACC-58 near to the biplot origins have balanced trait profiles.