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Vandna

Department of Horticulture,
Rajasthan College of Agriculture,
Maharana Pratap University of
Agriculture & Technology,
Udaipur, Rajasthan, India

KD Ameta

Department of Horticulture,
Rajasthan College of Agriculture,
Maharana Pratap University of
Agriculture & Technology,
Udaipur, Rajasthan, India

Partha Pratim Behera

Department of Plant Breeding &
Genetics, Assam Agricultural
University, Jorhat, Assam, India

Roopali Patel

Department of Horticulture,
Assam Agricultural University,
Jorhat, Assam, India

Pooja Kumari

Department of Plant Breeding &
Genetics, DRPCA, Pusa,
Samastipur, Bihar, India

Sheetal Rawat

Department of Horticulture,
Swami Keshwanand Rajasthan
Agricultural University, Bikaner,
Rajasthan, India

Corresponding Author:

Vandna

Department of Horticulture,
Rajasthan College of Agriculture,
Maharana Pratap University of
Agriculture & Technology,
Udaipur, Rajasthan, India

Genetic divergence analysis in greater yam (*Dioscorea alata* L.)

Vandna, KD Ameta, Partha Pratim Behera, Roopali Patel, Pooja Kumari and Sheetal Rawat

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Abstract

An assessment of genetic diversity was made based on the data recorded for twenty-two tuber yield and quality contributing characters in thirty greater yam genotypes using Mahalanobis's D^2 statistics. The greater yam genotypes were characterised based on morphological and bio-chemical characters and clustered into five groups. Cluster I was the largest one, with 26 genotypes, and the rest of the clusters contained one genotype each. There was considerable variability among the genotypes for most of the characters. The inter-cluster distance was the minimum between clusters I and II, while the maximum inter-cluster distance was recorded between clusters III and V, suggesting the highest genetic divergence existing between the genotypes of these clusters. The cluster mean for both the tuber yield and quality is the highest in cluster V and the lowest in cluster III. The weight of the tuber (kg), followed by TSS ($^{\circ}$ B), diameter of tuber (cm), stem girth (cm), ascorbic acid (mg), vine length at harvest (cm) and tuber yield per vine (kg) contributed the most to the total diversity. The hybridization between genotypes MPY-5 (cluster III) x Sree Kartika (cluster V) could be suggested for transgressive breeding and also be used to develop mapping populations. These mapping populations could be further utilised in marker assisted breeding and other advanced molecular breeding for tuber yield and quality improvement.

Keywords: Cluster, D^2 statistics, genetic divergence, greater yam, hybridization

Introduction

Vegetables constitute an important component of a balanced diet for human beings. These are natural protective foods and are rich in vitamins and minerals. The production of vegetables is estimated to be 196.27 million tonnes in 2020–21 compared to 188.28 million tonnes in 2019–20, an increase of 4.24%. India's varied agro-climate zones make the country more suitable for the production of various vegetable crops. There is a great scope for increasing the production and consumption of vegetables to ensure a balanced diet for the masses (Tak *et al.*, 2021) [13]. Yams constitute a group of *Dioscorea* species cultivated widely in the tropics for their edible tubers. Winged yam, water yam, greater yam, and ten month yam are the names variously used for *Dioscorea alata*. Greater yam is mostly cultivated in Asia, Africa, and tropical America. In India, it is cultivated in all the states except the major yam producing states of Kerala, West Bengal, Bihar, Orissa, Assam, Gujarat, Maharashtra, Karnataka and Rajasthan. Among the *Dioscorea* species, greater yam (*Dioscorea alata* L.) is the most important species grown throughout India. Yams are also considered famine food and play a prime role in the food habits of small and marginal rural families and forest-dwelling communities during food scarcity periods. It is recognised as the fourth most important tuber crop after potatoes, cassava, and sweet potatoes and contributes about 10% of the total root and tuber production around the world (Viruel *et al.*, 2016) [14]. Yam tubers are used mostly for human consumption. They are primarily starchy staple foods; because of this, their protein content is appreciable (4.6%) and contributes significantly to dietary value (Coursey and Haynes, 1970) [3]. It is a very nutritive vegetable and contains starch (27.88 g), energy (108 kcal), vitamin A (138 μ g) protein (1.53 g) and fibre (0.65-1.40%) per 100 g of edible part. In addition, they (purple in colour) are rich in powerful plant compounds and antioxidants; including anthocyanins and vitamin C. Yam tubers have a wide range of culinary uses. Tubers are widely used for chips, curries, puris, soups, fried vegetables, and for canning, dehydration, and flour manufacture (Padhan *et al.*, 2020) [9]. Many greater yams have various medicinal values, as reported by many researchers. Their powerful antioxidants reduce blood pressure and blood sugar levels.

Tuber crops have immense potential for contributing to a particular area of food production because they are well adapted to existing as well as adverse environmental conditions and are generally resistant to pests and pathogens. India has a diverse germplasm of greater yam, which will provide enormous potential for popularising this crop through breeding programs. Currently, new crop breeding technologies are continually being developed. It also helps to increase the food and nutritional value of yam (Otoo *et al.*, 2015) [8].

The greater yam breeding strategy involves assembling or generating variable germplasm and selecting superior genotypes for utilising them and breeding for high yield, good quality of tubers, resistance to diseases (anthracnose and yam mosaic virus) and nematodes. To achieve these targets, collection of germplasm from various sources is very important, and utilisation of these genetic resources requires their proper and systematic evaluation to understand and estimate the genetic variability, heritability, genetic advance, and character association with yield components. Genetic diversity is an essential aspect of any heritable improvement. Knowing the nature and extent of genetic diversity is useful for selecting desirable parents from a germplasm for a successful breeding program. The Mahalanobis D^2 technique appears to be a fruitful approach which is based on multivariate analysis and serves as a good index of genetic diversity. Hence, in the present study, an attempt was made to assess the genetic diversity among 30 genotypes of greater yam.

Material and Methods

To study genetic divergence in the present investigation, thirty genotypes of greater yam were collected from different main growing places in Rajasthan and Kerala. These genotypes were evaluated during kharif 2018-2019 at the Hi-tech unit, Department of Horticulture, at RCA, MPUAT, Udaipur in Randomized Block Design (RBD) with three replications. In an in-situ study, it was very complicated to select plants of similar age and environment, so observations were recorded for those characters that were relatively less affected by these factors and were easily assessable at the

time of data recording. Observations were recorded on randomly selected plants of each genotype for 22 characters, viz., days to emergence, first leaf emergence, number of leaves (30 DAE), number of sprouts per seed tuber, vine length at 45 DAE, internode length, vine length at harvest, leaf width, petiole length, tuber length, diameter of tuber, number of tubers per vine, weight of tuber, stem girth, tuber yield per vine, starch, ascorbic acid, moisture, TSS, total sugar, total Phenol, and dry matter. Five randomly selected plants for each genotype were considered for observations of different characters.

Mean values of 22 characters studied were subjected to statistical analysis adopting standard statistical procedure. Genetic divergence was calculated by using Mahalanobis's D^2 (1936) [5] statistics as suggested by Rao (1952) [10]. Genotypes were grouped into various clusters by Tocher's method as described by Rao (1952) [10].

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the traits under study. A set of 30 genotypes of greater yam were subjected to D^2 analysis for 22 characters, and based on D^2 values, five clusters were formed. The distribution of genotypes into five clusters is presented in Table 1 and illustrated in Fig 1. This indicated that substantial diversity existed in all the genotypes evaluated in the present study. The present study also suggests that there is no relationship between geographical and genetic diversity as genotypes chosen from different eco-geographical regions are grouped into different clusters. The 30 greater yam genotypes were grouped into five clusters on the basis of their relative magnitude of D^2 values. Cluster I was the largest one, with 26 genotypes, and the other clusters each had a single genotype. Genetic diversity between genotypes may be a result of variables such as selection history, heterogeneity, selection under varied environmental conditions, and genetic drift. Therefore, while selecting parents for hybridization; particular attention should be paid to genetic diversity in addition to per se performance and the breeder's practical knowledge (Behera *et al.*, 2018) [2].

Table 1: Cluster composition of 30 greater yam genotypes into different clusters (Tocher's method)

Clusters	Number of Genotypes	Genotypes Name
I	26	MPY-1, MPY-2, MPY-3, MPY-4, MPY-6, MPY-7, MPY-8, MPY-9, MPY-10, MPY-11, MPY-12, MPY-13, TGY-12-6, TGY-12-3, TGY-17-2, TGY-17-3, TGY-17-4, TGY-17-8, TGY-17-9, TGY-12-2, TGY-14-3, TGY-14-5, TGY-14-7, TGY-14-8, TGY-14-9, Jai White
II	1	TGY-14-11
III	1	MPY-5
IV	1	TGY-14-4
V	1	Sree Kartika

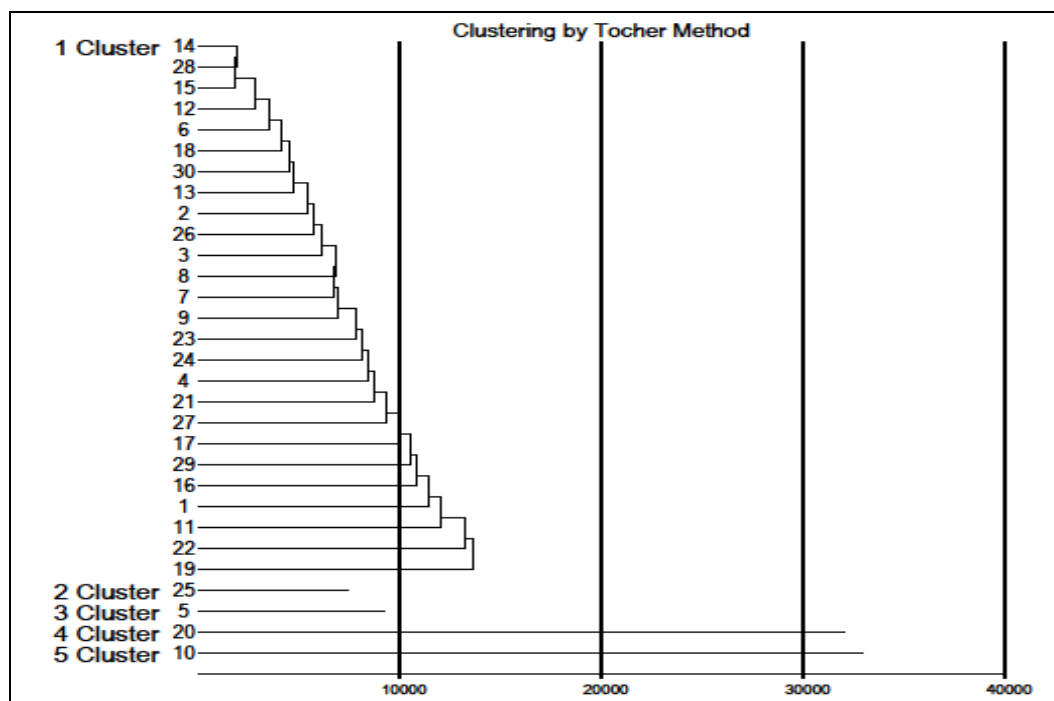


Fig 1: Clustering of 30 greater yam genotypes by using Tocher Method

The magnitude of inter-cluster distance measures the genetic distance between two clusters, while intra-cluster distance measures the extent of genetic diversity between the genotypes of the same cluster. The mean intra and inter-cluster distances among the genotypes are given in Table 2. The maximum mean intra-cluster distance was in cluster I (99.19) and the minimum was recorded as a 0.00 value for the rest of all the clusters as they had only a single genotype each. The highest intra-cluster distance among the genotypes of the clusters was mainly due to the wide genetic diversity of the genotypes. The minimum inter-cluster D^2 values were recorded between clusters I and II (128.77), while the maximum D^2 value was found between cluster III and V (274.49), followed by cluster II and IV (272.52), cluster III and IV (272.48), cluster I and cluster V (231.45), cluster I and cluster IV (225.85), cluster II and cluster III (149.55) and cluster I and cluster III (132.01). The inter-cluster distance

was shortest between clusters I and II, indicating close relationships and similarity for most of the Greater yam genotypes in these clusters, while the greatest inter-cluster distance was found between clusters III and V, indicating the greatest genetic divergence between the genotypes in these clusters. Hence, the crosses between genotypes MPY-5 (cluster III) x Sree Kartika (cluster V) and TGY-14-11 (cluster II) x TGY-14-4 (cluster IV) could be suggested for transgressive breeding for tuber yield and quality. The heterotic effect of progeny is anticipated to increase with hybridization of these genotypes from widely different clusters Jyothy *et al.*, (2017) [4]. The inter-cluster distances were greater than the intra-cluster distances, indicating strong parental diversity. Similar results of inter and intra cluster distances in greater YAM were reported by Sheela *et al.*, (2014) [12] and Sartie *et al.*, (2012) [11].

Table 2: Average Inter-cluster and Intra-cluster (diagonal) distance based on corresponding D^2 Values in 30 greater yam genotypes

Cluster	I	II	III	IV	V
I	99.19	128.77	132.01	225.85	231.45
II		0.00	149.55	272.52	271.54
III				272.48	274.79
IV					219.58
V					0.00

The cluster means for various quantitative and qualitative traits indicated differences between the clusters for all the characters listed in Table 3. The cluster I recorded the highest mean values significant for dry matter (%) (53.41). The cluster II recorded the highest mean values significant for days to emergence (24.33), number of sprouts per seed tuber (2.13), number of tubers per vine (1.93), ascorbic acid (mg) (24.11) and TSS ($^{\circ}$ B) (13.60). The cluster III recorded the highest mean values significant for moisture (%) (67.79). Cluster IV had the highest significant mean values for the number of leaves (30 DAE) (89.30), vine length (cm) (148.34), vine length at harvest (cm) (378.33), and starch

content (g/100g) (59.28). The cluster V recorded the highest mean values significant for days to first leaf emergence (26.0), internode length (cm) (15.38), leaf width (cm) (13.91), petiole length (cm) (12.08), tuber length (cm) (30.59), diameter of tuber (cm) (9.99), weight of tuber (kg) (3.01), stem girth (cm) (5.65), tuber yield per vine (kg) (3.26), total sugar (g/100g) (8.73) and Total Phenol (mg/100g) (94.11). Cluster V had the greatest mean tuber yield features, whereas cluster III had the lowest mean tuber yield traits. To maximise the number of transgressive segregants that may be used in crop breeding operations, hybridization programme should cross chosen germplasm belonging to clusters V and III.

Similar kinds of results were also reported by Obidiegwu *et al.*, (2009) [7] and Sheela *et al.*, (2014) [12]. The clustering pattern made it evident that none of the asra rice germplasm clusters could be chosen and used directly as varieties since

none of the clusters had all the desired features. In order to avoid this, various clusters' germplasm must be combined via hybridization.

Table 3: Cluster means for 22 characters in 30 greater yam genotypes (Tocher's method)

Cluster	Days to emergence	Days to first leaf emergence	No. of leaves (30 DAE)	No. of sprouts per seed tuber	Vine length (cm)	Internode length (cm)	Vine length at harvest (cm)	Leaf width (cm)	Petiole length (cm)	Tuber length (cm)	Diameter of tuber (cm)
I	17.98	20.72	84.07	1.81	144.14	13.27	347.32	9.83	9.93	28.66	7.68
II	24.33	26.00	69.66	2.13	110.66	9.90	365.70	8.30	8.60	25.44	6.72
III	22.00	25.00	76.40	1.27	125.00	14.01	216.80	8.80	10.20	26.48	7.03
IV	16.33	18.66	89.30	2.00	148.34	12.49	378.33	11.89	9.60	29.34	9.02
V	23.00	26.00	73.00	1.73	116.33	15.38	371.90	13.91	12.08	30.59	9.99

Table 3: Contd...

Cluster	Number of tuber per vine	Weight of tuber (kg)	Stem girth (cm)	Tuber yield per vine (kg)	Starch content (g/100g)	Ascorbic acid (mg)	Moisture (%)	TSS (°B)	Total sugar (g/100g)	Total Phenol (mg/100g)	Dry matter (%)
I	1.52	1.37	4.35	1.67	55.94	17.48	64.59	8.97	7.17	92.44	53.41
II	1.93	1.07	5.02	1.78	56.59	24.11	64.32	13.60	6.87	93.16	35.68
III	1.60	0.83	3.14	1.21	51.42	22.30	67.79	7.87	3.53	91.58	32.21
IV	1.20	2.45	3.14	1.97	59.28	19.77	64.86	11.27	8.46	90.51	35.14
V	1.13	3.01	5.65	3.26	54.79	21.60	67.20	9.63	8.73	94.11	32.80

Apart from divergence, the performance of genotypes and the trait that contributes the most to divergence should be considered since they seem to be desirable for higher yam improvement. The relative percent contribution of individual traits towards total divergence was given in Table 4. Among all the characters, weight of tuber (kg) contributed the maximum (22.07%) to the diversity, followed by TSS (°B) (17.7%), diameter of tuber (cm) (11.26%), stem girth (cm)

(11.26%), ascorbic acid (mg) (11.03%), Vine length at harvest (cm) (7.36%), Tuber yield per vine (kg) (6.67%), No. of leaves (30 DAE) (3.45%), Leaf width (cm) (3.45%), Petiole length (cm) (3.45%), and the remaining characters all contributed very little to total genetic divergence. Similar results in greater yam were also reported by Agreeta *et al.*, (2019) [1] and Norman *et al.*, (2011) [6].

Table 4: Relative Percent contribution of 22 different characters to the total genetic divergence in 30 greater yam genotypes.

S. No.	Characters	Percent Contribution
1	Days to emergence	0.00
2	Days to first leaf emergence	2.07
3	No. of leaves (30 DAE)	3.45
4	No. of sprouts per seed tuber	0.00
5	Vine length (cm)	0.00
6	Internode length (cm)	0.00
7	Vine length at harvest (cm)	7.36
8	Leaf width (cm)	3.45
9	Petiole length (cm)	3.45
10	Tuber length (cm)	0.00
11	Diameter of tuber (cm)	11.26
12	Number of tuber per vine	0.00
13	Weight of tuber (kg)	22.07
14	Stem girth (cm)	11.26
15	Tuber yield per vine (kg)	6.67
16	Starch content (g/100g)	0.00
17	Ascorbic acid (mg)	11.03
18	Moisture (%)	0.00
19	TSS (°B)	17.70
20	Total sugar (g/100g)	0.00
21	Total Phenol (mg/100g)	0.23
22	Dry matter (%)	0.00

Conclusion

In the present investigation, the 30 greater yam genotypes were characterized based on morphological and bio-chemical characters and clustered into five groups. Cluster I was the largest one, with 26 genotypes, and the rest of the clusters

contained one genotype each. There was considerable variability among the genotypes for most of the morphological characters. The inter-cluster distance was the minimum between clusters I and II, while the maximum inter-cluster distance was recorded between clusters III and V,

suggesting the highest genetic divergence existing between the genotypes of these clusters. The cluster mean for both the tuber yield and quality is the highest in cluster V and the lowest in cluster III. The characteristics: weight of tuber (kg), followed by TSS (°B), diameter of tuber (cm), stem girth (cm), ascorbic acid (mg), vine length at harvest (cm) and tuber yield per vine (kg) contributed the most to the total diversity. The hybridization between genotypes MPY-5 (cluster III) x Sree Kartika (cluster V) could be suggested for transgressive breeding and also be used to develop mapping populations. These mapping populations could be further utilised in marker assisted breeding and other advanced molecular breeding for tuber yield and quality improvement.

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