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# Recent genetic variability studies in taro (*Colocasia esculenta* L. Schott) in India: An overview

**T Aiswarya[1], KT Chandramohanan[2]**
[1] Junior Research Fellow, Department of Botany, Government Brennen College, Dharmadam, Thalassery, Kerala, India
[2] Associate Professor and Head, Department of Botany, Government Brennen College, Dharmadam, Thalassery, Kerala, India

## Abstract

Genetic diversity of crop plants is the basis of a successful plant breeding programme. *Colocasia esculenta* L. Schott is one of the major edible tuber crop cultivated in different regions of India. It exhibits great genetic variability. Morphological and molecular studies support the existence of high genetic variability between *C. esculenta* germplasm accessions. It will enhance the probability of success of a plant breeding programme. Most of these studies were concentrated on North East states of India. Only a few genetic variability studies at molecular level were reported in India. Hence the present work is an attempt to summarise the genetic variability studies in taro in India.

**Keywords:** *Colocasia esculenta*, taro cultivars, genetic variability

## Introduction

Analysis of genetic diversity plays a vital role in plant breeding as well as in conservation biology. Genetic variability studies provide more background knowledge regarding conservation strategies and it also determines the success of a plant breeding programme. In addition it also helps to study about the evolutionary trends within the species. Taro, *Colocasia esculenta* L. Schott belongs to the aroid family Araceae. It is one of the popular edible tuber crops of India. It is ranked 9th among the world food crops [11]. It is believed that taro is originated in Asia [20]. Hence it is expected to have more genetic diversity in Asia continent. Taro is a good source of carbohydrates. Tubers contain 70-80% starch. It also contains protein and mineral like sodium, magnesium, iron, calcium, potassium, zinc, manganese, copper and phosphorus. Phenolic acids, terpenoids and flavonoids with various pharmacological properties were also present in taro. It shows anti cancerous, anti oxidant and anti inflammatory properties [3, 14]. Hence taro is a medicinally and nutritionally important crop.

The present work is envisaged to summarise genetic variability studies in *C. esculenta* in India. Recent morphological and molecular studies on genetic variability of taro in India are discussed below.

## Materials and Methods

A systematic review was done by collecting and analysing published works related to the topic of study. Literature review was conducted with the help of databases and search engines such as Google Scholar, Semantic Scholar, ResearchGate, Web of Science, Scopus, ScienceDirect and Academia.

## Results and Discussion

### Morphological studies

Genetic variability analysis plays vital role in plant breeding programme. Heritable morphological traits are important in plant breeding. The results of morphological studies conducted by various authors to estimate the degree of taro diversity in India are discussed here. Morphological screening of fourteen *C. esculenta* germplasm accessions collected from hill areas of Arunachal Pradesh revealed existence of high genetic variability within taro genotypes. In this study, they observed various morphological characters like height and width of taro plant, number of leaves, leaf length, lamina breadth, number of cormels, weight of cormels, size of corm, weight of corms, number of suckers and tuber yield. Study reveals wide range of variability in plant girth, number of side suckers, number of cormels and cormel yield [6]. Naskar and Sreekumar [25] reported extensive variation among taro cultivars in India. They have analysed agronomic characters of 43 taro genotypes collected from North East states of India. These 43 genotypes are grouped into eight clusters through cluster analysis with wide range of variability. Tuber yield per plant varies from 0.29 Kg to 2.38 Kg.

Singh *et al.* [31] analysed genetic diversity of taro accessions in Andaman Islands. They have studied 20 wild genotypes collected from different regions of the Island along with one cultivated form. Based on morphological traits, these accessions were classified into two clusters with 75% variability. Mandal *et al.* [19] reported high variability in number of leaves, number and weight of cormels and tuber yield among taro cultivars collected from Kerala, Assam, Orissa and West Bengal. On the basis of $D^2$ statistics, high morphological diversity of taro was recorded in West Bengal [2].

Vinutha *et al.* [32] reported high level of phenotypic diversity among taro germplasm accessions collected from North East India. They studied 27 phenotypic characters of taro and found that variability was very higher for characters like tillering and plant size with coefficient of variation 51.91 and 54.04 respectively. Mukherjee *et al.* [22] studied about 14 taro cultivars collected from Uttar Pradesh, West Bengal and Bihar. They evaluated different agronomic traits including height of taro plant, number of leaves, leaf size, number of side tuber, weight of side tuber per plant, weight of corm, proportion of dry matter in tubers and corm yield. Study revealed that highest Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation

(PCV) was observed in case of dry matter percentage of tuber and greater heritability was observed in agronomic characters like number of cormels per plant and proportion of dry matter in tubers. High genetic variability as well as high heritability of characters will support plant breeding programme.

According to Kathayat *et al.* [13], Uttarakhand forms a big pool of taro genetic diversity. Nineteen traits of 45 genotypes were analysed in this study. Genotypes were classified into seven clusters with high intra and inter cluster distances. Devi *et al.* [10] analysed yield characters of 9 traditional taro cultivars from Manipur state and found that number of cormels and yield of corms and cormels varies considerably from one cultivar to another. Tuber yield per plant varies from 205g/plant to 604g/ plant. Similarly number of cormels per plant varies from 0 to 12.

Sachen [27] observed different agronomic characters of 24 taro cultivars collected from Nagaland and estimated GCV, PCV, broad sense heritability and genetic advance. Highest GCV and PCV were reported in case of number of side tuber per plant. Number of cormels formed per plant and corm weight show high heritability. According to Singh *et al.* [30] maximum GCV was observed in case of number of side tuber and weight of the corm. High heritability was observed in case of leaf length and weight of cormels per plant. Existence of high heritability in yield contributing characters of taro indicates that selection approach can be considered as a good tool for improvement of taro varieties.

Narayan *et al.* [24] studied about five agronomic traits of 28 germplasm accessions of *C.esculenta* collected from Bihar. PCV is high in morphological characters such as the weight of the central corm and the number of buds seen on the central corm. Corm yield and corm length show high heritability and genetic advance. Taro accessions were grouped into six clusters with inter cluster distance varies from 1.096 to 28.970. Cluster 3 and cluster 4 shows wide inter cluster distance (28.970). Kathayat *et al.* [12] analysed 19 characters of 45 germplasm accessions of taro collected from different parts of North India. Study shows high inter and intra cluster distance between different taro accessions. Cluster 3, cluster 4 and cluster 6 show high intra cluster distance. Wide range of inter cluster distance was recorded between cluster 5 and cluster 6. These studies reveal that North East India harbouring rich taro diversity.

Devi *et al.* [9] grouped 40 taro accessions from North East India into seven clusters with high inter cluster distance. In this case inter cluster distance was found to be substantially greater than the intra cluster distance. Highest inter cluster distance was reported between clusters 2 and cluster 7 (218.30), suggesting great genetic variability. Large inter cluster distance will help in taro breeding programme for the production of superior genotypes. Khatemenla *et al.* [16] studied 22 taro cultivars from Meghalaya, Assam, Nagaland, Arunachal and Kerala. In their study taro cultivars from Kerala and Assam grouped together during cluster analysis. Cultivar from Assam grouped along with cultivars from four other states mentioned above. It suggests that morphological features of taro cultivars do not give any idea about their place of origin.

Genetic variability and correlation studies of 23 taro accessions were done by Kumar *et al.* [17]. Study reveals that number of side tubers and tuber yield show elevated genotypic and phenotypic coefficient of variability. Tuber yield per plant shows positive correlation with corm width, corm weight, leaf length, plant height and number of cormels. Choudhary *et al.* [5] revealed that taro cultivars show great variability in leaf characteristics. Genotypes show variability in arrangement, colour and orientation of leaves. Colour and pattern of leaf margin, sinus, vein and leaf sheath also varies considerably. Shellikeri *et al.* [29] detected considerable variation in yield characteristics of taro accessions collected from Konkan region of Maharashtra. Maximum total yield was observed on accession number M-9-111 (26.15 ton/ hectare) and smallest total yield is shown by accession number M-12-429(9.17 ton/ hectare).

Above studies show that *C. esculenta* is a complex species with large number of morphotypes. Existence of high GCV, PCV, and heritability gives a greater hope for future plant breeding programs.

## Molecular studies

In India, genetic variability of *C. esculenta* studied at molecular level using various molecular techniques like Random Amplified Polymorphic DNA (RAPD), Inter Simple Sequence Repeat (ISSR), Microsatellites marker or simple sequence repeats (SSR) and Amplified Fragment Length Polymorphism (AFLP).

Lakhanpaul *et al.* [18] characterised 32 taro genotypes which are collected from different regions of India. Thirteen RAPD primers were used in the study with an average polymorphism of 78.89%. These 32 accessions were grouped into 4 clusters with 3 outliers. This study reveals that genotypic variability does not imply any idea about place of occurrence of that genotype. Pillai and Lekha [26] studied about 45 taro varieties through RAPD analysis followed by cluster analysis. Eleven RAPD primers were used in the study, in which three primers (B 11, AN 2 and AM 3) produced polymorphic bands. Percentage of similarity between these genotypes ranges from 60-100%.

Sharma *et al.* [28] carried out AFLP analysis of taro accessions collected from Kerala, *Uttarakhand,* Uttar Pradesh, West Bengal and Orissa states of India. These genotypes are grouped into two clusters with dissimilarity coefficient ranging from 0.01- 0.38. Observed heterozygosity and expected heterozygosity were 0.3341 and 0.3657 respectively. This study also point out high genetic diversity of taro in India.

Beevi *et al.* [1] characterised sixty accessions of taro including 43 cultivars and 17 wild genotypes collected from Kerala, Tamil Nadu and Andhra Pradesh through RAPD analysis. Twenty primers were used in the study and nine primers produced polymorphic bands. These 9 RAPD markers (OPA 03, OPA 04, OPA 08, OPA 09, OPA 12, OPA 13, OPA 15, OPA 16 and OPA17) grouped taro genotypes into 5 clusters, among which cluster V includes triploid genotypes and remaining clusters include diploid forms. Study suggests high degree of polymorphism among south Indian genotypes. Taro collected from Kerala shows more variability than other genotypes.

RAPD and ISSR analysis of 21 *C. esculenta* germplasm accessions of Andaman Islands along with three released varieties from CTCRI (Central Tuber Crop Research Institute) were done by Singh *et al.* [31]. Two major clusters are formed by RAPD analysis, one with three released varieties Sree Pallavi, Sree Rashmi and Sree Kiran and second with 21 local cultivars. ISSR markers also grouped 24 accessions into two major groups, one with released variety Sree Kiran and the other with remaining 23 accessions. Das *et al.* [7] characterised ten drought resistant taro genotypes through RAPD markers. Genotypes show wide range of polymorphism (3.7%- 41.9%) which point out great genetic variability. Sixty primers were used in the study and fourteen primers produced polymorphic bands with an average polymorphism of 34.34%. These fourteen primers divided ten taro accessions into two clusters.

Chaïr *et al.* [4] studied about 321 taro cultivars collected from Asia, Africa, America and Pacific region. Among these 43 genotypes were collected from India. Eleven microsatellite markers with M- 13 tail were used in the study. These molecular markers divided accessions into two clusters. Maximum genetic diversity was observed within Indian cultivars. According to Mezhii *et al.* [21], Nagaland is rich in taro genetic diversity. They have analysed fifty taro genotypes by using microsatellite markers (Simple Sequence Repeat analysis). Twenty eight SSR markers were used in the study among which sixteen microsatellite markers produced polymorphic bands. Genotype 9 and genotype 45 show wide range of variations.

Molecular characterisations of leaf blight resistant and susceptible genotypes of *C. esculenta* were carried out by Nair *et al.* with the aid of ISSR markers [23]. In this study fourteen ISSR primers generated 108 bands which show 95.7% polymorphism. Khatemenla *et al.* [15] used SSR markers for analysing genetic variability of taro in North East India. Molecular characterisation of 22 genotypes was done using 10 SSR primers. This study also supports high genetic variability of taro in North East India with no genotypes with 100% similarity.

High genetic variability exhibited by Indian taro genotypes support the concepts of its origin in India [8]. Above studies show that *C. esculenta* shows great morphologic and genotypic variability in various characters. It will help in the better survival of the plant species. It also enhances the possibilities of success of plant breeding programme.

## Conclusions

Highest genotypic and phenotypic variability exhibited by taro shows its greater adaptability to withstand changing environmental conditions. It will also support maximum heterosis during plant breeding. Correlation analysis of different yield contributing characters of taro can be used in crop improvement programmes. Presence of natural variability is a promising scope for crop improvement programmes. Due to its highly polymorphic nature, species *C. esculenta* comprises large number of morphotypes and local cultivars. Only few researches have done on its genomic level in India. Most of the genetic variability studies were concentrated on North East States of India. Hence characterisation and evaluation of traditional and local cultivars of taro in other regions are also very significant.

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