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Genetic variability among taro (*Colocasia esculenta* L. Schott Var. *antiquorum*) Germplasm related to morphological and nutritional characters: A review

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Abstract

Taro (*Colocasia esculenta* (L.) is one of the important among tuber crops grown in various parts of India and African countries. But there are few standard cultivars available for commercial cultivation and local germplasms across various parts of the world have a lot of genetic variation. For any crop improvement programme, aimed to achieve maximum productivity and production, a detailed knowledge of facts such as genetic variability, genetic diversity, heritability, genetic advance, correlation and path coefficient of various qualitative and quantitative traits and their contribution towards yield is essential. Studies in this direction are very less and can not be generalized for every climatic condition and with other genetic materials. Hence, the information regarding some indigenous genotypes of taro used to formulate a sound breeding plan for its improvement has been reviewed here.

Keywords: Correlation, genetic diversity, taro, path coefficient, variability

Introduction

Taro, *Colocasia esculenta* (L.) Schott. var. *antiquorum* known as *eddoe* type or *Arvi* belongs to the monocotyledonous family Araceae, whose member is known as aroid. It is an ancient crop which originated in the Indo-Malayan region probably in Eastern India and Bangladesh and it is being grown throughout the humid tropics. It is believed that the origin of domesticated taro is from 'wild type' *C. esculenta* var. *aquatilis*, which is from North East India or South East Asia. In India it is grown an area of 0.052 million ha with production of 0.654 million tonnes and productivity of 12.57 t/ha. Taro is one of the few edible species of the genus *Colocasia*. Cultivated ones are mostly diploid ($2n=2x=28$), although some triploids ($2n=3x=42$) are found. There are about thousand recognized cultivars, but basically fall into two groups, eddoe type (*Colocasia esculenta* (L.) Schott var. *antiquorum*) which has a relatively small corm surrounded by several well developed cormels and the dasheen (*Colocasia esculenta* (L.) Schott var. *esculenta*) popularly known as "Gaderi" in hills, which has a large central corm and smaller cormel attached more compactly and clustered cormels.

The corms are consumed as cooked vegetables or are made into pudding breads or poi. The large nutrient rich leaves are commonly eaten stewed. Petioles are given to pigs after boiling with broken rice or rice bran. They are a good source of thiamine, riboflavin, iron, phosphorus, zinc and a very good source of vitamin B6, vitamin C, niacin, potassium, copper, and manganese. It is also a rich source of amino acids. Gave the composition of corms as it contains water (63-85 per cent), protein (1.3-4.0 per cent), fat (2.0-4.0 per cent), carbohydrate (13 - 29 per cent), ash (0.6-1.3 per cent), fibre (0.6-1.2 per cent) and vitamin B & C in appreciable quantities. Besides, this crop has high medicinal importance and it is used in many Ayurvedic preparations. The juice of the leaves is used against colic and constipation, the acrid juice extracted from leaf stalk is astringent and styptic.

Why genetic diversity is require

Success of any breeding programme depends much on genetic diversity available to the breeders and the judicious selection of parents. The success of breeding programme is achieved by the efficient utilization of heritability and variability available in the population. The importance of genetic diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been realized by several workers (Kurian and Peter, 1994)^[11]. Mahalanobis (1936)^[12] has been used distance as an efficient tool in

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quantitative estimation of genetic diversity and a rational choice of potential parents for a breeding programme. Knowledge of interrelationship between yield and its components is obvious for efficient selection of desirable plant type. Unlike the correlation coefficient values, which measure the extent of relationship, path coefficient (Wright, 1921; Dewey and Lu, 1959) [28, 9] measure the magnitude of direct and indirect effects of characters on complex dependent characters like yield and thus enable the breeders to judge best about the important component characters during selection.

Genetic variability, heritability and genetic advance related yield and quality contributing traits

Genetic variability is an important feature of considerable importance in crop improvement. It is the basic necessity for any breeding programme to be successful. The knowledge of existing variability with respect to yield and yield attributing traits in the germplasm of a crop is the basic requirement in order to select the desirable types. Vavilov (1951) [27] for the first time perceived the importance of genetic variability and advocated that the wide range of variability provides better scope of selecting desired genotypes.

According to Allard (1960) [2], heritability is the proportion of observed variability which is due to genetic causes, the remainder being due to the environmental cause. Heritability of a character indicates the extent to which the character can be transmitted from one generation to another (Balouch *et al.*, 2003) [3] and is a valuable tool to predict the magnitude of genetic gain that follows selection for a character (Adeniji and Kehinde, 2003) [1]. Mukherjee *et al.* (2003) [13] observed that cormels per plant showed high genetic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percent of mean.

Genotypic and phenotypic coefficients of variation were high for number of leaves per plant, oxalate content, number of corms and cormels per plant, total yield per plant and corm weight. High heritability coupled with higher genetic advance observed for all the above characters suggesting the importance in the selection programme of yield improvement (Cheema *et al.*, 2007) [6].

Yadav *et al.* (2007) [29] observed high genotypic coefficient of variation and heritability among leaves per plant, corm weight, cormel weight, corm length, yield and leaf blight incidence. Three important characters, namely, corm weight per plant, cormel weight per plant and yield (q/ ha) recorded high heritability coupled with high genetic and coefficient of variability and advance and indicating a possible role of additive gene effect for the genotypic variance for these characters.

Pandey *et al.* (2009) [18] found that phenotypic coefficient of variation was higher than genotypic coefficient of variation, which indicates that environment plays an important role in expression of these traits.

Sarma *et al.* (2010) [23] revealed highly significant differences among the germplasm for different traits and exhibited higher range of variation. For all the characters phenotypic coefficient of variance was found higher than genotypic coefficient of variance.

Choudhary *et al.* (2011) [7] reported that there was more variability in the characters like plant girth, number of side suckers, number of cormels and cormel yield. The high values of genetic advance coupled with high estimates of heritability suggest that real progress in improvement through selection could be made for yield and associated traits like number of

leaves, lamina length and breadth, cormel weight and cormel size.

Devi *et al.* (2013) [8] reported highest phenotypic and genotypic coefficient of variation for the characters like weight of corm per plant, average weight of cormel, average weight of corm, tuber yield per plant, starch content, number of cormel per plant and weight of cormel per plant in taro. High heritability (broad sense) and genetic advance in percent of mean for the characters like weight of corm per plant, average weight of corm, tuber yield per plant, starch content, number of cormel per plant and weight of cormel per plant in taro.

Bhattacharjee *et al.* (2014) [5] observed that length of main sucker and girth of main sucker had high heritability with moderately to high genetic advance percentage as a mean, which indicates additive nature of genetic variance and less influence of the environment and there is more possibility of character improvement through selection. Whereas number of side sucker per plant had moderately low heritability with moderate genetic advance over mean indicating less possibility of improvement of the character through selection.

Poddar *et al.* (2015) [21] at Bhubaneswar conducted experiment on variability and heritability of one forty five genotypes of taro. They observed that in general phenotypic coefficient of variation was higher than genotypic coefficient of variation and it indicated the environmental influence over the expression of these characters. They observed high PCV and GCV values among the evaluated genotypes which indicated the presence of considerable variability. Maximum heritability was noticed in yield, number of cormels, corm length and plant height.

Singh *et al.* (2015) [25] at Faizabad observed high phenotypic and genotypic coefficient of variation for corm yield (g) and corm yield per plant. Mukherjee *et al.* (2016) [14] observed highest genotypic and phenotypic coefficient of variation for dry matter percentage. Higher heritability and genetic advance were exhibited by number of cormels per plant and dry matter percentage, indicating the potentiality of selection for improvement of such characters.

Correlation and path coefficient studies

Correlation coefficient is a statistical measure to determine the extent of association, whether positive or negative, between various plant characters and thus, helps to identify the character on which selection can be imposed for improvement in associated characters. Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation into direct and indirect effects. In other words, it measures the direct and indirect contribution of various independent characters on a dependent character. The concept of path analysis was developed by Wright (1921) [28] and the technique was first used by Dewey and Lu (1959) [9] that helps in determining yield contributing characters thus, useful in indirect selection. Correlation coefficients along with path coefficients together provide more reliable information, which can be effectively predicted in crop improvement program. If the correlation between yield and a character is due to direct effect of a character, it reveals true relationship between them and direct selection for the trait will be rewarding for yield improvement. However, if the correlation coefficient is mainly due to indirect effect of the character through another component trait, indirect selection through such trait will be effective in yield improvement.

Sivam *et al.* (1983) ^[26] reported that the Corm development could be noticed from 8th week after planting in upland taro and the corm weight increased continuously reaching a peak value at 40-46 weeks after planting. Under Fiji condition varieties differ significantly in leaf production. Usually a plant produces 20-35 leaves at a time with longevity of 30-50 days depending upon the cultivar.

Cheema *et al.* (2007) ^[6] observed fourteen characters in twenty four clones of taro collected from different parts of North India. Studies revealed that there is strong positive and significant correlation between total yield per plant and number of corms, number of cormels per plant, oxalate content, protein content and corm length. The analysis of path reported that number of cormels per plant, protein content, corm weight and length showed direct and positive effects while number of corms per plant and oxalate content had indirect and positive effects on total yield per plant. Similarly Pandey *et al.* (2009) ^[18] observed that the total yield per plant was positively and significantly associated with number of cormel per plant.

Paul and Bari (2011) ^[19] evaluated thirty accessions of taro (*Colocasia esculenta* L.) the genotypic level of plant height, petiole length, corm breadth, cormel number and cormel length showed direct effect on yield per plant whereas at the phenotypic level cormel weight and cormel breadth showed the highest direct effect on yield per plant. Devi *et al.* (2013) ^[8] revealed that weight of corm per plant had maximum positive direct effect on tuber yield per plant followed by weight of cormel per plant at genotypic and phenotypic level in *Colocasia*.

Paul *et al.* (2014) ^[20] reported that significant and positive correlation with yield per plant was shown by leaf length, leaf number, LAI, cormel length, corm weight and cormel weight. Buragohain *et al.* (2013) ^[4] conducted morphological and chemical analysis of twenty locally grown taro (*Colocasia esculenta* L. Schott.) cultivars. Wide variability was recorded in nutritional and other quality parameters like starch, calcium oxalate, dry matter etc. among the different taro cultivars. Strong positive correlation was found between corm length and specific gravity, calcium oxalate and moisture content.

Singh *et al.* (2015) ^[25] observed that length of lamina showed positive and highly significant correlation with width of lamina, number of corm per plant, corm yield per plant, diameter of corm, diameter of cormel and cormel yield per plant.

Pandey and Singh (2006) ^[17] estimated the variance, heritability and genetic advance for 18 characters in taro. He reported the gcv was highest in number of cormel per plant, heritability and genetic advance were also high for number of cormel per plant and cormel weight per plant. Among the accessions and cultivars of this species for all characters showed significant variations.

Mukherjee *et al.* (2016) ^[14] observed that genotypic and phenotypic co-efficients of variation, heritability, genetic advance at 5 per cent selection intensity. results indicated that highest genotypic co-efficient of variation for dry matter percentage (47.91), which was 95.78 per cent of the phenotypic co-efficient of variation, whereas tuber yield per plant showed the widest range (819.37). Number of cormels per plant and dry matter percentage exhibited considerably higher heritability (84.90% and 91.70%, respectively) and genetic advance (81.19 and 79.00, respectively), indicating the potentiality of selection for improvement of such characters. These two characters were found to be positively correlated to tuber yield per plant.

Genetic divergence studies

Genetic diversity in the available gene pool is the source of variation, which is raw for the improvement work. For effective conservation and utilization of *Colocasia* genetic resources, a clear understanding of genetic diversity and relationships of varieties is essential. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite for an effective breeding program. Genetic diversity is a useful tool in quantifying the degree of divergence in a biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Jatasara and Paroda, 1978) ^[10].

Solanki *et al.* (2001) ^[22] studied fifteen varieties of *Colocasia* for eleven yield and its contributing traits to estimate their genetic variability and related parameters. High heritability coupled with high genetic advance were observed for number of corms per plant, corm length, corm yield per plant and corm yield per hectare showing additive gene effect while other characters were found to have high to moderate heritability with low genetic advance showing non additive gene effects.

Naskar and Sreekumar (2011) ^[16] identified three vectors with minimal Eigenvalue criterion through Principal component analysis, which explained 78% of the variation in the traits. The accessions TL-3 and Megh-1 (Meghalaya) were found to be far apart from other accessions and can be utilized for further breeding programs.

Bhattacharjee *et al.* (2014) ^[5] assessed the genetic diversity within the population of twenty genotypes of taro collected from different districts of West Bengal and other parts of India by using D2 statistics and principal component analysis. On basis of magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters it was found that FC-4, FC-11, PKS-1, BCC-32, BCC-30 and Muktakeshi might be used as parental material for future breeding program. Similarly stated that fifty genotypes were grouped into ten clusters in first year and in second year, nine clusters were observed. The clustering patterns indicate that geographic diversity has impact on genetic diversity.

Poddar *et al.* (2015) ^[21] observed narrow genetic base among the taro germplasm collection through PCA derived scatter plot. Three major groups were obtained and maximum number of genotypes found to be in major group-II. 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.

Conclusion

The literature reviewed in this paper highlighted the genetic divergence and variability available in taro genotypes. Overall reviewed that is yield and its components are very useful for efficient selection of desirable plant type regarding quantitative and qualitative characteristics. Therefore, genetically divergent genotypes could be utilized for crop improvement in taro and can be developed improved cultivar in colocasia genotypes.

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