

Studies on Genetic Variation for Yield and its Attributing Characters in Taro (*Colocasia esculenta* var. *antiquorum* L. Schott)

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Abstract: The present investigation was carried out to studies the genetic variation, heritability and genetic advance for important yield attributing traits involving 24 selected taro (including check) germplasm of colocasia in a complete randomized block design with three replication during summer season of 2018 and 2019. The estimation of genetic variation observed that there was significant genetic variation in the experiment. Among all the genotypes evaluated, genotype IGCOL-GB-17-1 was recorded highest cormels and corms yield ha⁻¹ followed by IGCOL-LHDD-18-1 suitable to further crop improvement programme. Among the attributes studied, high PCV and GCV were observed for characters like number of suckers plant⁻¹ (46.80 and 46.23 respectively), Leaf Area Index (43.90 and 42.70 respectively) and corm yield plant⁻¹ (43.04 and 42.66 respectively) indicating high variability available in the genotypes for these characters for further improvement. A high heritability (>60 %) coupled with high genetic advance was observed for LAI, number of suckers plant⁻¹ and corm yield plant⁻¹ which suggested that there may be presence of additive gene action and selection will be beneficial for improving of such characters.

INTRODUCTION

Colocasia (*Colocasia esculenta* var. *antiquorum* L. Schott) also known as 'Taro' is one of the oldest known tuber crop and has been grown for more than 10,000 years ago in Tropical Asia (Lebot, 2009). It is a tropical tuber crop belongs to the monocotyledonous own family *Araceae* of the order *Arales* whose participants are called aroids (Henry, 2001). *Araceae* includes about 100 genera and 1500 widely distributed species. It has been probably originated as of the wet tropical place flanked by India and Indonesia (Matthews, 2004) and has been cultivated within the South Pacific for hundreds of years (FAO, 1992). *Colocasia* grows wild in tropical Asia, extending as far as east as New Guinea region near Indonesia and possibly Northern Australia. Taro serves as staple

supply of diet for community in the region of the globe and it is the fourteenth mainly enthusiastic vegetable globally (Rao *et al.*, 2010). Worldwide taro is grown in an area of approximately 1.35 M ha in the midst of a yearly production of 10.2 MT and average productivity of 6.82 t/ha. In Asia, average yields reach 12.6 t ha⁻¹ (Anonymous, 2019).

Available literature expressed that, an insufficient systematic breeding effort for developing the quantifiable traits in taro has been concluded so a ways and a small number of indigenous cultivars are handy for its growing. Hence, a dire need had once felt for systematic breeding work for improvement of taro specifically in Chhattisgarh which is blessed with the adequate variety of taro. In view of this the knowledge of genetic variability, heritability

and genetic advance of important economic characters and their genotypic and phenotypic correlation coefficients amongst themselves play a significant role in framing the breeding works of the any crops. The achievement of breeding work depends largely on the genetic variability, which is existing in the population. Hence, segregation of the phenotypic variance in to the genetic & environmental variance is essential. The amount of transmission of quantitative traits from parent to the offspring depends upon the heritability (h^2b) of the particular traits. The value alone does no longer have much importance as it fails to account for the magnitude of absolute variability. It is therefore crucial to make use of heritability along with genetic improve whilst predicting for selection. A large amount of the agro-nomically essential traits inclusive of yield are poly genetically and are maximum effects by environmental factors. In view of the fact that yield is a complex trait dependent on several to huge number of component characters.

The same genotypes were raised during 2017-18 for another season evaluation and tubers were planted on 07th February 2019 with the same design and plot size and similar agronomic practices.

MATERIALS AND METHODS

The experiments were conducted at SG, College of Agriculture and Research Station, IGKV, Instructional cum Research Farm, Kumhrawand, Jagdalpur, Bastar, Chhattisgarh during the summer season from 1st year February to August 2018 and 2nd year during February to August 2019. The experiment was laid out in Randomized Complete Block Design (RCBD) with 24 genotypes of colocasia grown in three replications. The genotypes were grown randomly in each replication/block in a total of 72 plots at 3m x 3m spacing each containing 50 plants per plot at each locations.

Estimation of genetic parameters

a) Component of variance

(i) Phenotypic Variance

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

(ii) Genotypic Variance

$$\sigma_g^2 = \frac{TMS - EMS}{r} = \sigma_p^2 - \sigma_e^2$$

(iii) Environmental Variance

$$\sigma_e^2 = EMS = \sigma_p^2 - \sigma_g^2$$

b) Coefficient of Variation

The genotypic and phenotypic Coefficient of variance was calculated as per the formulae of Burton, (1952)

(a) Genotypic Co- efficient of variation

$$GCV(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

(b) Phenotypic Co- efficient of variation

$$PCV(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

2. Heritability in broad sense [h^2b] (per cent)

Heritability in broad sense in per cent was estimated as per Burton (1952).

$$h^2(bs) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

As suggested by Johnson *et al.* (1955), $h^2(b)$ estimates were categorized

Low= 0 -30%

Moderate = 31-60%

High= 61% and above

Genetic advance as per cent of mean (GAM)

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K.h^2(b).\sigma_p$$

Genetic advance as per cent for mean

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed as follows.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

- Low = Less than 10%
 Moderate = 10-20%
 High = More than 20%

RESULTS AND DISCUSSIONS

Analysis of Variance

The analysis of variance of all the characters under study is presented in Table 1. This analysis of variance revealed that mean sum of squares due to genotypes was highly significant for all the characters over all the locations studied. This is an indication of existence of sufficient variability among the genotypes for yield and its components traits is in directive of applying various analyses in the material. Significant mean sum of squares due to yield and attributing characters revealed existence of considerable variability in materials studied for improvement for various traits. These findings are in general agreement with the findings of Chand *et al.* (1987), Muluaem and Weldemichael (2013), Tewodros (2013) and Bhanuprakash *et al.* (2019)

The environmental coefficients of variation (ECV), genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), heritability, genetic advance and expected genetic advance as per cent of mean (GAM) for the different characters were studied and presented in Table 2. The estimates of phenotypic variance were greater than the corresponding estimates of genotypic variance for all the traits, indicating thereby, the influence of environment in the expression of these traits. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) for all the traits under study.

Coefficient of Variance

Phenotypic variance was higher than the genotypic and environmental variances. Similarly, phenotypic coefficient of variation was higher in magnitude than the genotypic coefficient of variation also had higher genotypic

coefficient of variation. In Table 1, the highest value of environmental coefficient of variation was recorded for leaf area index (9.46) followed by number of cormels plant⁻¹ (9.05), girth of pseudo-stem (8.11), number of suckers plant⁻¹ (7.45), cormel length (6.97), cormel weight g (5.86) and corm yield plant⁻¹ (5.73), whereas corms and cormels yield ha⁻¹ had the lowest ECV (3.35). The highest value of PCV was found for number of suckers plant⁻¹ (46.80) followed by leaf area index plant⁻¹ (43.90), corm yield plant⁻¹ (43.04), cormels yield plant⁻¹ (39.17), corms & cormels yield plant⁻¹ (37.66), corm length (26.31) and number of cormels plant⁻¹ (25.68). The lowest PCV had recorded for dry matter per cent cormel (4.90). The highest value of GCV was recorded for number of suckers plant⁻¹ (46.23) followed by leaf area index plant⁻¹ (42.70), corm yield plant⁻¹ (42.66), cormels yield plant⁻¹ (38.86), corms & cormels yield ha⁻¹ (37.51), corm length (cm) (25.88) and number of cormels plant⁻¹ (24.04), whereas dry matter per cent of cormel had the lowest GCV (2.60).

The estimates of moderate PCV and GCV, high heritability coupled with high GAM were observed for this trait indicated the preponderance of additive gene action governing the inheritance of this character and offers the possibility of improvement through direct selection. These finding are in accordance with findings of Mukherjee *et al.* (2003) Pandey *et al.* (2009), Paul *et al.* (2011), Choudhary *et al.* (2011), Muluaem and Weldemichael (2013), Tewodros *et al.* (2013), Bhattacharjee *et al.* (2014), Poddar *et al.* (2015), Eze and Nwofia (2016a), Ashok *et al.* (2017) in sweet potato, Singh *et al.* (2017) and Narayan *et al.* (2018) in taro.

The estimates of PCV and GCV were low for this trait which is in accordance with the findings of Choudhary *et al.* (2011), Tewodros *et al.* (2013) and Mukherjee *et al.* (2016) in taro whereas, Alam *et al.* (2014) in greater yam. The high PCV and GCV for number of suckers plant⁻¹ revealed that variation among the genotypes was also high. High PCV for this trait was in accordance with the findings of Chand *et al.* (1987). The results were in accordance with findings of Alam *et al.* (2014) in greater yam, Kumar *et al.* (2017), Yadav *et al.* (2017) in taro, Bhanuprakash (2018) in taro.

Table 1: Analysis of variance for yield and its component characters in colocasia: during 2018 and 2019

S. No.	Traits	Mean sums of square		
		Replicate	Treatments	Error
	df	2	23	46
1	Plant height (cm)	2.30	514.59**	7.23
2	No. of suckers Plant ⁻¹	0.01	1.40**	0.01
3	Petiole length (cm)	6.72	197.36**	4.10
4	Girth of pseudo-stem (cm)	0.18	1.21**	0.09
5	LAI	0.00	0.54**	0.01
6	No. of cormels plant ⁻¹	0.22	12.74**	0.57
7	Cormel length (cm)	0.12	2.15**	0.15
8	Cormel girth (cm)	0.07	0.18**	0.01
9	Cormel weight (g)	5.61	80.80**	2.17
10	Cormels yield Plant ⁻¹ (g)	51.52	10565.33**	55.74
11	Dry matter % of cormel	1.29	2.64*	1.21
12	Corm length (cm)	0.18	7.96**	0.09
13	Corm girth (cm)	0.14	1.03**	0.04
14	Corm yield plant ⁻¹	55.85	6530.08**	39.04
15	Dry matter % of corm	4.05	12.55**	1.34
16	Corms & cormels yield ha ⁻¹	37.55	8921.69**	23.67

* & ** Significant at 5% & 1% respectively

Heritability (h²b)

Heritability in broad sense was estimated for all the 16 traits under study and presented in Table 2. In the location-Jagdarpur the magnitude of heritability ranged from 28.11% to 99.21%. The corms & cormels yield ha⁻¹ had the high heritability estimate (99.21%) followed by cormels yield plant⁻¹ (98.43%), corm yield plant⁻¹ (98.23%), number of suckers plant⁻¹ (97.46%), corm length (96.73%), plant height (95.90%) leaf area index (95.35%) petiole length (94.01%) and cormel weight (92.34%). The moderate heritability was estimated in the characters *viz.*, corm girth (88.49%), number of cormels plant⁻¹ (87.59%), cormel girth (84.44%), and dry matter per cent of corm (73.67%). The low heritability was estimated for character dry matter per cent of cormel (28.11%).

The heritability value alone however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. The heritability estimates would be reliable; if it is limited in broad sense and h²b along cannot give reliable gain. It indicates the preponderance of additive and non additive gene effect if accompanied with high genetic advance. To facilitate the comparison of progress in various characters of different genotypes genetic advance was calculated as percentage of mean.

High heritability in conjunction with high GAM was observed for corms & cormels yield ha⁻¹ trait which indicated the role of additive gene action governing the inheritance of this trait and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects. These findings are in agreement with Mukherjee *et al.* (2003), Cheema *et al.* (2007), Choudhary *et al.* (2011), Paul *et al.* (2011), Devi *et al.* (2013), Bhattacharjee *et al.* (2014), Alam *et al.* (2014) in greater yam, Eze and Nwofia (2016a), Kumar *et al.* (2017) and Yadav *et al.* (2017) in taro cultivars.

Presence of moderate to high heritability is in agreement with Choudhary *et al.* (2011), Tewodros *et al.* (2013), Poddar *et al.* (2015), Kumar *et al.* (2017), and Yadav *et al.* (2017) in taro, Paul *et al.* (2011) in aqua edible aroids cultivars and Paul *et al.* (2011) in aqua edible aroids and Muluaem and Weldemichael (2013) in aerial yams,

Genetic advance as percentage of mean

The magnitude of genetic advance as percentage of mean ranged from 2.83% to 93.96% (Table 2) estimated for all 16 characters in colocasia.

The character number of suckers plant⁻¹ showed higher genetic advance (93.96%) followed by character *viz.*, corm yield plant⁻¹

Table 2: Genetic parameters of variance for corms & cormels yield and its components characters: pooled mean of colocasia

S. No.	Traits	Mean	Range		Coefficient of Variation (%)			$I^2 b$ (Broad Sense)	Genetic Advancement 5%	GA as percent of mean 5%
			Min ^m	Max ^m	ECV	GCV	PCV			
1	Plant height (cm)	73.52	61.03	105.36	3.66	17.69	18.06	95.90	26.23	35.68
2	No. of suckers plant ⁻¹	1.47	38.56	67.75	7.45	46.23	46.80	97.46	1.38	93.96
3	Petiole length (cm)	48.68	38.56	67.75	4.16	16.49	17.00	94.01	16.03	32.93
4	Girth of pseudo-stem (cm)	3.60	2.67	4.95	8.11	16.98	18.84	81.45	1.14	31.61
5	LAI	0.98	0.55	2.18	9.46	42.70	43.90	95.35	0.85	86.23
6	No. of cormels plant ⁻¹	8.38	6.26	12.67	9.05	24.04	25.68	87.59	3.88	46.34
7	Cormel length (cm)	5.46	4.47	7.48	6.97	14.99	16.53	82.20	1.53	27.99
8	Cormel girth (cm)	2.78	2.33	3.22	3.65	8.50	9.26	84.44	0.45	16.10
9	Cormel weight (g)	25.14	15.97	35.80	5.86	20.36	21.19	92.34	10.13	40.31
10	Cormels yield plant ⁻¹ (g)	152.32	52.26	301.58	4.90	38.86	39.17	98.43	120.97	79.42
11	Dry matter% of cormel	26.55	25.39	28.32	4.15	2.60	4.90	28.11	0.75	2.83
12	Corm length (cm)	6.26	4.57	9.63	4.75	25.88	26.31	96.73	3.28	52.43
13	Corm girth (cm)	5.53	4.66	6.54	3.74	10.38	11.03	88.49	1.11	20.11
14	Corm yield plant ⁻¹	109.04	63.23	200.37	5.73	42.66	43.04	98.23	94.97	87.10
15	Dry matter % of corm	25.23	22.33	28.46	4.58	7.66	8.93	73.67	3.42	13.55
16	Corms & cormels yield ha ⁻¹	145.20	82.44	278.86	3.35	37.51	37.66	99.21	111.74	76.96

(87.10%), leaf area index (86.23%), cormels yield plant⁻¹ (79.42%) and corms & cormels yield ha⁻¹ (76.96%). Similarly moderate GA as percentage of mean was recorded for the characters corm length (52.43%), number of cormels plant⁻¹ (46.34%), cormel weight (40.31%) plant height (35.68%), petiole length (32.93%) and girth of pseudo stem (31.61%). The rest of the characters exhibited low magnitude of genetic advance as per cent of mean were *viz.*, cormel length (27.99%), corm girth (20.11%), cormel girth (16.10%) and dry matter per cent of cormel had the lowest magnitude of GA in colocasia (2.83%).

The genetic advance is a useful measure to predict genetic gain at specified selection intensity, but when it is considered along with h^2 becomes more valuable from selection point of view and to predict response to selection. The heritability value alone, however, provides no indication of the amount of genetic improvement that would result from selecting the best individuals. Hence, genetic gain in quantitative traits can be predicted only when heritability and genetic advance over mean are considered together (Johnsen *et al.*, 1955)

High h^2 estimates coupled with high GAM was recorded for number of suckers plant⁻¹ followed by corm yield plant⁻¹ in location Jagdalpur and Kanker, while high GAM was recorded for corm yield plant⁻¹ in location Dantewada. Thus, it is apparent from the present finding that, these traits being governed by additive gene and their effects could be exploited for improving corms and cormels yield and its attributes in colocasia. Also, early selection for these traits would be precious for accumulating desirable genes in selected genotypes. Similar finding had also been reported by Mukherjee *et al.* (2003), Choudhary *et al.* (2011) in taro, Paul *et al.* (2011), Devi *et al.* (2013), Bhattacharjee *et al.* (2014), Choudhary *et al.* (2011), Tewodros *et al.* (2013), Alam *et al.* (2014) in greater yam Bhattacharjee *et al.* (2014), Mukherjee *et al.* (2016), Kumar *et al.* (2017), Yadav *et al.*, (2017) in taro genotypes.

Moderate to high GAM for this trait were in accordance with the findings of Singh *et al.* (2003), Alam *et al.* (2014) in greater yam, Kumar *et al.* (2017) and Ashok *et al.* (2017).

The estimates of PCV and GCV were low for this dry matter per cent of cormel which is in accordance with the findings of Tewodros *et al.* (2013), Choudhary *et al.* (2011) and Mukherjee *et al.* (2016) in taro whereas, Alam *et al.* (2014) in greater yam. High heritability in conjunction with moderate to high GAM was observed for this trait indicating the role of additive gene action governing the inheritance of the trait and offers the best possibility of improvement through progeny selection or any modified selection procedures aiming to exploit the additive gene effects. Presence of moderate to high heritability is in agreement with Cheema *et al.* (2007), Choudhary *et al.* (2011), Paul *et al.* (2011) in aqua edible aroids cultivars, Poddar *et al.* (2015) in yam, Ashok *et al.* (2017) in sweet potato and Yadav *et al.* (2017) in taro genotypes.

CONCLUSIONS

The data of ANOVA revealed the significant difference between the evaluated genotypes in almost all traits. The PCV evaluation was higher than GCV estimation for all the observed traits. The number of suckers plant⁻¹, LAI, corm yield plant⁻¹ and cormels yield plant⁻¹ revealed a wide range of PCV and GCV as well as high broad-sense heritability that indicated these characters to have additive gene effect and more reliable for successful selection. In a population, a population with a broad GCV is effective for selection to obtain superior variety. The 24 genotypes can be utilized in assembling varieties especially for traits which have a broad GCV value. **Hence, these accessions may be finalized for further breeding programme.**

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