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Screening of taro (*Colocasia esculenta* L.) genotypes for yield optimization and related traits in Nagaland

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ABSTRACT

Colocasia commonly known as taro holds significant agricultural, nutritional, and ecological value, particularly in Mon district, Nagaland. The crop is a staple among the Konyak Naga tribe, thriving in the region’s agro-climatic conditions. This study aimed to assess genetic variability, yield traits, and storage potential of 18 Colocasia genotypes collected from varying altitudes. Observations were made on physicochemical, biometrical, and storage traits. High genotypic and phenotypic variation was recorded for traits like weight of corm per plant, number of cormels per plant, and yield per hectare, indicating significant scope for selection and improvement. Most of the traits were recorded high heritability, with high genetic advance observed in parameters such as corm weight and starch content, suggesting additive genetic influence. Correlation and path analysis revealed that weight of corms and cormels had the most substantial positive effects on yield. This variability underscores the potential of Colocasia for sustainable agricultural practices and food security, warranting further research and conservation.

Keywords: Colocasia, Genetic variability, Heritability, Correlation, Sustainable agriculture

INTRODUCTION

Colocasia (*Colocasia esculenta* L.), commonly known as taro, is an ancient crop with significant cultural, nutritional, and agricultural importance. Originating in the Indo-Malayan region, likely in eastern India and Bangladesh, it has adapted to diverse agro-climatic conditions, making it a staple in tropical and subtropical regions (Matthews, 1991). Known for its enlarged starchy roots, taro is cultivated for its corms and cormels, which are rich in starch, protein, and minerals. Additionally, its leaves and petioles, rich in provitamins A and C, are used as vegetables in many cuisines (Chopra *et al.,* 1956). Taro contributes to sustainable agriculture by requiring minimal inputs like fertilizers and pesticides, which reduce environmental hazards. It aids in soil health improvement through symbiotic relationships with nitrogen-fixing bacteria and plays a role in erosion control due to its extensive root system and dense foliage. Moreover, its ability to thrive in wetlands and marshy areas makes it an efficient crop for filtering pollutants and sequestering atmospheric carbon dioxide, further enhancing its ecological value (Jolly *et al.,* 2010). Despite its global significance, the potential of taro remains underexplored, particularly in terms of genetic variability and genotype suitability for different agro-climatic zones. The northeast region of India, especially Mon district of Nagaland, serves as a reservoir of colocasia diversity, hosting both cultivated and wild species in jhum fields, homestead gardens, and riverbanks (Thirugnanavel *et al.,* 2013). Mon district, a biodiversity hotspot, has ideal conditions for colocasia cultivation. However, the conservation and characterization of landraces remain neglected. With colocasia as a staple food in Konyak households, there is an urgent need to study its genetic variability to identify high-yielding and quality genotypes.

The evaluation of genetic variability within colocasia germplasm is vital for estimating the potential genetic improvement achievable through breeding for traits like yield, environmental adaptation, and quality (Yen and Wheeler, 1968). The yield of colocasia is influenced by complex interactions between genotype, environment, and soil conditions. Therefore, direct reliance on heritability for selecting high-yielding genotypes may be limiting. A combination of biometrical analysis, correlation studies, and path coefficient analysis provides insights into traits that

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substantially impact yield and adaptability. Consequently, the current study was conducted on 18 Colocasia genotypes collected from Mon district of Nagaland to characterise, assess variability, and examine trait associations to identify elite lines with high yield potential.

MATERIALS AND METHODS

The study was conducted during 2017-2018 at the experimental farm of the School of Agricultural Sciences (SAS), Nagaland University, Medziphema, Nagaland, India. The experimental site is located in the foothills of Nagaland, at an altitude of 304.8 meters above mean sea level, and lies between 25°45'43"N latitude and 93°53'04"E longitude. The climate is subtropical with high humidity (70-80%), moderate temperatures, and average annual rainfall ranging from 2000 to 2500 mm. The study used a randomized complete block design (RCBD) with three replications to account for soil fertility variability. Eighteen Colocasia genotypes were collected from different altitudes in Mon district, Nagaland (foothills, mid-hills, and high hills). Each genotype was planted in 3m × 1.8m plots with a spacing of 60 × 45 cm, containing 20 plants per plot. Standard agricultural practices were followed, including field preparation (ploughing, harrowing, and levelling) and the application of farmyard manure (10 t/ha). Fertilization included urea, single super phosphate, and muriate of potash at 100 kg N, 60 kg P_2O_5, and 80 kg K_2O per hectare. Nitrogen was applied in two splits, with half before planting and the rest 30 days later. Intercultural operations like weeding and earthing up were carried out, with irrigation provided until sufficient rainfall was received. A total of 15 quantitative characters of Colocasia were taken for experimentation. For each characteristic, data were gathered from five randomly sampled plants from each genotype and in each replication. The quantitative data encompassed various traits, including, plant height (cm), number of leaves, LAI, no of suckers per plant, no. of corms per plant, no of cormels/plant, weight of corm/plant(g), weight of cormels/plant(g), moisture content (%), protein content (%), vitamin C (mg/100g), starch content (%), oxalic acid (%), yield/plot (kg) and yield/ha (q).

Table 1: Details of the place of collection of genotypes

Sl. No.	Local Name	Place of collection	Latitude, Longitude & Altitude	
1.	Nalon	Tekang	26°53’56” N& 95°4’39” E	Foothill Region
2.	Tosat	Tizit	26.903287°N&95.08262°E	
3.	Tomei	Ngangting	26°53’56” N& 95°4’39” E	
4.	Poangmen Along	Ngangting	26.8102°N & 94.8048°E	
5.	Tiru Baishi	Tiru	26.8820°N& 94.8819°E	
6.	Kongan Tongnyak	Kongan Naginimora	26.7457°N& 94.8127°E	
7.	Tongmok	Chohnyu	26.546066°N& 95.05719°E	Mid hill Region
8.	Hoakto	Leangha	26.5787°N& 95.0527°E	
9.	Muksang	Sheanghah	26.66661°N& 94.98926°E	
10.	Bahnuh	Chenwetnyu	26.5913°N& 94.8986°E	
11.	Tongmih	Tuimei	26.5809°N& 95.0790°E	
12.	Tongphak	Totok Chingnyu	26.5913°N&94.8986 °E	
13.	Pangtong	Kenchenshu	26.4530°N& 94.9891°E	High Hill Region
14.	Hentong	Yonghong	26.3789°N& 95.0463°E	
15.	Yakteeen	Changlangshu	26.4533°N& 94.9872°E	
16.	Eang	Tobu	26.4208°N& 95.0136°E	
17.	Bujong	Tobu	26.3628°N& 94.9349°E	
18.	Tongshe	Monnyakshu	26.3628°N& 94.9349°E	

Statistical analysis

Data were subjected to analysis of variance (ANOVA) using the OPSTAT open-source software to evaluate treatment effects. The phenotypic, genotypic, and environmental coefficients of variation were computed as per the methodology outlined by Burton (1952). Heritability estimates in the broad sense were determined following the approach of Allard (1960), while the expected genetic advance under selection was calculated according to the formula proposed by Johnson *et al.* (1955). Phenotypic and genotypic correlation coefficients between traits were analyzed based on the method described by Al-Jibouri *et al.* (1958). Additionally, genotypic correlations were partitioned into direct and indirect effects using path coefficient analysis as suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Mean and range

The mean and range values for various traits in Colocasia indicate significant variability, reflecting the genetic diversity present in the population as shown in Table 2. Plant height showed a mean of 71.35 cm, with a range of 47.24 to 98.43 cm, suggesting a wide variability among genotypes. The number of leaves averaged 14.04, ranging from 6.06 to 21.11, demonstrating a considerable spread, likely influenced by genetic or environmental factors. Leaf area index (LAI) had a lower mean of 0.20, with a narrow range (0.13-0.28), indicating minimal variation. The number of suckers per plant ranged widely (2.06–6.11) with a mean of 4.18, highlighting potential for selection. Similarly, the number of corms per plant averaged 1.65 (1.14 to 2.42), and the number of cormels per plant had a mean of 6.91 with a broad range (2.82 to 11.25), suggesting high genetic variability. Weight of corms per plant (185.68 g) and cormels per plant (227.56 g) showed substantial ranges (105.6 to 430.94 g and 94.49 to 363.89g, respectively), emphasizing their potential for improvement. Moisture content exhibited moderate variability with a mean of 71.65% (48.61 to 84.46%), while protein content (2.11%, 1.23 to 2.44%) and vitamin C (112.5 mg/100g, 91.52 to 134.04 mg) demonstrated narrower ranges. Starch content showed a mean of 13.24% (10.52 to 16.87%), and oxalic acid averaged 0.58% (0.30 to 0.83%), both with moderate variability. Yield per plot (9.05 kg, 5.64 to 12.93 kg) and yield per hectare (166.18 q, 104.29 to 241.49 q) reflected high genetic diversity, indicating scope for selection. These results collectively suggest that traits with wide ranges, such as weight of corms, number of cormels, and yield, offer substantial potential for genetic improvement through breeding programs. Similar findings were reported by Yimchunger *et al.* (2018) and Patton *et al.* (2024).

Genetic variability analysis

The study of genetic variability, heritability, and genetic advance provides valuable insights for crop improvement. In this study, traits of Colocasia were analyzed to estimate phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as a percentage of the mean (GAM). Results indicate significant genetic variability and high potential for selection in several yield related traits. The PCV and GCV values were computed to differentiate environmental influence from total variability, enabling accurate genotype identification. Traits were categorized as having low (<10%), moderate (10-20%), and high (>20%) variability following Sivasubramanian and Madhavamenon (1973). High variability was observed in weight of corm per plant (46.48%, 45.91%), number of cormels per plant (31.40%, 30.47%), weight of cormel per plant (31.29%, 30.68%), number of suckers per plant (29.13%, 27.88%), number of leaves (28.32%, 27.32%), number of corm (26.72%, 24.22%), and yield per hectare (21.90%, 21.28%). Moderate variability was recorded for moisture content (15.92%, 14.89%), vitamin C (15.04%, 9.73%), protein content (14.90%, 13.66%), and starch content (14.43%, 12.93%). The narrow differences between PCV and GCV for most traits suggest minimal environmental influence, with high variability traits demonstrating greater potential for improvement through selection. Similar findings were reported by Vinutha *et al.* (2015), Pratibha *et al.* (2013), and Juri *et al.* (2013). Heritability (h^2bs) estimates the proportion of genetic variance to total variance, while genetic advance (GA) predicts potential improvement after selection. High heritability indicates the predominance of genetic factors in trait expression but must be considered alongside GA for effective breeding strategies. High heritability (>60%) was observed for all traits, with the highest in weight of corm per plant (97.6%), weight of cormel per plant (96.1%), and yield per plant (94.5%). High GAM (>20%)

was recorded for weight of corm per plant (93.42%), weight of cormel per plant (61.95%), number of cormels per plant (60.90%), number of suckers (54.96%), number of leaves (54.90%), and yield per hectare (42.61%), while moderate GAM (10-20%) was observed for Vitamin C (12.98%) as shown in Table 2. High heritability coupled with high GAM indicates additive gene effects, making traits such as weight of corm, weight of cormel, and number of cormels ideal for selection. Moderate GAM suggests both additive and non-additive genetic effects. The results align with earlier studies by Vinutha *et al.* (2015), Pratibha *et al.* (2013), and Juri *et al.* (2013). The high PCV, GCV, heritability, and genetic advance for key yield related traits in Colocasia suggest substantial genetic variability and potential for improvement through selection. Traits governed by additive genes can be effectively targeted in breeding programs, ensuring significant genetic gains.

Table 2: Genetic parameters of yield and its component characters in Colocasia

Characters	Mean± SE(m)	Range		Coefficient of variability (%)		Heritability (h^2)	Genetic Advance as % of mean (Genetic gain)
		Min.	Max.	PCV	GCV		
Plant height	71.35	47.24	98.43	22.02	21.26	93.2 %	42.29
Number of leaves	14.04	6.06	21.11	28.32	27.32	93.1%	54.29
LAI	0.20	0.13	0.28	24.66	20.24	67.3%	34.21
No of suckers per plant	4.18	2.06	6.11	29.13	27.88	91.6%	54.96
No. of corms per plant	1.65	1.14	2.42	26.72	24.22	82.2%	45.24
No of cormels/plant	6.91	2.82	11.25	31.40	30.47	94.1%	60.90
Wt. of corm/plant(g)	185.68	105.6	430.94	46.48	45.91	97.6%	93.42
Wt. of cormels/plant(g)	227.56	94.49	363.89	31.29	30.68	96.1%	61.95
Moisture content (%)	71.65	48.61	84.46	15.92	14.89	87.5%	28.69
Protein content (%)	2.11	1.23	2.44	14.92	13.66	83.8%	25.77
Vit. C (mg/100g)	112.5	91.52	134.04	15.04	9.73	41.9%	12.98
Starch content (%)	13.24	10.52	16.87	14.43	12.93	80.3%	23.86
Oxalic acid (%)	0.58	0.30	0.83	23.97	21.23	78.4%	38.72
Yield/plot (kg)	9.05	5.64	12.93	22.11	21.44	94.0%	42.81
Yield/ha (q)	166.18	104.29	241.49	21.90	21.28	94.5%	42.61

Correlation studies

In the study, it was found that the traits *viz.* plant height, which exhibited positive phenotypic correlations with LAI (0.72) and number of suckers (0.49), and negative correlations with number of cormels (-0.56) and weight of cormels (-0.56), show notable associations with yield related traits. Number of leaves, with phenotypic correlations of 0.81 with number of suckers, 0.45 with weight of corm per plant, and 0.56 with yield per hectare, also demonstrated strong genotypic correlations with starch content (0.53), protein content (0.32), and yield per hectare (0.52). LAI showed positive phenotypic associations with plant height (0.72) and negative correlations with weight of cormels (-0.50) and protein (-0.44), while genotypically it correlated with weight of corm (0.48) and oxalic acid (-0.48). Weight of corm per plant had strong phenotypic and genotypic correlations with starch content (0.49 and 0.58) and yield per hectare (0.80 and 0.85), and negative correlations with oxalic acid (-0.64 and -0.84, respectively). Protein content showed positive phenotypic correlations with weight of cormels (0.47) and starch content (0.50), and genotypically with yield per hectare (0.51). Yield per hectare exhibited strong phenotypic correlations with weight of corm (0.80), moisture (0.31), and starch content (0.65), and genotypically with ascorbic acid (0.30) and negative correlations with oxalic acid (-0.74) as shown in table 3. In conclusion, the genotypic correlations generally being stronger, indicating a higher genetic association and the traits *viz.* plant height, number of leaves, LAI, and weight of corm per plant show positive correlations with yield-related traits, while certain traits like oxalic acid and number of cormels exhibit negative correlations. These findings underscore the importance of these traits in improving both yield and quality in

Table 3: Correlation coefficient (r) between 13 characters of Colocasia

Correlation Studies (Phenotypic/Genotypic)													
Traits (P/G)	Plant height	No. of leaves	LAI	No. of suckers/ plant	No. of corms/ plant	No. of cormels/ plant	Wt. of corm/ Plant (g)	Wt. of cormels/ Plant (g)	Moisture (%)	Protein (%)	Vit. C (mg/ 100g)	Starch content (%)	Oxalic acid (%)	Yield/ ha (q)
Plant height	1	0.31	0.72	0.49	-0.15	-0.56	0.31	-0.56	0.20	-0.37	-0.08	-0.21	-0.28	0.05
		0.32	0.91	0.51	-0.21	-0.60	0.32	-0.58	0.21	-0.44	-0.10	-0.22	-0.35	0.04
No. of leaves		1	0.15	0.81	0.25	0.28	0.45	0.31	0.05	0.30	-0.15	0.46	-0.14	0.50
			0.14	0.86	0.27	0.30	0.47	0.33	0.05	0.32	-0.20	0.53	-0.15	0.52
LAI			1	0.35	-0.14	-0.37	0.40	-0.50	0.22	-0.44	0.12	-0.13	-0.37	0.12
				0.39	-0.18	-0.43	0.48	-0.62	0.30	-0.57	0.23	-0.14	-0.48	0.10
No. of suckers/plant				1	0.09	0.07	0.28	0.10	0.13	-0.04	-0.26	0.35	-0.09	0.24
					0.11	0.09	0.30	0.10	0.11	-0.05	-0.34	0.39	-0.03	0.25
No. of corms/plant					1	0.64	0.12	0.71	-0.13	0.25	0.19	0.25	-0.03	0.37
						0.73	0.10	0.77	-0.13	0.34	0.53	0.33	0.02	0.39
No. of cormels/plant						1	0.08	0.87	-0.21	0.42	0.12	0.40	0.18	0.31
							0.09	0.90	-0.22	0.48	0.19	0.45	0.20	0.33
Wt. of corm/plant(g)							1	-0.10	0.27	0.32	0.27	0.49	-0.73	0.80
								-0.12	0.28	0.36	0.43	0.58	-0.84	0.85
Wt. of cormels/plant (g)								1	-0.23	0.47	-0.03	0.35	0.24	0.30
									-0.23	0.52	-0.03	0.39	0.25	0.30
Moisture (%)									1	-0.06	0.13	0.36	-0.27	0.31
										-0.02	0.11	0.40	-0.33	0.37
Protein (%)										1	0.15	0.50	-0.12	0.48
											0.17	0.63	-0.21	0.51
Vit. C (mg/100g)											1	0.17	-0.32	0.17
												0.37	-0.50	0.30
Starch content (%)												1	-0.23	0.65
													-0.27	0.72
Oxalic acid (%)													1	-0.64
														-0.74

Table 4: Direct and Indirect effect of yield component on yield per ha at Genotypic level in colocasia

Genotypic Path Studies													
Traits	Plant height	No. of leaves	LAI	No. of suckers/ plant	No. of corms/ plant	No. of cormels /plant	Wt. of corm/ plant (g)	Wt. of cormels/ plant(g)	Moisture (%)	Protein (%)	Vit. C (mg/ 100g)	Starch content (%)	Oxalic acid (%)
Plant height	-0.18	-0.06	-0.17	-0.09	0.04	0.11	-0.06	0.11	-0.04	0.08	0.02	0.04	0.06
No. of leaves	-0.04	-0.11	-0.02	-0.10	-0.03	-0.03	-0.05	-0.04	-0.01	-0.04	0.02	-0.06	0.02
LAI	-0.39	-0.06	-0.42	-0.17	0.07	0.18	-0.20	0.26	-0.13	0.24	-0.10	0.06	0.20
No. of suckers/plant	-0.20	-0.34	-0.16	-0.40	-0.04	-0.03	-0.12	-0.04	-0.05	0.02	0.14	-0.16	0.01
No. of corms/plant	-0.10	0.13	-0.08	0.05	0.48	0.35	0.05	0.37	-0.06	0.16	0.25	0.16	0.01
No. of cormels/plant	0.92	-0.45	0.66	-0.13	-1.12	-1.53	-0.13	-1.37	0.33	-0.73	-0.29	-0.69	-0.30
Wt. of corm/plant(g)	0.76	1.11	1.14	0.72	0.23	0.20	2.37	-0.28	0.67	0.86	1.01	1.37	-1.99
Wt. of cormels/plant(g)	-0.91	0.52	-0.96	0.16	1.19	1.39	-0.18	1.55	-0.36	0.81	-0.04	0.60	0.39
Moisture (%)	0.04	0.01	0.05	0.02	-0.02	-0.04	0.05	-0.04	0.17	-0.004	0.02	0.07	-0.06
Protein (%)	0.34	-0.25	0.44	0.04	-0.27	-0.38	-0.29	-0.41	0.02	-0.78	-0.13	-0.50	0.17
Vit. C (mg/100g)	0.03	0.07	-0.08	0.12	-0.18	-0.06	-0.14	0.01	-0.04	-0.06	-0.33	-0.12	0.17
Starch content (%)	-0.02	0.05	-0.01	0.04	0.03	0.05	0.06	0.04	0.04	0.07	0.04	0.11	-0.03
Oxalic acid (%)	-0.21	-0.09	-0.29	-0.02	0.01	0.12	-0.50	0.15	-0.20	-0.13	-0.30	-0.16	0.60
Yield/ha(q)	0.04	0.52***	0.11	0.25	0.39***	0.33***	0.85***	0.30***	0.37***	0.51***	0.30***	0.72***	-0.74***
Partial R^2	-0.008	-0.0589	-0.0445	-0.098	0.187	-0.5013	2.0047	0.4732	0.0633	-0.3971	-0.1024	0.0762	-0.4477

Residual effect = 0.27

colocasia, aligning with previous studies by Orji and Ogbonna (2015), Pranabjyoti (2007), and Vellayudhan *et al.* (2000). This research provides valuable insights for future breeding and selection programs.

Path coefficient analysis

Path coefficient analysis was carried out at the genotypic level to separate the direct and indirect effects of different yield contributing characters and it was presented in Table 4. This revealed that the maximum positive direct effect on yield per plant was exerted by weight of corm per plant (2.3718), weight of cormels per plant (1.5528), and oxalic acid (0.6036). Conversely, the maximum negative direct effect on yield per plant was observed for number of cormels per plant (-1.5301), followed by protein content (-0.7387) and leaf area index (-0.423). The maximum positive indirect effect on yield per plant was imposed by number of cormels per plant through weight of cormels per plant (1.3946), followed by starch content through weight of corm per plant (1.372) and number of corms per plant through number of cormels per plant (1.1905). The maximum negative indirect effect on yield per plant was imposed by oxalic acid through weight of corm per plant (-1.9921), followed by weight of cormels per plant through number of cormels per plant (-1.3743) and number of corms per plant through number of cormels per plant (-1.1175). These results suggest that selection of genotypes with higher weight of cormels per plant, weight of corm per plant, number of corms per plant, and number of cormels per plant should be prioritized, as all these traits directly or indirectly showed a positive effect on yield, confirming findings from Orji and Ogbonna (2015), Pranabjyoti (2007), and Vellayudhan *et al.* (2000).

Conclusion

In the present study, traits *viz.* plant height, number of leaves, number of suckers, number of cormels, weight of corm per plant, and yield showed high heritability and genetic advance, indicating they are controlled by additive gene effects and are reliable for selection. High phenotypic and genotypic variation in these traits suggests significant scope for improvement. Correlation studies revealed that Leaf Area Index (LAI), number of suckers, weight of cormels, and starch content have strong positive correlations with yield, making them key traits for selection. Path coefficient analysis identified weight of corm per plant and weight of cormels per plant as having the greatest direct impact on yield, highlighting their importance for breeding programs.

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