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Evaluation of morpho-physiological parameters of Arvi [Colocasia esculenta (L.) Schott)] genotypes using multivariate analysis



Rishabh Kumar¹, BS Dogra¹, Nikhil Thakur^{1*}, Jasdeep Kaur², Monica Sharma³ and Sanchita Gautam⁴

¹Department of Vegetable Science, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Solan-173230, Himachal Pradesh, India

²Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishwavidyalaya Palampur-176062, Himachal Pradesh, India

³Department of Plant Pathology, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Solan-173230, Himachal Pradesh, India

⁴Department of Plant Science, Central University of Himachal Pradesh, Shahpur, Kangra-176206, Himachal Pradesh, India

ABSTRACT

The research titled "Evaluation of morpho-physiological parameters of Arvi [Colocasia esculenta (L.) Schott)] genotypes using multivariate analysis" was carried out in Dr. YSP University of Horticulture and Forestry, Solan (H.P). The experiment was laid out in randomized block design comprising 23 diverse genotypes of colocasia, to ascertain the heritability, genetic advance, correlation, path analysis and cluster analysis for yield and other horticultural traits among the genotypes. The PCV and GCV were recorded high for the number of cormels per plant, tuber yield per plot, weight of cormels per plant, plant height and width of cormels and high heritability along with high genetic advance was observed for width of corms, tuber yield per plot, plant height, dry matter percentage in tubers, width of cormels and weight of corms per plant. The correlation coefficient studies showed that tuber yield per plot had a significant and positive correlation with width of corms, number of cormels per plant, length of leaf lamina, number of corms per plant, width of cormels and plant height at both genotypic and phenotypic levels. Path coefficient showed that the maximum positive direct effect on tuber yield per plot was exhibited by width of corms, number of cormels per plant, length of leaf lamina, dry matter percentage in tubers, width of cormels, number of corms per plant and breadth of leaf lamina. The dendrogram reveals three main clusters, each containing multiple sub-clusters based on similarity. Hence, these characteristics should be given more helpful in the selection program of high-yielding genotypes in colocasia.

Keywords: Correlation, Colocasia esculenta, Genotypes, Path coefficient, Selection, Tubers

I.INTRODUCTION

Colocasia (Colocasia esculenta (L.) Schott) is a monocotyledonous plant belongs to the family Araceae, largely cultivated for its edible corms and leaves. All plants and members belonging to the family Araceae are known as aroids [20]. It is very popular crop of ancient times and Indo-Malyalam region. Bangladesh and Eastern India were considered as the native places of origin [22]. Though, colocasia is one of the popular and important edible tuber crops, but still not much attention is still given for genetic improvement of this crop. The introduction about the sexual reproduction of this crop is very fragmentary. Most of the improvement programmes are generally based on genetic variability among various cultivars [10]. The corms and cormels of colocasia are used as vegetables after the thorough cooking because corms are acrid due to the presence of calcium oxalates. The corms of colocasia are rich in starch (13-30%) but contains comparatively low amounts of fats and proteins. Colocasia contains water (63-85 %), proteins (1.3-4.0%), fiber (0.6-1.2%), fats (2.0-4.0%) etc. [5].

*Corresponding Author: Nikhil Thakur

DOI: https://doi.org/10.21276/AATCCReview.2025.13.02.80 © 2025 by the authors. The license of AATCC Review. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/). Path coefficient analysis was used for analyzing the direct and indirect contribution of various independent characters to a dependent character. The correlation coefficient on the other hand indicates the degree and direction of the relationship between two variables but does not provide an insight into the amount of contribution of a trait on another. In turmeric, rhizome yield cannot be improved by direct selection of highyielding genotypes alone but, it also requires a complete study of yield contributing traits and thus path and correlation coefficient are two major statistical techniques to quantify the relation between two traits and for improving tuber yield [12].

II. MATERIALS AND METHODS

The present investigation was carried out in the Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, HP. The experimental material comprised of Colocasia tubers (Local). 23 genotypes (*Table I*) were grown under open field conditions. The experiment was conducted under a randomized Complete Block Design (RCBD) with three replications of each genotype. Rhizomes of different genotypes were planted at a spacing of 30×20 cm in a plot size of 1×1 m which accommodate 16 plants/plot. The standard cultural practices as recommended in the package of practices for vegetable crops were followed to ensure a healthy crop stand [2].

The observations were recorded for plant height (cm), the number of leaves per plant, length of leaf lamina (cm), Breadth of leaf lamina (cm), number of petioles per corm, number of cormels per plant, number of corms per plant, width of corms (cm), width of cormels (cm), weight of cormels per plant (gm), dry matter percentage in tubers (%), disease severity (%) and tuber yield per plot (Kg) from five randomly selected plants in each replication for all characters.

III. RESULTS AND DISCUSSION

The analysis of variance revealed that there were significant differences between genotypes for all of the horticultural traits. Variability among 28 genotypes of pea for each of the traits measured in terms of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent of the mean are given in Table II.

Heritability

Heritability is a concept of transmitting the genetic makeup of a particular species from one generation to another. The genotypic variation is the portion of heritability that is transmitted from parent to progeny. The heritability estimates together with genetic advance provides a better response during selection than either of the parameters alone [7]. High heritability was observed for most of the traits under study for different genotypes ranging from 49.36% to 99.40%. High heritability (>80%) was observed for width of corms per plant (99.40%), tuber yield per plot (99.38%), plant height (98.80%), weight of cormels per plant (96.45%), number of cormels per plant (92.67%), width of cormels per plant (89.72%), weight of corms per plant (89.07%), disease severity (87.10%), length of leaf lamina (86.02%), dry matter percentage in tubers (85.93%). While, Moderate heritability (50-80%) was calculated for the breadth of leaf lamina (74.28%) and leaf number (68.82%). The number of corms per plant (49.36%) recorded a low range of heritability. The observations of the present study were closely supported by [8], [4], [16] and [9].

Genetic Advance

The values of the genetic gain for different characters are presented in Table II. the genetic gain ranged from 15.39% to 84.60% which included high, moderate and low ranges for genetic gain. High range for genetic gain (>50%) was observed for number of cormels per plant (84.60%), followed by tuber yield per plot (74.18%), disease severity (73.22%), plant height (53.72%) and weight of cormels per plant (53.07%). While, moderate magnitude of genetic gain was observed for width of cormels (46.48%), dry matter percentage in tubers (36.58%), leaf number (32.08%), number of corms per plant (30.91%), width of corms (30.91%) and weight of corms per plant (26.66%). The low genetic gain was recorded in the length of leaf lamina (20.61%) and breadth of the leaf lamina (15.39%). Similar findings were also reported by [3], [11], [9], [4] and [8].

Correlation studies

Results of a correlation analysis showed that genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients indicating the inherent association between various characters (figure 1). Phenotypic and genotypic coefficient of correlation revealed that tuber yield per plot showed significant and positive correlation with plant height (0.276, 0.279), length of leaf lamina (0.376, 0.405),

number of cormels per plant (0.856, 0.893), number of corms per plant (0.240, 0.338), width of cormels (0.249, 0.263), weight of corms per plant (0.555, 0.588) and weight of cormels per plant (0.522, 0.538). However, Disease severity was negatively and significantly associated with plant height (-0.346), length of leaf lamina (-0.306), the width of cormels (-0.341) and weight of cormels per plant (-0.467). These results are similar to the findings of [21], [17], [11] and [8].

Path coefficient analysis

The path coefficient analysis quantifies the direct and indirect impact of various independent variables on a dependent variable (Table III). Path coefficient analysis was exercised at genotypic level and revealed that the maximum positive direct effect on tuber yield per plot was observed in (Table III) with width of corms (0.726), number of cormels per plant (0.367), length of leaf lamina (0.233), dry matter percentage in tubers (0.142), width of cormels (0.102), number of corms per plant (0.053) and breadth of leaf lamina (0.028). While, maximum negative direct effects were recorded for the weight of cormels per plant (-0.162), the weight of corms per plant (-0.160), the number of leaves per plant (-0.116), plant height (-0.097) and disease severity (-0.039). These results are similar to the findings of [13], [18], [15], [14], [3] and [19].

Cluster analysis

Hierarchical clustering is a crucial statistical tool for identifying genetic relationships, detecting variability, and assisting in breeding decisions. It provides a structured classification of genetic resources, which is essential for germplasm conservation and selection. The dendrogram reveals three main clusters (figure 2), each containing multiple sub-clusters based on similarity. The first main cluster includes genotypes LC-A-9-18, LC-A-5-18, and LC-A-19-18 in one sub-cluster, while LC-A-8-18, LC-A-7-18, LC-A-16-18, and LC-A-10-18 form another, with LC-A-6-18, LC-A-4-18, and LC-A-13-18 grouped separately. The second main cluster consists of LC-A-17-18, LC-A-15-18, and LC-A-20-18 in one sub-group, LC-A-21-18 and LC-A-23-18 in another, and LC-A-3-18 with LC-A-1-18 forming the last subgroup. The third main cluster includes LC-A-18-18, LC-A-12-18, and LC-A-11-18 together, LC-A-2-18 and LC-A-14-18 in another sub-group, while LC-A-22-18 stands more independently, possibly as an outlier. Similar findings have been reported in Colocasia, where hierarchical clustering effectively grouped genotypes based on morphological and agronomic traits, aiding in their classification and potential breeding applications. These results highlight the importance of dendrogram-based clustering in plant breeding and genetic research. Similar findings were incorporated by [6] and [1].

IV. CONCLUSION

The estimates of PCV and GCV were recorded high for the number of cormels per plant, disease severity, tuber yield per plot, number of corms per plant, weight of cormels per plant, plant height and width of cormels. High heritability was observed for width of corms, tuber yield per plot, plant height, weight of cormels per plant, disease severity, length of leaf lamina, dry matter percentage in tubers, the width of cormels and weight of corms per plant. Genetic advance was recorded high for number of cormels per plant, tuber yield per plot, disease severity, plant height and weight of cormels per plant. Positive and significant correlation coefficient of tuber yield per plot was recorded for width of corms, number of cormels per plant, weight of corms per plant, weight of cormels per plant, length of leaf lamina, number of corms per plant, width of cormels and plant height. Path coefficient analysis at the genotypic level revealed that the width of corms, number of cormels per plant length of leaf lamina, dry matter percentage in tubers, width of cormels, number of corms per plant and breadth of leaf lamina had positive and direct effects on tuber yield per plot. The promising genotypes may be released as a variety (es) after further evaluation or can be used for crop improvement by way of different breeding programmes.

Compliance with ethical standards

Conflict of interest: The authors declare that they have no conflict of interest.

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Author's contribution

RK (Rishabh Kumar) experimented and analyzed the data; B.S.D. (Balbir Singh Dogra) and M.S. (Monica Sharma) conceptualized the research and guided throughout the experiment; J.K. (Jasdeep Kaur) and N.T. (Nikhil Thakur) helped in main manuscript writing and forming tables; S.G. (Sanchita Gautam) helped in data curation.

Genotypes	Source
LC-A-1-18, LC-A-2-18, LC-A-3-18, LC-A-	
4-18, LC-A-5-18, LC-A-6-18, LC-A-7-18,	
LC-A-8-18, LC-A-9-18, LC-A-10-18, LC-A-	Department of Vegetable Science, COHF, Neri Hamirnur [Dr Y S Parmar University
11-18, LC-A-12-18, LC-A-13-18, LC-A-14-	of Horticulture and Forestry, Nauni, Solan (HP)]
18, LC-A-15-18, LC-A-16-18, LC-A-17-18,	
LC-A-18-18, LC-A-19-18, LC-A-20-18, LC-A-	
21-18, LC-A-22-18, LC-A-23-18	

			Coefficients of	variability (%)			Gen	
Characters	Range	Mean± SE(d)	Phenotypic	Genotypic	Heritabilit y (%)	Genetic advance	etic gain (%)	
Plant height (cm)	45.66- 126.22	86.38±2.04	26.40	26.24	98.80	46.41	53.72	
Number of leaves per plant	1.87- 3.93	2.81±0.29	22.63	18.77	68.82	0.90	32.08	
Length of leaf lamina (cm)	22.27- 35.07	29.28±1.04	11.63	10.79	86.02	6.03	20.61	
Breadth of leaf lamina (cm)	19.27- 27.20	23.55±0.98	10.06	8.67	74.28	3.63	15.39	
Number of cormels per plant	3.20- 9.60	5.71±0.56	44.32	42.66	92.67	4.83	84.60	
Number of corms per plant	1.07- 2.80	1.80±0.32	30.40	21.36	49.36	0.56	30.91	
Width of corms (cm)	4.10- 6.56	5.46±0.05	14.93	14.88	99.40	0.56	30.57	
Width of cormels (cm)	2.27- 3.28	2.51±0.17	25.15	23.82	89.72	1.17	46.48	
Weight of corms per plant (gm)	109.67- 177.35	137.45±5.39	14.53	13.71	89.07	36.65	26.66	
Weight of cormels per plant (gm)	101.80- 166.05	120.94±4.97	26.71 26.23		96.45	64.18	53.07	
Dry matter percentage in tubers (%)	21.20- 45.13	33.49±2.12	20.66	19.15	85.93	12.25	36.58	
Disease severity (%)	6.67- 37.33	18.46±2.21	40.81	38.09	87.10	13.52	73.22	
Tuber yield per plot (Kg)	0.96- 4.39	3.03±0.07	36.24	36.12	99.38	2.25	74.18	

	PH	NLPP	LoLL	BoLL	NCsPP	NCPP	WC	WCs	WoCPP	WoCsPP	DMP	DS	GCCTYPP
РН	-0.097	-0.037	0.119	0.011	0.063	0.001	0.199	-0.014	-0.028	0.030	0.019	0.013	0.279*
NLPP	-0.031	-0.116	0.123	0.011	-0.025	0.012	0.014	-0.009	-0.002	0.023	0.032	-0.005	0.027
LoLL	-0.050	-0.061	0.233	0.023	0.118	0.000	0.220	0.016	-0.058	-0.048	0.001	0.012	0.405**
BoLL	-0.039	-0.043	0.186	0.028	0.046	-0.007	0.019	0.004	-0.038	-0.016	0.015	0.007	0.162
NCsPP	-0.017	0.008	0.075	0.004	0.367	0.025	0.609	0.040	-0.110	-0.100	-0.012	0.005	0.893**
NCPP	-0.001	-0.026	-0.002	-0.004	0.171	0.053	0.219	-0.011	-0.068	-0.009	0.017	-0.001	0.338**
WC	-0.027	-0.002	0.070	0.001	0.308	0.016	0.726	0.010	-0.097	-0.069	-0.023	0.004	0.918**
WCs	0.013	0.010	0.036	0.001	0.144	-0.006	0.069	0.102	-0.002	-0.126	0.008	0.013	0.263*
WoCPP	-0.017	-0.002	0.085	0.007	0.253	0.023	0.441	0.001	-0.160	-0.030	-0.011	-0.001	0.588**
WoCsPP	0.018	0.017	0.069	0.003	0.227	0.003	0.308	0.079	-0.030	-0.162	-0.012	0.018	0.538**
DMP	-0.013	-0.026	0.002	0.003	-0.030	0.006	-0.116	0.006	0.013	0.013	0.142	-0.003	-0.003
DS	0.034	-0.015	-0.071	-0.005	-0.043	0.001	-0.080	-0.035	-0.006	0.076	0.009	-0.039	-0.174

PH = Plant height (cm), NLPP= Number of leaves per plant, LoLL = Length of leaf lamina (cm), BoLL = Breadth of leaf lamina (cm), NoCsPP = Number of cormels per plant, NCPP = Number of corms per plant, WC = Width of corms (cm), WCS = Width of cormels (cm), WoCPP = Weight of corm per plant (gm), WoCsPP = Weight of cormels per plant (gm), DMP = Dry matter percentage in tubers (%), DS = Disease severity (%) and GCCTYPP = Genotypic Correlation Coefficient with Tuber yield per plot (Kg).





Where, PH = Plant height (cm), NLPP= Number of leaves per plant, LoLL = Length of leaf lamina (cm), BoLL = Breadth of leaf lamina (cm), NoCsPP = Number of cormels per plant, NCPP = Number of corms per plant, WC = Width of corms (cm), WCs = Width of cormels (cm), WoCPP = Weight of corm per plant (gm), WoCsPP = Weight of cormels per plant (gm), DMP = Dry matter percentage in tubers (%), DS = Disease severity (%) and GCCTYPP = Genotypic Correlation Coefficient withTuber yield per plot (Kg).

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Figure 2. Dendrogram showing the genetic diversity within 23 genotypes through agro-morphological traits



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