

Genetic Variability, Trait Association, and Path Analysis Studies for Nut Yield and Yield-Related Traits in Cashew (*Anacardium occidentale* L.)

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ABSTRACT

This study was carried out to determine the genetic variability and the relationship between twenty traits for nut yield in fourteen cashew genotypes. The genotypes show considerable variation, and nut yield tree⁻¹ had the highest genotypic coefficient of variation and phenotypic coefficient of variation. The number of nuts panicle⁻¹, kernel weight and nut yield tree⁻¹ all had substantial heritability and genetic advance in percent of mean. Plant height, canopy spread, leaf size, flowering intensity, length of inflorescence, percentage fruit set, number of nuts panicle⁻¹, nut weight, shell thickness, kernel weight, apple weight and TSS of juice all showed a significant positive association with nut yield tree⁻¹. Path analysis revealed that the main factors influencing nut yield tree⁻¹ were canopy spread (east-west direction), apple weight, length of the inflorescence and the number of nuts panicle⁻¹. The information on these statistical metrics would be useful in identifying genotypes with greater yield potential that can be used in the cashew improvement program.

Keywords: Canopy spread, Cashew genotypes, Genotypic coefficient of variation.

INTRODUCTION

Cashew (*Anacardium occidentale* L.) is a tropical crop introduced from eastern Brazil to India by the Portuguese (Preethi *et al.*, 2021), with the Amazonia forest of Brazil standing as the center of origin (Mitchell and Mori, 1987). Commercial cashew production is currently practiced in over thirty three countries worldwide, with Vietnam, India, Ivory Coast, Philippines, Benin, Mozambique, Guinea-Bissau, Tanzania, Indonesia, Brazil, Burkina Faso, Nigeria, Ghana, Mali and Colombia being the main cashew producers. In India, cashew occupies 1.035 million hectare and produces 0.779 million metric ton of raw

nuts (Anon., 2017). It has adapted well to the coastal regions in the Indian states of Odisha, Maharashtra, Andhra Pradesh, Kerala, Karnataka, Goa and Tamil Nadu. India is not only the country with the large area under this crop, but it also has a solid track record of exporting cashew kernels to gain foreign currency. The USA, UK, UAE, Netherlands, Saudi Arabia, Italy, the Middle East, Australia, Japan, Germany, Austria, Canada, and France are the top foreign purchasers of cashews from India (Preethi *et al.*, 2021). Cashew kernels are commonly used in confectionery and desserts. The shells contain high-quality oil termed Cashewnut Shell Liquid (CSNL) that has a wide range of industrial applications. Cashew apples are processed into many value-added

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products like cashew apple ready to serve, juice, jelly, jam, syrup, chutney and beverage, which provide consumers with vitamins A and C (Dewangan *et al.*, 2021). Even though attempts have been made to improve this crop for agronomic attributes, such as nut yield and quality, through conventional breeding approaches, production of cashews is unfortunately constrained by low and variable nut yields, poor nut quality, and susceptibility to a pest, tea mosquito bug (Ramteke, 2022). Because of its cultivation across varied ecologies and employment of rural women in its value chain, cashew has been identified as a crop with enormous potential to alleviate poverty.

Meager tree production continues to be a major concern for cashew growers, restricting investment in the cashew processing business. A fundamental strategy for achieving a sustainable and investable cashew sector is the development of stable, high-yielding cultivars to boost nut production. It is necessary to produce variations in the genetic makeup of cashews in order to get vital information on the availability of variation in populations (Sethi *et al.*, 2020). To make the most of the available gene pool, it is essential to understand the kind, degree and interrelationships of genetic population variability as well as the correlations between characters in order to create an effective selection strategy based on several features. The most efficient technique to improve cashew productivity and kernel quality attributes is to utilize available genetic resources. In the cashew breeding program, it is essential to identify genotypes that generate high nut yields with semi-vigorous canopies and favorable kernel characteristics (Eradasappa *et al.*, 2020; Ramteke, 2022). Further, the cashew breeding program needs to carefully evaluate germplasm clones from both domestic and international sources across certain ecologies for survival, vigor and yield in order to effectively compare and choose clones for subsequent breeding efforts (Paul *et al.*, 2019). Surprisingly, data

on cashew genetic resources to drive improvement are only now becoming available (Sethi *et al.*, 2020; Preethi *et al.*, 2021).

Yield is one of the major complex traits that are an outcome of the interaction of plant traits that are highly influenced by environmental fluctuation (Dakuyo *et al.*, 2022). The direct selection based on the nut yield without considering other traits of interest may be ambiguous. In the examination of yield and yield contributing traits in cashew, conducting association studies together with a path coefficient analysis is a more effective method (Sethi *et al.*, 2016a). Path analysis is a structural technique to assess the relationships between a dependent variable and two or more independent traits. However, correlation of traits and path coefficient analysis must be considered to understand the impact of genotype and environment towards the final yield before selection (Faysal *et al.*, 2022). The current study employed variability, correlation path coefficient analysis approaches to evaluate the relationships and effect of significant yield contributing components on the yield of cashew.

Evaluation of variability is the initial step in any breeding program, and the extent of genetic variability present in distinct biometric traits in the gene pool determines success in selection of superior genotypes. Earlier studies showed that genotypes H-303 and H-68 were promising with respect to flowering, nut yield and shelling parameters in the south Chhattisgarh Region (Ramteke, 2022). However, there are few reports on the level of heterogeneity in cashew on various quantitative characteristics. Since most plant traits of economic value are polygenic in nature and strongly influenced by environmental changes, determining whether the observed variability is attributable to the environment or the genetics of an individual is difficult (Sethi *et al.*, 2020). Furthermore, it is important to identify key characteristics that are critical in comprehending the type of diversity present in breeding materials. As a result, an

attempt was made in this study to estimate the variability, heritability, genetic advance, genotypic and phenotypic correlations, as well as their direct and indirect effects in cashew to determine the contribution of the most important characters towards nut yield, which ultimately aids in the selection of superior cross combinations.

MATERIALS AND METHODS

The present study was undertaken at Shaheed Gundadhoor College of Agriculture and Research Station (SG CARS), Kumhrawand, Jagdalpur, Bastar, Chhattisgarh, during the years 2015-18. The topographic situation of the field, where the cashew genotypes were planted in midland to upland (*Tikra*) of Bastar-Plateau agro-climatic region of Chhattisgarh. The soil of the experimental site was silty-loam texture with pH varying from 5.5 to 6.2. The nitrogen and potassium content of the soil was low, while the phosphorus level was medium to low. The experiment comprised 14 cashew genotypes, viz., BPP 30/1, BPP 3/33, BPP 10/19, BPP 3/28, H-68, H-255, H-303, H-320, H-367, Vengurla-4, M-15/4, M-44/3, NRCC Selection-1 and NRCC Selection-2, collected from Bapatla (Andhra Pradesh), Vridhachalam (Tamil Nadu) and Vengurla (Maharashtra). These genotypes had been planted at 7.5×7.5 m spacing in three replications, under randomized complete block design during the year 2000, at AICRP on Cashew Experimental Field, Kumhrawand, Jagdalpur, Chhattisgarh, India. The clonally multiplied softwood grafted plants of each genotype were planted in the experimental plot. Six grafts of each genotype were planted in each replication. Observations on vegetative, yield and yield-attributing traits were recorded as per the standard descriptor of cashew (Swamy *et al.*, 2000). The Total Soluble Solids (TSS) content of the cashew apple juice was measured using a 0-32 % range 'Zeiss-Hand' refractometer.

After testing the homogeneity, using Bartlett's test (Bartlett, 1937), the mean values of twenty characters were pooled for

three years and subjected to Analysis Of Variance (ANOVA) for testing the presence of significant differences among genotypes (Panse and Sukhatme, 1978) following randomized complete block design. The Genotypic Coefficients of Variation (GCV) and Phenotypic Coefficients of Variation (PCV) were computed using the formula suggested by Burton (1952).

$$GCV = \frac{\sigma_g \times 100}{\bar{X}}$$

$$PCV = \frac{\sigma_p \times 100}{\bar{X}}$$

Where, σ_g is genotypic standard deviation, σ_p is phenotypic standard deviation and \bar{X} is general mean.

Heritability estimate in broad sense (h^2) was calculated as the ratio of genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and expressed in percentage (Falconer, 1981).

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

Genetic Advance in per cent of the Mean (GAM), assuming selection of the superior 5% genotypes were estimated in accordance with the methods illustrated by Johnson *et al.* (1955).

$$GA = h^2 \times k \times \sigma^2_p$$

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

Where, k is 2.06 at 5% selection intensity, h^2 is heritability, σ^2_p is phenotypic variance.

Correlation coefficients were calculated for all possible combinations among the characters at genotypic and phenotypic levels and were estimated as per method described by Searle (1961). Estimation of the path coefficient using genotypic correlation values and path coefficient analysis was done following the procedure of Dewey and Lu (1959). The results were analyzed using OPSTAT statistical software.

RESULTS AND DISCUSSION

The mean square due to genotype (Table 1) for all characters showed a significant

**Table 1.** Analysis of variance for growth parameters and nut yield in cashew.

Observations	df	Mean sum of square		
		Replication	Genotype	Error
		2	13	26
1. Plant height (m)		0.069	1.714**	0.144
2. Canopy spread E-W (m)		0.156	1.737**	0.183
3. Canopy spread N-S (m)		0.00705	2.352**	0.158
4. Leaf size (cm ²)		12.861	3351.92**	9.465
5. Number of flowering laterals (m ⁻²)		2.292	18.518**	1.0272
6. Flowering intensity (m ²)		65.237	154.367**	22.642
7. Sex ratio		0.00002	0.00093**	0.00002
8. Duration of flowering (days)		41.285	1023.14**	46.140
9. Length of inflorescence (cm)		0.0482	28.316**	0.462
10. Width of inflorescence (cm)		0.515	63.205**	0.848
11. Fruit set (%)		0.017	9.570**	0.212
12. Number of nuts panicle ⁻¹		0.013	7.479**	0.329
13. Nut weight (g)		0.032	10.344**	0.155
14. Shell thickness (mm)		0.011	1.306**	0.024
15. Shelling (%)		2.411	86.884**	1.068
16. Kernel weight (g)		0.0030	1.695**	0.0058
17. Apple weight (g)		4.700	198.795**	22.181
18. Juice content (%)		42.542	702.631**	35.814
19. TSS of juice (°Brix)		0.0065	7.776**	0.092
20. Nut yield tree ⁻¹ (kg)		0.974	6.770**	0.301

** Significant at $P \leq 0.01$ by the F test.

difference ($P < 0.05$), indicating the presence of adequate amount of variability to be harnessed in the cashew for an improvement program. The extent of variability and inheritance pattern present in the germplasm was estimated in terms of range, Phenotypic and Genotypic Coefficient of Variation (PCV and GCV) and heritability in broad sense (h^2) along with Genetic Advance as percentage of the Mean (GAM). PCV was slightly higher than the GCV, indicating less influence of the environment on the traits under study. This indicated that there was considerable scope for choosing superior and diverse genotypes for inclusion in a program aimed at increasing the genetic yield potential of cashew. Similar results on cashew were also reported by Sethi *et al.* (2016b) and Paul *et al.* (2019). In pooled analysis (Table 2.), the higher value of the GCV was recorded for nut yield tree⁻¹ followed by the number of nuts panicle⁻¹, kernel weight, fruit set, leaf size, juice content, width of inflorescence and nut weight, whereas the flowering intensity showed the lowest GCV. The high amount

of GCV is indicative of inherent variability arising due to genetic cause and more useful for breeder in crop improvement program (Tiwari *et al.*, 2019). The higher value of PCV was recorded for nut yield tree⁻¹ followed by the number of nuts panicle⁻¹, kernel weight, fruit set, leaf size, juice content, the width of inflorescence and nut weight. The lowest PCV was recorded for sex ratio indicating that the environment seemed to have some impact on how this characteristic was expressed phenotypically. Traits with high PCV and GCV values indicate high levels of genetic diversity, while traits with low PCV and GCV values show low levels of genetic diversity (Das *et al.*, 2021). Significant diversity indicates the possibility of successful selection for character development. In the present research, nut yield tree⁻¹ had the highest GCV and PCV, followed by number of nuts panicle⁻¹, kernel weight and fruit set. This suggests that nut yield tree⁻¹ might be improved by using these features as a selection criterion. The result is in line with the previous research that reported that nut

Table 2. Estimates of phenotypic and genetic parameters for various characters in cashew.

Characters	Mean	Range		GCV (%)	PCV (%)	h ²	GAM
		Minimum	Maximum				
Plant height (m)	3.60	2.52	4.57	14.20	17.70	0.643	23.478
Canopy spread E-W (m)	4.29	3.03	5.24	11.83	15.48	0.584	18.642
Canopy spread N-S (m)	4.48	2.88	5.15	13.51	16.17	0.698	23.261
Leaf size (cm ²)	118.65	72.40	165.01	19.89	20.06	0.983	40.633
No. of flowering laterals (m ⁻²)	13.64	10.96	17.04	12.51	14.55	0.739	22.169
Flowering intensity (m ⁻²)	75.68	63.80	82.05	6.19	8.82	0.492	8.948
Sex ratio	0.24	0.21	0.27	7.58	8.18	0.859	14.483
Duration of flowering (days)	92.17	73.00	110.33	13.84	15.68	0.779	25.173
Length of inflorescence (cm)	19.44	15.80	23.75	11.07	11.61	0.909	21.765
Width of inflorescence (cm)	19.65	14.45	25.46	16.40	17.06	0.924	32.495
Fruit set (%)	5.20	3.91	8.65	24.01	25.60	0.880	46.407
Number of nuts panicle ⁻¹	3.91	2.91	5.98	27.88	31.50	0.783	50.839
Nut weight (g)	8.04	5.70	10.06	16.19	16.91	0.916	31.929
Shell thickness (mm)	3.12	2.60	4.25	14.80	15.63	0.897	28.902
Shelling (%)	27.05	20.42	33.16	13.98	14.48	0.930	27.772
Kernel weight (g)	1.95	1.13	2.74	27.16	27.44	0.979	55.383
Apple weight (g)	49.52	42.83	64.98	10.95	14.50	0.570	17.041
Juice content (%)	63.95	44.63	82.91	16.48	18.95	0.756	29.532
TSS of juice (⁰ Brix)	13.62	11.92	15.38	8.30	8.60	0.932	16.528
Nut yield (kg tree ⁻¹)	7.03	5.65	8.75	34.23	38.73	0.781	62.343

yield tree⁻¹ of cashew could be improved through the selection of traits like number of nuts panicle⁻¹ and fruit set (Sethi *et al.*, 2016b; Chandrasekhar *et al.*, 2018; Eradasappa *et al.*, 2020). Considerably lower GCV and PCV were found for flowering intensity (m⁻²), sex ratio, TSS of juice and apple weight indicating that selection for nut yield would not be effective based on these traits.

Heritability in a broad sense (h²) was calculated for all the twenty characters. In the pooled analysis (Table 2) the magnitude of heritability ranged from 49.2 to 98.3%. The leaf size had the highest heritability estimate followed by kernel weight, shelling (%), TSS of juice, nut weight, the width of inflorescence, shell thickness, fruit set (%), sex ratio, number of nuts panicle⁻¹, and nut yield tree⁻¹. The moderate heritability was estimated in the characters *viz.*, canopy spread in north south direction (N-S), plant height, canopy spread in east west direction (E-W) and apple weight, whereas low heritability was recorded for flowering intensity. The magnitude of GAM ranged

from 8.94 to 62.34% (Table 2.). The nut yield (kg tree⁻¹) showed the highest GAM followed by kernel weight and the number of nuts panicle⁻¹. The characters that showed moderate GAM were fruit set (%), leaf size, the width of inflorescence and nut weight. Genetic advance in any population would depend upon its genetic architecture. Heritability estimates are considered in understanding the pattern of inheritance of quantitative characters like nut yield (Mohapatra *et al.*, 2018). Similarly, genetic advance is also a useful measure to predict gains in specified selection intensity. However, when it is considered along with heritability, it becomes more valuable to predict response to selection than the heritability estimates alone (Neelima *et al.*, 2018). The characters having a high magnitude of heritability have an immense value of selection because they indicate low environmental influence. The selection of a trait in any breeding program requires both a high heritability and a high genetic advance of the trait. In the present study, high heritability along with high GAM were



reported for nut yield (kg tree^{-1}), kernel weight and the number of nuts panicle⁻¹, indicating the additive gene action for the traits, therefore, selection based on such traits might contribute significantly to the improvement of cashew for nut yield trait. A high GAM and high heritability were previously reported for various yield-related traits in cashew (Ushavani and Jeyalekshmy, 2009; Sethi *et al.*, 2016b; Chandrasekhar *et al.*, 2018). These findings are in agreement with those obtained in cashew by Lenka *et al.* (1998), wherein the number of nuts panicle⁻¹ and nut yield tree⁻¹ have high GCV, high heritability and high genetic advance, indicating the scope for selection in these traits.

Relationship between genetic parameters for biometric and yield traits were examined through the rank procedure (Table 3) on a pooled basis, indicating maximum variability for leaf size, number of nuts panicle⁻¹ and kernel weight, whereas the minimum variability was observed for the characters sex ratio, flowering intensity and canopy spread. Hence, based on genetic variability, it could be concluded that the characters like the number of nuts panicle⁻¹, kernel weight and nut yield tree⁻¹ had high heritability coupled with high

GAM indicate the predominance of additive gene effects (Chandrasekhar *et al.*, 2018). High heritability with moderate GAM was recorded for the character nut weight. This indicates that nut weight is governed by both additive and non-additive gene action (Eradasappa *et al.*, 2020). The practical applicability of these findings would be profitably realized in selection of promising genotypes for nut yield-related traits.

The correlation coefficient among different characters was worked out at phenotypic and genotypic levels (Table 4). Correlation studies revealed that the growth parameters such as plant height, canopy spread (E-W and N-S) and leaf size showed a significant positive association with nut yield tree⁻¹. Among flowering parameters, flowering intensity, number of flowering laterals (m^{-2}), number of nuts panicle⁻¹ and nut weight have significant positive association with nut yield tree⁻¹. That means any factor that impairs the performance of these parameters will ultimately affect the nut yield. The number of nuts panicle⁻¹ had a highly significant and positive correlation with plant height, number of flowering laterals (m^{-2}), fruit set, TSS of juice, and nut yield tree⁻¹ at a phenotypic as

Table 3. Relationship between different parameters of cashew rank procedure.

S. No.	Characters	GCV (%)	PCV (%)	h^2	GAM	Total
1	Plant height (m)	10	7	17	12	64
2	Canopy spread E-W (m)	15	13	18	16	81
3	Canopy spread N-S (m)	13	10	16	13	68
4	Leaf size (cm^2)	5	5	1	5	17
5	No. of flowering laterals (m^{-2})	14	14	15	14	66
6	Flowering intensity (m^{-2})	20	18	20	20	84
7	Sex ratio	19	20	10	19	88
8	Duration of flowering (days)	12	11	13	11	49
9	Length of inflorescence (cm)	16	17	7	15	63
10	Width of inflorescence (cm)	7	8	5	6	33
11	Fruit set (%)	4	4	9	4	32
12	Number of nuts panicle ⁻¹	2	2	11	3	31
13	Nut weight (g)	8	9	6	7	40
14	Shell thickness (mm)	9	12	8	9	55
15	Shelling (%)	11	16	4	10	46
16	Kernel weight (g)	3	3	2	2	25
17	Apple weight (g)	17	15	19	17	72
18	Juice content (%)	6	6	14	8	37
19	TSS of juice (^o Brix)	18	19	3	18	70
20	Nut yield (kg tree^{-1})	1	1	12	1	29

Table 4. Correlation coefficient analysis (phenotypic and genotypic) among total nut yield and its components of cashew.

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆	X ₁₇	X ₁₈	X ₁₉	Nut yield tree ⁻¹
X ₁	1.000	0.759***	0.765***	0.280*	0.610**	0.594***	-0.140	-0.148	0.223	0.280*	0.256*	0.659***	0.397**	-0.019	0.069	0.318**	0.476**	0.383**	0.488**	0.541**
X ₂	1.000	0.609***	0.658**	0.233*	0.372**	0.393**	-0.119	-0.166	0.171	0.219*	0.187	0.474**	0.312**	-0.012	0.047	0.259*	0.324**	0.276*	0.365**	0.458**
X ₃	1.000	0.974**	0.564**	0.564**	0.504**	0.629**	-0.118	0.017	0.378**	0.241*	0.068	0.301*	0.710**	0.050	0.378**	0.660**	0.787**	0.607**	0.440**	0.611**
X ₄	1.000	0.798**	1.000	0.443**	0.365**	0.403**	-0.093	0.012	0.265**	0.177	0.016	0.230*	0.545**	0.018	0.237*	0.499**	0.602**	0.329**	0.333**	0.473**
X ₅	1.000	1.000	0.449**	0.596**	0.828**	0.828**	-0.260	0.058	0.273*	0.079	0.026	0.564**	0.710**	0.229*	0.238*	0.574**	0.737**	0.510**	0.377**	0.638**
X ₆	1.000	1.000	0.377**	0.417**	0.472**	0.472**	-0.196	-0.013	0.229*	0.066	-0.006	0.269*	0.577**	0.138	0.169	0.474**	0.561**	0.535**	0.361**	0.528**
X ₇	1.000	0.841**	0.211	0.288	0.422**	0.422**	0.025	0.011	0.647**	0.559**	0.095	0.221*	0.720**	0.484**	0.748**	0.878**	0.618**	0.402**	0.680**	0.558**
X ₈	1.000	0.378**	0.024	0.024	0.024	0.024	-0.076	-0.076	0.482	0.142	0.749**	0.851**	0.757**	0.327**	0.048	0.505**	0.468**	0.555**	0.560**	0.953**
X ₉	1.000	0.378**	-0.002	-0.029	-0.029	-0.029	-0.036	-0.036	0.391**	0.116	0.609**	0.649**	0.641**	0.283**	0.029	0.439**	0.368**	0.384**	0.469**	0.782**
X ₁₀	1.000	0.378**	-0.002	-0.029	-0.029	-0.029	-0.036	-0.036	0.391**	0.116	0.609**	0.649**	0.641**	0.283**	0.029	0.439**	0.368**	0.384**	0.469**	0.782**
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* Significant at P<0.05, ** Significant at P<0.01 respectively

- X₁ - Plant height (cm)
- X₂ - Canopy spread E-W (m)
- X₃ - Sex ratio
- X₄ - Duration of flowering (days)
- X₅ - Length of inflorescence (cm)
- X₆ - Width of inflorescence (cm)
- X₇ - Flowering intensity (m⁻²)
- X₈ - Flower set (%)
- X₉ - Number of nuts panicle⁻¹
- X₁₀ - Nut weight (g)
- X₁₁ - Shell thickness (mm)
- X₁₂ - Shelling (%)
- X₁₃ - Fruit set (%)
- X₁₄ - Number of nuts panicle⁻¹
- X₁₅ - Nut weight (g)
- X₁₆ - Shell thickness (mm)
- X₁₇ - Shelling (%)
- X₁₈ - Kernel weight (g)
- X₁₉ - Apple weight (g)
- X₂₀ - Juice content (%)
- X₂₁ - TSS of Juice (°Brix)



Table 5. Genotypic path coefficient analysis for nut yield (kg tree⁻¹) and its components in cashew. ^a

	\bar{X}_1	\bar{X}_2	\bar{X}_3	\bar{X}_4	\bar{X}_5	\bar{X}_6	\bar{X}_7	\bar{X}_8	\bar{X}_9	\bar{X}_{10}	\bar{X}_{11}	\bar{X}_{12}	\bar{X}_{13}	\bar{X}_{14}	\bar{X}_{15}	\bar{X}_{16}	\bar{X}_{17}	\bar{X}_{18}	r_e with yield
X_1	0.237	0.586	-0.879	-0.164	-0.384	-0.187	0.043	-0.049	0.119	-0.034	0.058	0.369	-0.007	-0.105	0.630	0.255	0.005	0.048	0.541**
X_2	0.180	0.772	-1.119	-0.330	-0.318	-0.198	0.036	0.006	0.201	-0.029	0.015	0.169	0.019	-0.572	1.306	0.422	0.008	0.043	0.611**
X_3	0.182	0.752	-1.148	-0.263	-0.375	-0.260	0.080	0.019	0.145	-0.010	0.006	0.204	0.086	-0.361	1.136	0.396	0.007	0.043	0.638**
X_4	0.067	0.436	-0.516	-0.585	-0.234	-0.091	-0.130	0.009	0.365	-0.068	0.022	0.124	0.183	-1.132	1.737	0.301	0.005	0.067	0.558**
X_5	0.145	0.390	-0.685	-0.217	-0.629	-0.264	-0.007	-0.025	0.256	-0.017	0.169	0.477	0.124	-0.074	0.999	0.251	0.007	0.055	0.953**
X_6	0.141	0.486	-0.952	-0.169	-0.530	-0.314	0.103	-0.098	0.231	-0.004	0.087	0.282	0.166	-0.171	1.065	0.342	0.006	0.031	0.703**
X_7	-0.033	-0.091	0.299	-0.248	-0.015	0.106	-0.307	0.013	0.151	-0.050	0.002	-0.079	-0.005	-0.246	0.409	0.167	0.002	0.013	0.085
X_8	-0.035	0.013	-0.067	-0.015	0.048	0.093	-0.012	0.329	-0.054	0.000	-0.042	-0.066	-0.005	-0.138	-0.001	-0.176	0.002	0.022	-0.102
X_9	0.053	0.292	-0.314	-0.402	-0.304	-0.137	-0.087	-0.033	0.531	-0.101	0.069	0.099	0.106	-0.736	1.229	0.197	0.003	0.030	0.494**
X_{10}	0.067	0.187	-0.091	-0.327	-0.089	-0.009	-0.127	-0.001	0.443	-0.122	0.013	0.015	0.021	-0.567	0.672	0.045	0.003	0.015	0.146
X_{11}	0.061	0.053	-0.030	-0.056	-0.472	-0.121	-0.003	-0.061	0.162	-0.007	0.226	0.429	0.021	-0.183	0.588	0.006	0.005	0.033	0.651**
X_{12}	0.157	0.232	-0.419	-0.129	-0.536	-0.159	0.043	-0.039	0.094	-0.003	0.173	0.560	0.098	0.077	0.505	0.066	0.005	0.061	0.787**
X_{13}	-0.005	0.039	-0.263	-0.283	-0.206	-0.139	0.004	-0.004	0.149	-0.007	0.013	0.146	0.377	-0.388	0.811	0.081	0.001	0.029	0.354**
X_{14}	0.016	0.292	-0.274	-0.437	-0.031	-0.036	-0.050	0.020	0.258	-0.046	0.027	-0.028	0.097	-1.513	1.673	0.134	0.004	0.052	0.168
X_{15}	0.076	0.510	-0.660	-0.514	-0.318	-0.169	-0.063	0.010	0.330	-0.041	0.067	0.143	0.154	-1.280	1.978	0.335	0.007	0.066	0.620**
X_{16}	0.113	0.607	-0.847	-0.328	-0.295	-0.201	-0.095	-0.108	0.195	-0.010	0.002	0.069	0.057	-0.377	1.235	0.536	0.005	0.030	0.588**
X_{17}	0.091	0.469	-0.586	-0.235	-0.350	-0.144	-0.039	0.063	0.126	-0.025	0.096	0.226	0.034	-0.460	1.007	0.198	0.013	0.032	0.516**
X_{18}	0.116	0.340	-0.503	-0.398	-0.353	-0.101	-0.042	0.073	0.164	-0.018	0.075	0.350	0.113	-0.799	1.334	0.163	0.004	0.098	0.617**

^a Residual effect= 0.014, r_e = Genotypic correlation coefficient, Underlined figures are the direct path coefficient values, **Significant at P< 0.01.

- X_1 - Plant height (cm)
- X_2 - Canopy spread E-W (m)
- X_3 - Canopy spread N-S (m)
- X_4 - Leaf size (cm²)
- X_5 - No. of flowering laterals (m⁻²)
- X_6 - Flowering intensity (m⁻²)
- X_7 - Sex ratio
- X_8 - Duration of flowering (Days)
- X_9 - Length of inflorescence (cm)
- X_{10} - Width of inflorescence (cm)
- X_{11} - Fruit set (%)
- X_{12} - Number of nuts panicle⁻¹
- X_{13} - Shell thickness (mm)
- X_{14} - Shelling (%)
- X_{15} - Kernel weight (g)
- X_{16} - Apple weight (g)
- X_{17} - Juice content (%)
- X_{18} - TSS of juice (^bBriggs)

well as genotypic level. Nut weight had a highly significant and positive correlation with leaf size, flowering laterals (m^2), kernel weight, apple weight, TSS of juice and nut yield $tree^{-1}$. Kernel weight had a highly significant and positive correlation with leaf size, nut weight, shelling percent, TSS of juice and total nut yield $tree^{-1}$ at the phenotypic as well as genotypic level. Selection should be based on the correlation coefficient analysis of nut yield and its component characters, in addition to heritability and genetic advancement to increase nut yield genetically. The ability to identify traits through indirect selection that may increase nut yield is made possible by the relationship between nut yield and yield-related traits. The green leaves absorb sunlight to create sugars and carbohydrates, which are then delivered to the regions where they are needed, such as inflorescence, buds, flowers, and fruits (Adiga *et al.*, 2020). Thus, larger leaf size is potentially more capable for producing higher number of flowering laterals and number of nuts $panicle^{-1}$. Higher cashew yield can thus be attained by selecting these strongly associated features, as an increase in the weighted mean of either one of them would greatly increase the values of the others (Pedroza de Azevedo *et al.*, 1998). The results of the present study are also similar to earlier reports by Swarnapirria and Manivannan (1999) and Aliyu (2006). It is interesting to note that the flowering duration showed a negative association, though not significant, with nut yield. A similar observation was also reported by Lenka *et al.* (2001) and Rao *et al.* (2002).

Path coefficient analysis revealed that the plant height expressed a positive indirect effect on nut yield $tree^{-1}$ viz., kernel weight, canopy spread (E-W), number of nuts $panicle^{-1}$, apple weight, length of inflorescence, fruit set, TSS of juice, sex ratio, and juice content. However, the rest of the characters showed indirect negative values. The positive indirect effect of the number of nuts $panicles^{-1}$ on nut yield $tree^{-1}$ was observed viz., kernel weight, canopy

spread (E-W), length of inflorescence, shelling (%), apple weight, TSS of juice, sex ratio and juice content, while the rest of the characters showed indirect negative values. Kernel weight showed a positive indirect effect on nut yield $kg tree^{-1}$ through canopy spread (E-W), apple weight, length of inflorescence, shell thickness, number of nuts $panicle^{-1}$, plant height, fruit set, TSS of juice, duration of flowering and juice content at a genotypic level, whereas, shelling per cent, canopy spread (N-S), number of flowering laterals m^2 , leaf size, flowering intensity, sex ratio and width of inflorescence expressed negative direct effects. The need to primarily choose traits to augment nut yield in cashew is highlighted by the positive relationship between the number of flowering laterals m^2 , the number of nuts $panicle^{-1}$ and the canopy spread in an east-west direction. The findings were consistent with those of Sethi *et al.* (2016a), who found that canopy spread (N-S), the number of flowering laterals (m^2) and the number of nuts $panicle^{-1}$, all directly correlated positively with nut yield. Our research findings showed that canopy spread (E-W), length of inflorescence and number of nuts $panicle^{-1}$ were the major attributes contributing to nut yield. Despite specific character selection that can enhance yield, long-term yield gain is more likely to arise from improvements in all of the characters that influence the manifestation of the yield attributes. According to Aliyu (2006), nut yield was significantly positively associated with nut weight, number of nuts $panicle^{-1}$, nut yield and hermaphrodite flowers $panicle^{-1}$. Ushavani and Jayalekshmy (2009) found that nut weight and kernel weight had significant positive direct effects and moderately positive relationships with yield. The small magnitude of residual effect at the genotypic level indicated that enough character was included in the present study. The results of this study suggest that the selection process should pay particular attention to traits with a direct path coefficient in the positive direction and a



positive and extensive assembly with nut yield.

CONCLUSIONS

From the current study, it can be concluded that high heritability coupled with high genetic advance was noticed for the number of nuts panicle⁻¹, kernel weight and nut yield, indicating that heritability due to additive gene action and selection based on these characters may be effective. The characters viz., plant height, canopy spread (E-W and N-S), leaf size, length of inflorescence, fruit set (%), number of nuts panicle⁻¹ and nut weight must be given importance for further cashew improvement program. The characters like kernel weight, canopy spread (E-W), number of nuts panicle⁻¹, length of inflorescence, plant height, fruit set (%) and TSS of juice exhibited highest positive direct effect on nut yield tree⁻¹. It indicated that these characters would influence nut yield directly. These findings suggest the possibilities of achieving desirable genetic gain through direct selection of the above-mentioned characters in cashew.

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بررسی تغییرات ژنتیکی، ارتباط صفات و تحلیل مسیر برای عملکرد و صفات مرتبط با عملکرد در بادام هندی (*Anacardium occidentale* L.)

و. رامتکه، م. س. پایکرا، ر. س. نتام، آ. کرکتا، ی. س. نیوالا، د. پ. سینگ، گ. ل. وینا، ج. د. آدیگا، گ. س. مهنا، و ت. ن. راویپراساد

چکیده

این پژوهش برای تعیین تنوع ژنتیکی و ارتباط بین ۲۰ صفت برای عملکرد بادام هندی (nuts) در ۱۴ ژنوتیپ بادام هندی انجام شد. ژنوتیپ‌ها تنوع قابل توجهی داشتند و عملکرد هر درخت دارای بالاترین ضریب تنوع ژنوتیپی و ضریب تغییرات فنوتیپی بود. تعداد بادام (nut) هرخوشه، وزن هسته و عملکرد هر درخت همگی دارای وراثت پذیری و بهبود ژنتیکی (genetic advance) قابل توجهی در درصد میانگین بودند. ارتفاع بوته، گسترش تاج پوشش، اندازه برگ، شدت گلدهی، طول گل آذین، درصد تشکیل میوه، تعداد بادام هر خوشه، وزن مهره، ضخامت پوسته، وزن هسته، وزن هر میوه محصول (apple weight) و TSS آب میوه همگی ارتباط مثبت و معنی داری با عملکرد بادام هر درخت نشان داد. تجزیه و تحلیل مسیر آشکار کرد که عوامل اصلی موثر بر عملکرد بادام هر درخت شامل گسترش تاج پوشش (جهت شرقی-غربی)، وزن میوه محصول، طول گل آذین و تعداد بادام هر خوشه بود. اطلاعات مربوط به این معیارهای آماری در شناسایی ژنوتیپ‌هایی با توان عملکرد بیشتر که می‌توانند در برنامه بهبود بادام هندی مورد استفاده قرار گیرند، مفید خواهد بود.