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Genetic variability and character association studies in Indigenous germplasm of cashew (*Anacardium occidentale* L.) in Bastar Plateau of Chhattisgarh

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ABSTRACT

The study evaluated 24 indigenous cashew genotypes along with the check variety Vengurla-4 in the Bastar Plateau region of Chhattisgarh, India, to assess genetic variability, heritability, and trait associations for yield and quality improvement. Significant genotypic differences were observed for vegetative, reproductive and nut quality traits over two consecutive years (2023–24 and 2024–25). Moderate genotypic coefficient of variation and phenotypic coefficient of variation were recorded for nut weight (20.84%, 20.98%), apple weight (25.71%, 26.35%) and nut yield tree^{-1} (20.01%, 20.61%), indicating substantial genetic variability. Broad-sense heritability was highest for nut weight (98.60%), apple weight (95.20%) and shelling percentage (98.00%), suggesting strong additive gene effects. A significant genetic advance as percentage of the mean was noted for apple weight (51.66%), nut weight (42.62%) and nut yield (40.03%). Nut yield tree^{-1} showed a strong positive correlation with number of nuts panicle^{-1} (r = 0.925) and fruit set (r = 0.789), while nut weight was positively associated with apple weight (r = 0.709). The study identified key traits like nut weight, kernel weight, shelling percentage and canopy size as ideal for direct selection to improve nut yield and nut quality. Indigenous genotypes having potential traits with high heritability and genetic advance can serve as potential donors for breeding plan targeting, high nut yield, bold nut and high-density planting for sustainable cashew cultivation in plateau regions.

Key words: Cashew genotypes, genetic variability, heritability, selection traits, nut yield.

INTRODUCTION

Cashew (*Anacardium occidentale* L.) is an economically important tropical nut crop, valued for its kernels, cashew nut shell liquid (CNSL) and agro-industrial uses. India is one of the largest producers and exporters of cashew, with Chhattisgarh's Bastar Plateau region emerging as a potential cultivation zone due to its suitable agro-climatic conditions (Ramteke, 13). However, productivity remains suboptimal due to limited genetic improvement and lack of region-specific high-yielding genotypes (Preethi *et al*., 10). Genetic diversity is fundamental to enhancing crops, allowing for the identification of better genotypes for traits related to yield and yield enhancement. Previous studies on cashew have focused on variability, heritability and trait associations in different regions (Mohapatra *et al.,* 9; Adu-Gyamfi *et al.,* 1), yet research specific to the Bastar Plateau remains scarce. While some investigations have highlighted significant variability in nut weight, apple weight and flowering duration (Chandrasekhar *et al*., 5; Ramteke *et al*., 11), a critical research gap persists in understanding the genetic potential of indigenous genotypes in this unique agro-ecological zone. Moreover, earlier studies often lacked comprehensive analysis of trait correlations with nut yield, limiting their utility in breeding programs.

Existing variability studies predominantly focus on coastal regions (Yadawad *et al*., 15), with scant attention to plateau ecosystems like Bastar, where soil and climatic factors differentially influence trait expression. This research tackles this issue by assessing twenty-four native promising cashew genotypes along with a commercial variety to examine genetic variability, heritability, and trait associations specifically in the Bastar Plateau. The results will aid in recognizing key tree characteristics in the existing genotypes for application in breeding plan designed to increase nut yield, produce larger nuts and create denser canopies suitable for high-density planting, thereby improving yield and sustainability in non-traditional cashew cultivation areas.

MATERIALS AND METHODS

The experimental material comprised 25 diverse cashew genotypes, including 24 local cashew genotypes and one commercial variety, Vengurla-4,

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as a check (Table 1), maintained at the NURI farm in Lamker under Zonal Agricultural Research Station, Indira Gandhi Krishi Vishwavidyalaya, Jagdalpur, Chhattisgarh. The study was conducted on seven-year-old trees over two consecutive cropping seasons, from 2023-24 to 2024-25. The experiment was laid out in a Randomized Block Design with four replications, where each replication consisted of one tree per genotype. Plants were arranged with a spacing of 7 × 7 m. The data collection concentrated on a wide range of traits, including 26 related to vegetative growth, reproductive aspects and nut quality, along with nut yield. The average data from the years 2023-24 and 2024-25 was employed for the analysis. All quantitative measurements were taken using appropriate instruments, and qualitative observations were scored based on established protocols (Bhat *et al.,* 2). The analysis of variance (ANOVA) for each trait was estimated according to Gomez and Gomez (6). Genetic variability parameters, such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), were computed following the method described by Burton and Devane (3). Broad-sense heritability and genetic advance as a percentage of the mean (GAM) were determined according to Johnson *et al.* (7). The genotypic correlation coefficient was estimated using the standard procedure suggested by Miller *et al.* (8). All statistical computations were carried out using the R software (RStudio) with the variability package.

RESULTS AND DISCUSSION

The combined two-year ANOVA revealed significant genotypic variation in cashew genotypes for key traits such as tree height, trunk girth, canopy spread, nut yield, and kernel quality, indicating strong genetic influence (Table 2). Flowering intensity, length

Table 1: Cashew genotypes used for studying the variability.

S. No.	Genotypes	Source of collection
1.	CARS-1	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
2.	CARS-2	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
3.	CARS-3	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
4.	CARS-4	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
5.	CARS-5	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
6.	CARS-6	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
7.	CARS-7	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
8.	CARS-8	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
9.	CARS-9	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
10.	CARS-10	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
11.	CARS-11	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
12.	CARS-12	Dhanpunji, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
13.	CARS-13	Dhanpunji, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
14.	CARS-14	Rajnagar, Block−Bakawand, Dist. Bastar, Chhattisgarh
15.	CARS-15	Rajnagar, Block−Bakawand, Dist. Bastar, Chhattisgarh
16.	CARS-16	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
17.	CARS-17	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
18.	CARS-18	Kumhrawand, Block−Jagdalpur, Dist. Bastar, Chhattisgarh
19.	CARS-19	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
20.	CARS-20	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
21.	CARS-21	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
22.	CARS-22	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
23.	CARS-23	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
24.	CARS-24	Kaudawand, Block−Bakawand, Dist. Bastar, Chhattisgarh
25.	Vengurla-4	Regional Fruit Research Station, Vengurla, Maharashtra

Table 2: ANOVA, mean, range, GCV, PCV, heritability and genetic advance for growth, flowering, nut yield, kernel and apple quality characters in cashew.

S. No.	Characters	Mean sum of squares			Mean	Range		GCV (%)	PCV (%)	h^2 (Broad sense) %	GAM
		Replication (df = 3)	Genotype (df = 24)	Error (df = 72)		Min.	Max.				
1	Tree height (m)	0.006	9.96**	1.27	3.37	2.72	4.38	12.93	14.10	84.10	24.42
2	Trunk girth (cm)	0.02	1488.70**	22.27	40.15	30.41	49.27	11.40	13.01	76.80	20.58
3	Canopy spread E-W (m)	0.03	21.85**	7.39	4.15	3.05	5.94	13.26	15.27	75.40	23.71
4	Canopy spread N-S (m)	0.47	20.52**	5.60	4.17	2.82	5.94	15.14	16.31	86.20	28.95
5	Leaf size (cm^2)	17.63	647.09**	1060.03	133.41	123.71	141.09	1.37	3.65	14.10	1.06
6	Number of flowering laterals per m^2	0.47	20.52**	0.23	15.76	14.00	18.06	4.58	7.51	37.20	5.75
7	Flowering intensity (m^2)	1.98	849.94	486.72	77.57	72.33	82.87	1.67	4.18	16.00	1.37
8	Duration of flowering (days)	96.99	648.33	798.35	92.49	85.54	102.78	2.34	5.66	23.00	2.68
9	Length of inflorescence (cm)	1.73	20.58	18.42	19.26	18.32	20.36	0.12	3.67	0.10	0.01
10	Width of inflorescence (cm)	2.21	45.53	72.91	20.58	19.63	22.15	2.15	5.43	25.80	2.88
11	Fruit set (%)	0.06	86.84	58.40	11.78	8.49	14.59	6.85	14.53	22.20	6.66
12	Number of nuts $panicle^{-1}$	6.53	45.54**	21.08	5.44	4.13	8.00	14.68	20.95	49.10	21.19
13	Nut weight (g)	0.10	111.75**	2.17	7.46	5.16	11.56	20.84	20.98	98.60	42.62
14	Apple weight (g)	0.25	7220.43**	192.58	47.41	28.61	82.28	25.71	26.35	95.20	51.66
15	Nut yield $tree^{-1}$ (kg)	0.07	42.53**	1.32	4.58	3.55	7.01	20.01	20.61	94.30	40.03
16	Shell thickness (mm)	0.00	7.54**	2.22	3.04	2.26	3.97	10.49	15.19	47.80	14.94
17	Shelling (%)	0.08	155.15**	3.09	28.71	24.98	31.50	6.69	6.75	98.00	13.64
18	Kernel weight (g)	0.11	9.08**	1.41	2.14	1.36	2.97	18.47	21.58	73.20	32.56
19	Juice content (%)	17.85	245.76	183.45	68.14	64.75	74.71	2.44	4.32	32.00	2.85
20	TSS (°Brix)	0.32	17.61	17.81	11.56	10.54	12.88	0.27	7.53	0.10	0.02
21	Acidity (%)	0.00	0.10	0.15	0.49	0.42	0.57	4.54	10.14	20.00	4.18
22	Ascorbic acid (mg100 ml^{-1})	81.10	1993.52	3418.11	196.55	182.05	207.85	2.46	5.40	22.60	2.51
23	Total sugars (%)	0.46	7.54	9.11	10.60	9.89	11.47	0.43	5.46	0.70	0.08
24	Reducing sugars (%)	0.09	6.11	5.48	8.90	8.11	9.67	1.35	5.93	5.20	0.64
25	Non reducing sugars (%)	0.13	1.70	2.74	1,51	1.13	1.74	4.45	14.29	9.70	2.85
26	Tannin (mg 100 ml^{-1})	39.83	6118.47	2273.47	161.95	140.33	188.49	4.64	9.34	24.60	4.74

of inflorescence and fruit set did not demonstrate any significant changes. Nut weight, shelling percentage, and kernel weight were highly significant, suggesting potential for selective breeding. Juice content, TSS, and sugar-related traits exhibited non-significant variation, implying minimal genetic control over these characteristics. Previous studies by Mohapatra *et al*. (9), Adu-Gyamfi *et al.* (1) and Ramteke *et al.* (11) similarly observed significant variability in morphological and yield-related traits among cashew genotypes.

Mean performance, variability range, and genetic parameters, including genetic advance as a percentage of the mean (GAM), heritability in the broad sense (h^2), PCV (phenotypic coefficient of variation), and GCV (genotypic coefficient of variation), are summarized in Table 2. All variables showed significant variability, with PCV values consistently greater than GCV, suggesting both genetic and environmental influences. The findings highlight substantial diversity among the studied traits, suggesting potential for selective breeding while accounting for external factors.

The GCV values highlight substantial genetic variability for several key traits. Nut weight (20.84 %) and apple weight (25.71%) showed the highest

GCV, indicating excellent potential for genetic improvement. Canopy spread N-S (15.14 %) and number of nuts per panicle (14.68 %) also exhibited considerable genetic variation. Moderate GCV was observed for trunk girth (11.40 %) and shell thickness (10.49 %). The high GCV for yield-related traits suggests these characteristics are particularly responsive to selection, whereas low GCV in vegetative traits implies limited genetic diversity for these features in the studied population (Chandrasekhar *et al.,* 2018). Apple weight (26.35%) and nut yield (20.61%) maintained high PCV, though with only slight increases over their GCV, indicating strong genetic control. The canopy traits showed moderate PCV (15.27-16.31%), with slightly higher values than GCV, suggesting some environmental modification of growth patterns. Traits like TSS (7.53% PCV vs 0.27% GCV) and total sugars (5.46% PCV vs 0.43% GCV) showed dramatic PCV-GCV disparities, highlighting their environmental sensitivity and poor suitability for direct selection.

The heritability in broad sense estimates reveal exceptionally strong genetic control for several economically important traits. Nut weight (98.60 %), apple weight (95.20 %) and shelling percentage (98.00 %) showed near-perfect heritability, indicating these traits are predominantly governed by additive gene effects. Canopy spread N-S (86.20 %) and tree height (84.10 %) also exhibited high heritability, suggesting reliable inheritance of growth habits. Moderate heritability was observed for number of nuts per panicle (49.10 %) and kernel weight (73.20 %). Apple weight (51.66%) and nut weight (42.62%) had particularly substantial GAMs, indicating enormous potential for rapid genetic improvement. Nut yield (40.03 %) and canopy spread N-S (28.95 %) also showed moderate potential. Traits with both high heritability and high GAM (nut weight, apple weight, yield) represent ideal targets for breeding, while those with low values (TSS, flowering traits) would require alternative improvement strategies.

The two-year data confirm the exceptional breeding potential of several key cashew traits. The combination of high heritability and high genetic advance for nut weight, apple weight, and yield components suggests these traits respond strongly to selection, with gains reliably transmitted to progeny. This supports the results of Adu-Gyamfi *et al.* (1) in Ghanaian cashew and supports the breeding strategies employed in Indian programs (Mohapatra *et al*., 9; Sethi *et al*., 14). These results strongly suggest that conventional breeding should focus on the high heritability-high GA traits, while genomic tools may be needed to address complex, low heritability characteristics. The stability of these findings across two years enhances confidence in their application to cashew improvement programs.

The genotypic correlation analysis revealed significant associations among 26 key traits in cashew, providing valuable insights for breeding strategies (Table 3). Strong positive correlations (p<0.01) were observed between vegetative traits, particularly

Table 3: Genotypic correlation coefficient among traits in cashew.

Traits	TH	TG	CSEW	CSNS	LS	NFL	FI	DF	LI	WI	FS	NNPP	NW
TH	1												
TG	0.899**	1											
CSEW	0.328*	0.358*	1										
CSNS	0.52**	0.7**	0.849**	1									
LS	-0.045	-0.192	0.005	0.006	1								
NFL	0.004	0.139	0.128	0.037	0.156	1							
FI	0.256*	0.275*	0.502**	0.435**	0.575**	0.456**	1						
DF	-0.021	0.034	0.178	0.312*	0.156	0.101	-0.198	1					
LI	0.199	0.167	-0.198	-0.078	-0.105	0.045	0.203	-0.289*	1				
WI	-0.154	-0.128	-0.056	0.198	0.109	0.023	-0.078	-0.089	-0.056	1			
FS	-0.179	-0.132	-0.14	0.185	0.312*	0.456**	0.278*	0.167	-0.186	-0.191	1		
NNPP	-0.264*	-0.087	0.145	0.306*	0.479**	0.542**	0.306*	0.174	0.124	0.034	0.678**	1	
NW	0.317*	0.476**	-0.063	-0.07	-0.673**	0.082	0.156	-0.204	0.109	-0.126	-0.456**	-0.464*	1
AW	0.515**	0.544**	-0.057	0.112	-0.399**	0.121	0.078	-0.076	0.045	-0.151	-0.265*	-0.409**	0.709**
NY	-0.078	-0.041	0.245*	0.254*	0.675**	0.769**	0.487**	0.095	-0.079	0.167	0.789**	0.925**	-0.178

Contd...

Table 3 contd...

Traits	TH	TG	CSEW	CSNS	LS	NFL	FI	DF	LI	WI	FS	NNPP	NW
STH	0.026	0.036	0.121	-0.15	-0.463**	0.316*	0.184	-0.245*	0.067	0.189	0.076	-0.188	0.256*
SHL	0.129	0.899**	0.328*	0.52**	-0.045	0.004	-0.067	0.087	0.167	-0.278*	-0.179	-0.264*	0.317*
KW	0.899**	0.089	0.358*	0.712**	-0.192	0.139	-0.043	-0.078	0.097	-0.032	-0.132	-0.087	0.476**
JC	0.328*	0.358*	-0.073	0.849**	0.005	0.128	0.264*	0.303*	-0.298*	-0.116	-0.147	0.306*	-0.063
TSS	0.52**	0.7**	0.849**	-0.103	0.006	0.037	0.222	0.045	-0.167	-0.206	0.185	0.306*	-0.07
ACID	-0.045	-0.192	0.005	0.006	0.046	0.156	-0.081	-0.089	-0.209	-0.076	-0.045	-0.198	-0.103
ASCOR	0.004	0.139	0.128	0.037	0.156	0.153	-0.176	0.145	-0.051	0.173	0.145	0.054	0.022
TSUG	0.154	0.094	0.032	-0.095	-0.054	-0.256*	-0.045	-0.174	-0.047	0.117	-0.132	-0.439**	0.156
RSUG	0.098	0.067	-0.045	-0.098	-0.045	-0.261*	-0.012	-0.176	-0.340	0.121	-0.129	-0.467**	0.109
NRSUG	0.108	0.132	-0.076	-0.043	0.256*	0.043	0.013	0.131	-0.045	-0.165	0.023	-0.041	0.087
TANN	0.208	0.098	0.143	0.045	-0.045	0.031	0.184	-0.124	-0.206	0.121	0.078	-0.149	0.561**

Traits	AW	NY	STH	SHL	KW	JC	TSS	ACID	ASCOR	TSUG	RSUG	NRSUG	TANN
TH													
TG													
CSEW													
CSNS													
LS													
NFL													
FI													
DF													
LI													
WI													
FS													
NNPP													
NW													
AW	1												
NY	-0.080	1											
STH	0.190	0.149	1										
SHL	-0.530**	0.172	-0.109	1									
KW	0.607**	-0.178	0.185	-0.135	1								
JC	0.115	0.761**	0.029	0.037	-0.252*	1							
TSS	0.045	0.145	-0.109	0.089	0.031	0.089	1						
ACID	0.049	0.078	-0.148	0.267*	0.131	-0.034	0.204	1					
ASCOR	-0.189	0.156	-0.134	-0.108	-0.121	-0.045	-0.387**	-0.418**	1				
TSUG	0.121	-0.085	0.456**	-0.205	0.145	-0.334*	0.178	-0.145	0.109	1			
RSUG	0.098	-0.091	0.317*	-0.145	0.156	-0.563**	0.298*	-0.034	0.034	0.987**	1		
NRSUG	0.198	0.134	0.412**	-0.167	0.106	0.323*	0.045	-0.178	0.187	0.476**	0.167	1	
TANN	0.563**	-0.234*	0.176	0.078	-0.045	-0.245*	0.145	0.104	-0.089	0.267*	0.289*	0.089	1

TH: Tree Height, TG: Trunk girth, CSEW: Canopy Spread in East West Direction, CSNS : Canopy Spread in North South Direction; LS : Leaf Size, NFL : Number of Flowering Laterals m-2, FI: Flowering Intensity, DF : Duration of Flowering : LI : Length of Inflorescence, WI : Width of Inflorescence, FS : Fruit Set, NNPP : Number of Nuts Panicle-1, NW : Nut Weight, AW : Apple Weight, STH : Shell Thickness, SHL : Shelling %, KW : Kernel Weight, JC : Juice Content, TSS : Total Soluble Solids, ACID : Titratable Acidity, ASCOR : Ascorbic Acid, TSUG : Total Sugars, RSUG : Reducing Sugars, NRSUG : Non Reducing Sugars, TANN : Tannin
*Significant at $p<0.05$; **Significant at $p<0.01$

tree height (TH) with trunk girth (TG, r=0.899) and kernel weight (AW, r=0.607). Canopy dimensions showed particularly strong interdependence (CSEW-CSNS, r=0.849), indicating their potential as complementary selection criteria. Leaf size showed significant negative association with nut weight (r= -0.673); however, it showed positive association with nut yield (r =0.675). For yield components, nut yield per plant (NY) demonstrated highly significant positive correlations with reproductive traits including number of flowering laterals (NFL, r=0.769), fruit set percentage (FS, r=0.789) and nut number per panicle (NNPP, r=0.925), highlighting panicle productivity as a primary yield determinant. The negative association between nut weight (NW) and NY (r=-0.178) revealed an important yield-component trade-off that breeders must consider when selecting for either trait. Kernel weight (KW), a key quality parameter, showed particularly strong relationships with TG (r=0.899) and CSNS (r=0.712), suggesting that robust canopy development supports kernel filling. Notably, tannin content (TANN) correlated positively with NW (r=0.561). Apple weight (AW) showed strong positive correlations with kernel weight (KW, r=0.607) and tannin content (TANN, r=0.563). For biochemical traits, total soluble sugars (TSS) showed a significant negative correlation with ascorbic acid (ASCOR, r=-0.387), while reducing sugars (RSUG) and non-reducing sugars (NRSUG) were strongly interrelated (r=0.987). The strong positive associations between vegetative traits (tree height, trunk girth, and canopy dimensions) suggest that selection for robust plant architecture could simultaneously improve multiple growth parameters. Notably, nut yield showed highly significant correlations with reproductive traits (flowering laterals, fruit set, and nut number per panicle), highlighting panicle productivity as a key yield determinant. However, the negative correlation between nut weight and yield emphasizes a critical trade-off that breeders must balance. The positive linkage between kernel weight and structural traits (trunk girth, canopy spread) indicates that vigorous growth supports kernel development. Biochemical analysis revealed important relationships, particularly the inverse correlation between TSS and ascorbic acid, which may influence fruit quality. The results agree with prior investigations by Sethi *et al.* (13), Chaithra *et al.* (4) and Yadawad *et al.* (15), who similarly indicated favourable associations between nut yield and fruit set; flowering intensity and the number of nuts panicle^{-1}.

AUTHOR'S CONTRIBUTION

Conceptualization and designing of the research work (VR, PB, JDA); Execution of field/lab experiments (VR, PT); Data collection (VR, PB); Analysis of data and interpretation (VR, PT, EE); Preparation of manuscript (VR, PT).

DECLARATION

The authors affirm that they do not have any potential conflicts of interest.

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