Genetic analysis in cashew (*Anacardium occidentale* L.)

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Abstract

Genetic analysis in cashew with 12 genotypes and 14 morphological traits revealed that the genotypes showed significant variation with respect to all characters except number of primary branches. Number of perfect flowers m^{-2}, number of nuts m^{-2}, apple weight, nut weight and kernel weight provided a clear separation of the genotypes. Number of perfect flowers m^{-2} and number of nuts m^{-2} had high heritability indicating the reliability of these traits in selection. Number of nuts m^{-2} also had significant positive correlation and direct effect on yield. Apple weight showed significant negative correlation and significant negative direct effect with yield. Cluster analysis could group the accessions into four clusters. Cluster I (Sulabha, Priyanka and P-3-2) and Cluster II (Mdk-1, AKM-1 and K-22-1) were the most divergent. Members of these two clusters can be utilized for hybridization in all possible combinations to yield superior cashew hybrids.

Keywords: Correlation, divergence, variability

Introduction

Cashew (*Anacardium occidentale* L.), a native of tropical America, was one of the first fruit trees from the New World to be widely distributed throughout the tropics by the early Portuguese and Spanish adventurers. Since then, it has acclimatized to Indian conditions and now, India exports about 1.2 lakh tonnes of cashew kernel to over 65 countries. Being a dollar-earning crop, it supports the economy of not only the farming community but also the industry and the export entrepreneurs.

Being a highly cross-pollinated heterozygous polyploid crop, cashew shows enormous variability in different morphological, physiological and anatomical characters. Considerable segregation due to heterozygosity creates lot of variation among the accessions (Rao and Bhat, 1996). Even though wide variation exists in cashew, it is difficult to obtain a single tree possessing all the desirable characters.

Crop improvement through conventional breeding methods in cashew includes introduction, clonal selection and hybridization followed by selection. Depending on the extent of natural variability among the genotypes and the association between yield and component characters, trees with desirable traits are identified and used for breeding programmes. Once the high-yielding trees are identified, commercial exploitation through suitable methods of vegetative propagation can be adopted in cashew. In the present study the vegetative, flowering and yield characters in cashew are assessed statistically to conclude the genetic basis of cashew for crop improvement.

Materials and Methods

The experimental material comprised of 12 genotypes (Table 1) maintained at the Demonstration Plot, Cashew Research Station, Madakkathara. Five plants for each genotype planted during 1993 at a spacing of 7.5 m x 7.5 m were selected for the study. The selection was based on the uniformity in morphology of trees within each genotype. The trees were critically observed during the vegetative and reproductive phases for the following morphological characters.

Vegetative characters

1   *Height of the tree*: Measured from the ground level to the tip of the topmost leaf expressed in m.

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Table 1. Details of the genotypes selected for the study

Code	Name of the genotype selected for the study	Year of release	Parentage
V1	Sulabha (K-10-2)	1996	Selection from Kottarakkara
V2	Dharasree (H-3-17)	1996	T 30 X Brazil-18
V3	H-1593	2004	BLA-139-1 X K-30-1
V4	Mdk-2 (NDR-2-1)	1990	Neduvellur Material
V5	Damodar (H-1600)	2002	BLA-139-1 X H-3-13
V6	Mdk-1 (BLA-39-4)	1990	T.No. 39 of Bapatla
V7	AKM-1 (BLA-139-1)	1982	T.No. 139 of Bapatla
V8	K-22-1	1987	Selection from Kottarakkara
V9	Priyanka (H 1591)	1995	BLA-139-1 X K-30-1
V10	Kanaka (H1598)	1993	BLA-139-1 X H-3-13
V11	Dhana (H-1608)	1993	ALGD-1 X K-30-1
V12	P-3-2	Not released	Exotic Genotype from Panama

ᴸ *Trunk girth*: Measured at 1.5 m above the ground level and expressed in cm.

ᴸ *Canopy spread*: Average of the East-West and North-South spread expressed in m.

ᴸ *No. of primary and secondary branches*: Visually recorded.

ᴸ *Leaf area*: Average of 3rd, 4th and 5th central leaves using Leaf Area Meter, LI-3000 A, Li-Cor. Inc., Nebraska, USA (Bhagwan and Mohan, 1983).

Flowering characters

ᴸ *Number of panicles m^{-2}*: Average of the number of panicles observed at 10 randomly selected quadrants of 1 m^2 in the canopy.

ᴸ *Number of hermaphrodite flowers m^{-2}*: Recorded in the western direction throughout the flowering season.

ᴸ *Number of mature nuts m^{-2}*: Recorded in all the four directions i.e. North, South, East and West.

Yield characters

ᴸ *Apple weight*: Average weight of 10 apples expressed in g.

ᴸ *Nut weight*: Average weight of 100 nuts expressed in g.

ᴸ *Shelling percentage*: Worked out as the ratio of weight of kernels to the weight of raw nuts.

ᴸ *Kernel weight*: Average weight of 100 kernels was recorded and expressed in g.

Analysis of growth and yield components

The data generated on morphological characters of the 12 genotypes were analysed using SPAR1 package developed at IASRI, New Delhi. Analysis of variance was performed on morphological characters. Genotypic and phenotypic coefficient of variation, heritability and genetic advance were worked out for each character separately. Morphological characters associated with yield were identified through genotypic and phenotypic correlation coefficient and path coefficient analysis. Non-hierarchial Euclidean cluster analysis was done using the package following the method suggested by Spark (1973).

Results and Discussion

Genetic analysis in cashew was undertaken using 14 morphometric traits in 60 cashew trees belonging to 12 cashew genotypes. Analysis of variance showed significant F value for all the variables except for the number of primary branches suggesting significant variation among the genotypes for these parameters (Table 2).

All the variables studied, except the number of primary branches, can be used to distinguish the genotypes from each other. The high F values for the characters such as number of perfect flowers m^{-2}, nut weight, number of nuts m^{-2}, apple weight and kernel weight provide a clear separation of the genotypes. The number of perfect flowers per panicle was found to vary significantly among cashew types by Sheshagiri (1996) and Reddy *et al.* (2001). Similarly, Sena *et al.* (1995) and Lenka *et al.* (1998) had found significant variation in apple weight among the various apple characters studied. Nut weight and kernel weight were found to show significant variation in 30 cashew accessions in the studies by Jayalekshmy and John (2004). Number of nuts per panicle was found to vary significantly by Lenka *et al.* (2001).

High Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability and genetic advance were found for the number of perfect flowers m^{-2} indicating the reliability of this trait for selection for high nut yield (Table 2). Lenka *et al.* (1999) had observed similar results for number of perfect flowers per panicle. In this study, GCV and PCV values were high and genetic advance was moderate for number of nuts m^{-2} and nut yield. Number of nuts m^{-2} showed very high heritability. Lenka *et al.* (2001) found high GCV, heritability and genetic advance for nut yield per plant, number of male flowers per panicle, number of perfect flowers per panicle and number of nuts per panicle.

Table 2. Mean values of different characters for the genotypes studied

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
V1	5.81	54.08	**2.25**	8.00	7.04	**81.14**	18.50	15.75	1099.25	84.58	9.05	2.58	27.90	8.28
V2	6.30	71.94	2.75	8.25	7.89	67.68	20.50	25.75	926.75	85.77	7.62	2.45	29.01	4.73
V3	5.46	67.41	2.75	7.25	7.82	69.15	21.00	**37.50**	1833.75	74.15	8.36	1.83	27.65	**10.00**
V4	6.12	79.75	3.00	9.75	7.90	64.59	**15.00**	15.50	**568.00**	46.71	8.52	1.76	25.96	7.94
V5	**6.31**	68.00	**2.25**	9.00	7.94	71.56	21.50	14.25	939.75	70.20	8.41	1.77	25.83	6.76
V6	5.38	72.88	3.25	10.25	**6.09**	**45.38**	24.50	22.00	1191.00	**42.44**	6.25	1.54	24.61	7.16
V7	5.69	59.04	3.25	**13.50**	7.55	59.83	**26.50**	22.50	1091.50	47.76	**6.04**	1.58	27.25	4.42
V8	6.03	60.50	2.75	10.00	6.36	57.87	22.25	22.50	1016.50	76.67	6.69	**1.45**	23.85	7.84
V9	5.94	59.50	3.00	10.25	7.87	79.99	17.25	20.75	**2802.00**	82.91	**11.87**	**2.65**	25.27	5.35
V10	6.04	78.75	**3.75**	9.75	**9.19**	58.35	25.00	21.25	1070.50	81.67	6.84	1.98	**29.04**	5.97
V11	6.19	**79.94**	2.75	11.75	8.31	58.83	20.25	17.50	1720.25	55.23	7.95	2.28	28.57	7.44
V12	**4.50**	**48.86**	3.00	**7.00**	6.18	68.27	**15.00**	**10.50**	1744.25	**103.56**	7.81	1.88	24.08	**2.77**
GM	**5.81**	**66.72**	**2.90**	**9.56**	**7.51**	**65.22**	**20.60**	**20.48**	**1333.63**	**70.97**	**7.95**	**1.98**	**26.58**	**6.55**
SEM	0.25	5.00	0.56	1.31	0.45	4.39	1.58	1.75	135.75	4.96	0.39	0.14	1.45	1.62
CD	0.72	14.35	1.61	3.77	1.28	12.60	4.54	5.02	389.71	14.25	1.11	0.40	4.16	4.65
F	8.43	8.60	1.12	3.99	8.71	10.45	11.00	31.07	38.83	29.21	32.27	22.09	3.41	3.03

V1 : Sulabha (K-10-2)	V9 : Priyanka (H-1591)	X1 : Tree height (m)	X9 : Number of perfect flowers m^{-2}
V2 : Dharasree (H-3-17)	V10: Kanaka (H-1598)	X2 : Tree girth (cm)	X10: Apple weight (g)
V3 : H-1593	V11: Dhana (H-1608)	X3 : Number of primary branches	X11: Nut weight (g)
V4 : Mdk-2 (NDR-2-1)	V12: P-3-2	X4 : Number of secondary branches	X12: Kernel weight (g)
V5 : Damodar (H-1600)	GM : Grand Mean	X5 : Canopy spread (m)	X13: Shelling percentage
V6 : Mdk-1 (BLA-39-4)	SEM : Standard Error of Means	X6 : Leaf area(cm^2)	X14: Yield (kg/ tree)
V7 : AKM-1 (BLA-139-1)	CD : Critical Difference (P=0.05)	X7 : Number of panicles m^{-2}	Bold figures show range and Grand Mean
V8 : K-22-1	F : F value	X8 : Number of nuts m^{-2}	

Yield in any crop is a complex character determined by a number of genetic factors and environmental conditions occurring at various growth stages of the plant. In cashew, it becomes more complicated due to high heterogenity and heterozygosity being a cross-pollinated polyploid showing polygenic inheritance for morphological traits (Rao *et al.,* 1998). Knowledge of the relationship of yield with other characters becomes essential for effective screening of genotypes for selection. Path coefficient analysis showing direct and indirect effects of individual components on yield supplements the correlation studies so that the breeder may be able to select superior trees based on some of the important characters.

In this study, the results of the correlations between yield and 13 other characters showed that nut yield was found to be significantly correlated with tree height, tree girth, number of primary branches, number of nuts m^{-2} and apple weight (Table 3). Among the vegetative traits, tree height and tree girth showed significant positive correlation with yield. The same was reported by Reddy *et al.* (1996) and Naik *et al.* (1997). Both tree height and number of primary branches had significant positive direct effect on yield. But number of primary branches

showed significant negative correlation with yield. This may be due to its significant negative indirect effect through tree girth, number of secondary branches, nut weight and kernel weight. In this study, canopy spread showed a weak positive correlation with yield.

Number of nuts m^{-2} was found to be most significantly and positively correlated with nut yield and its direct effect was significant and positive. Number of perfect flowers per m^2 showed a significant negative direct effect and a weak negative correlation with yield. Samal *et al.* (2001) found that perfect flowers and number of flowering panicles m^{-2} showed non-significant correlation with yield. Kumar and Udupa (1996) observed that number of perfect flowers per panicle was positively correlated with yield and that along with four other characters, significantly influenced yield. Lenka *et al.* (2001) had found that number of flowers per panicle, nut weight and number of nuts per panicle were the best contributors to nut yield and further, number of staminate flowers and perfect flowers showed high positive association with nut yield both at genotypic and phenotypic levels. This may be due to the significant positive indirect effects of number of perfect flowers m^{-2} on yield through nut weight and tree girth as

Table 3. Genotypic correlations between different characters

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
X1	1.000	0.665**	-0.463**	0.402**	0.668**	0.069	0.184	0.119	-0.334*	-0.304*	0.158	0.559**	0.566**	0.403**
X2		1.000	0.523**	0.276	0.688**	-0.512**	0.258	0.214	-0.359*	-0.596**	-0.224	0.142	0.474**	0.469**
X3			1.000	0.480**	0.648**	-1.426**	1.190**	0.243	0.095	-0.569**	-1.234**	-0.807**	-0.105	-1.508**
X4				1.000	0.225	-0.532**	0.655**	-0.065	-0.055	-0.775**	-0.310*	-0.049	0.073	-0.176
X5					1.000	0.180	0.178	0.204	0.014	-0.069	0.244	0.526**	0.963**	0.117
X6						1.000	-0.658**	-0.120	0.378*	0.621**	0.865**	0.592**	0.179	0.003
X7							1.000	0.466**	-0.280	-0.425**	-0.702**	-0.200	0.365*	0.108
X8								1.000	0.170	-0.104	-0.121	0.107	0.416**	0.564**
X9									1.000	0.343*	0.655**	0.336*	-0.196	-0.163
X10										1.000	0.346*	0.206	-0.009	-0.429**
X11											1.000	0.668**	-0.099	0.106
X12												1.000	0.674**	0.151
X13													1.000	0.072
X14														1.000

X1: Tree height (m)
X2: Tree girth (cm)
X3: Number of primary branches
X4: Number of secondary branches
X5: Canopy spread (m)
X6: Leaf area (cm^2)
X7: Number of panicles m^{-2}
X8: Number of nuts m^{-2}
X9: Number of perfect flowers m^{-2}
X10: Apple weight (g)
X11: Nut weight (g)
X12: Kernel weight (g)
X13: Shelling percentage
X14: Nut yield (kg)
** Significant at 1% level
* Significant at 5% level

reported in this study. Apple weight showed significant negative correlation with nut yield. Reddy *et al.* (1996) had also observed significant negative correlation of nut yield with apple weight both at phenotypic and genotypic levels.

Among the Interco relations of the different characters, number of nuts m^{-2} and apple weight had significant negative correlation. Samal *et al.* (2001) also had reported inverse correlation of number of nuts per panicle with apple weight. Therefore, both these parameters may not be considered simultaneously to improve nut yield in cashew. This is in corroboration

with the finding of Sena *et al.* (1995). Apple weight and nut weight had significant positive correlation with each other.

In order to study the direct and indirect effects of the 13 variables considered for the estimation of genotypic correlation coefficients, path coefficient analysis was done. The result showed that about 50 per cent of the variability in the nut yield was contributed by the 13 characters recorded in the study (Table 4). Significant positive direct effects and weak positive correlations with yield were reported for nut weight and kernel weight.

Table 4. Direct and indirect effects of thirteen characters on nut yield of cashew

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	**0.473***	-0.575*	-0.262	-0.343*	0.039	-0.023	-0.008	0.118	0.462*	0.299	0.192	0.485*	-0.454*
X2	0.314*	**-0.865***	0.295	-0.235	0.041	0.167	-0.011	0.211	0.495*	0.586*	-0.272	0.123	-0.381*
X3	-0.219	-0.452*	**0.565***	-0.409*	0.038	0.464*	-0.050	0.241	-0.132	0.559*	-1.498*	-0.700*	0.085
X4	0.190	-0.238	0.271	**-0.853***	0.013	0.173	-0.027	-0.065	0.076	0.762*	-0.377*	-0.043	-0.059
X5	0.316*	-0.596*	0.366*	-0.192	**0.059**	-0.059	-0.007	0.202	-0.020	0.068	0.296	0.456*	-0.773*
X6	0.033	0.443*	-0.806*	0.454*	0.011	**-0.326***	0.027	-0.119	-0.522*	-0.611*	1.050*	0.513*	-0.144
X7	0.087	-0.223	0.672*	-0.558*	0.011	0.214	**-0.042**	0.461*	0.387*	0.418*	-0.852*	-0.174	-0.293
X8	0.056	-0.185	0.138	0.056	0.012	0.039	-0.019	**0.989***	-0.235	0.102	-0.147	0.093	-0.334*
X9	-0.158	0.310*	0.054	0.047	0.001	-0.123	0.012	0.168	**-1.381***	-0.337*	0.795*	0.291	0.158
X10	-0.144	0.516*	-0.322*	0.661*	-0.004	-0.202	0.018	-0.103	-0.473*	**-0.983***	0.420*	0.179	0.008
X11	0.075	0.194	-0.697*	0.265	0.014	-0.282	0.029	-0.120	-0.904*	-0.340*	**1.214***	0.579*	0.079
X12	0.264	-0.123	-0.456*	0.042	0.013	-0.193	0.008	-0.106	-0.464*	-0.202	0.810*	**0.867***	-0.542*
X13	0.267	-0.410*	-0.060	-0.063	0.057	-0.058	-0.015	0.411*	0.271	0.009	-0.120	0.585*	**-0.803***

Residual effect: 0.5084

X1: Tree height (m)
X2: Tree girth (cm)
X3: Number of primary branches
X4: Number of secondary branches
X5: Canopy spread (m)
X6: Leaf area (cm^2)
X7: Number of panicles m^{-2}
X8: Number of nuts m^{-2}
X9: Number of perfect flowers m^{-2}
X10: Apple weight (g)
X11: Nut weight (g)
X12: Kernel weight (g)
X13: Shelling percentage
*Significant direct or indirect effects
**Significant at 1% level (correlation coefficients)
Bold figures indicate direct effects.

The high residual effect revealed in the path studies indicates the influence of other factors like environment on yield. Variability due to other yield contributing characters not included in the study may also account for high residual effect. Rao (2002) had also reported significant influence of climate on yield in cashew.

Non-heirarchial Euclidean cluster analysis grouped the twelve cashew genotypes into four clusters (Fig. 1). Cluster I consisted of 3 genotypes (Sulabha, Priyanka and P-3-2), Cluster II consisted of 3 genotypes (Mdk-1, AKM-1 and K-22-1), Cluster III, a single genotype (H-1593) and Cluster IV consisted of 5 genotypes (Dharasree, Mdk-2, H-1600, Kanaka and Dhana).
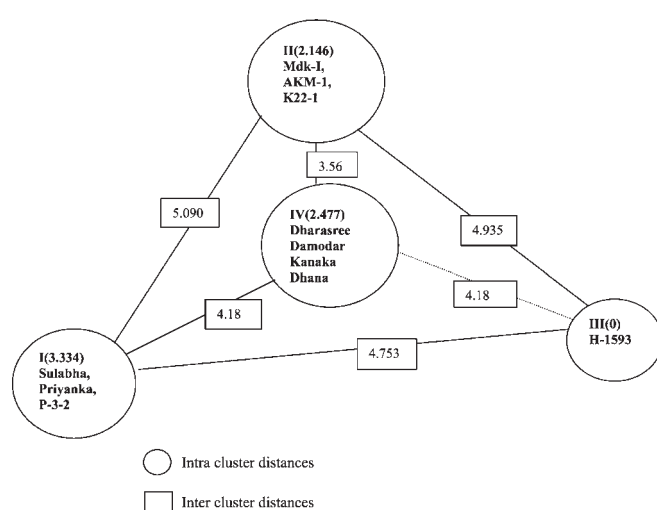

Fig. 1. Cluster diagram of cashew genotypes

Cluster I showed the highest mean for leaf area (76.47 m^2), number of perfect flowers per m^2 (1881.83), apple weight (90.35 g), nut weight (9.57 g) and kernel weight (2.17 g) (Table 5).

The average intracluster distances in the three clusters ranged from 0 (Cluster III) to 3.334 (Cluster I) with Cluster II having a value of 2.146 and Cluster IV with 2.477. This indicates that the members of cluster II (Mdk-1, AKM-1 and K-22-1) are more uniform with respect to the characters under study. The intercluster distances show that Cluster I and II were the farthest (5.090) and the Clusters II and IV were the closest (3.561). According to Falconer (1981), for obtaining maximum heterosis members possessing widest genetic distance have to be combined. Members of the Cluster I (Sulabha, Priyanka and P-3-2) and the Cluster II (Mdk-1, AKM-1 and K-22-1), the two farthest clusters can be used for hybridization programmes in all possible combinations to get maximum heterosis.

Table 5. Cluster means for different characters

Sl. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV
1.	Tree height (m)	5.42	5.7	5.46	**6.19**
2.	Tree girth (cm)	54.15	64.14	67.41	**75.68**
3.	Number of primary branches	2.75	**3.08**	2.75	2.90
4.	Number of secondary branches	8.42	**11.25**	7.25	9.70
5.	Canopy spread (m)	7.03	6.67	7.82	**8.25**
6.	Leaf area (cm^2)	**76.47**	54.36	69.15	64.20
7.	Number of panicles (m^{-2})	16.92	**24.42**	21.0	20.45
8.	Number of nuts (m^{-2})	15.67	22.33	**37.5**	18.85
9.	Number of perfect flowers (m^{-2})	**1881.83**	1099.67	1833.75	1045.05
10.	Apple weight (g)	**90.35**	55.62	74.15	67.92
11.	Nut weight (g)	**9.57**	6.33	8.36	7.87
12.	Kernel weight (g)	**2.17**	1.52	1.83	2.05
13.	Shelling percentage	25.75	25.24	27.65	**27.68**
14.	Nut yield (kg/plant)	5.47	6.47	**10.00**	6.57

Bold figures indicate the highest means among the clusters

Cluster I- Sulabha, Priyanka, P-3-2

Cluster II-Mdk-1,AKM-1,K 22-1

Cluster III- H 1593

Cluster IV-Dharasree,Damodar,Kanaka,Dhana

The present study shows that Cluster I with bold nut genotypes and Cluster II with small and medium nut weight were the farthest emphasizing the role of nut characters in assessing the genetic divergence. Jayalekshmy and John (2004) also reported the importance of nut characters in clustering cashew genotypes. But Lenka *et al.* (1999) had reported that apple weight contributed 36 % of genetic divergence and nut weight contributed only 17 % of genetic divergence.

Cashew is a perennial crop amenable to vegetative propagation and hence, superior varieties identified through selection can be easily multiplied by fixing the superiority. Characters which influence yield significantly and positively can help in fixing the selection criteria in cashew. This study could conclusively find that number of nuts m^{-2} influenced the yield positively and directly. This information can also be utilized for predicting the cashew yield during the middle of the bearing season. Hybridization and selection are the breeding techniques, which give the best opportunity to combine the desirable characters. Selection of suitable parents, which can contribute high heterosis, is one of the challenges faced by the breeders engaged in hybridization. This study suggests suitable parental combinations for obtaining high heterosis in cashew hybridizations. Varieties in cluster I (Sulabha, Priyanka, P-3-2) and varieties in cluster II (Mdk-1, AKM-1 and K-22-1) can be hybrized in all possible combinations to obtain superior cashew hybrids.

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