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Character Association and Multivariate Analysis in Cashew (*Anacardium occidentale* L.)

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Abstract

The cashew varieties tested in the experiment exhibited much variability among the vegetative and yield attributing traits. The heritability estimates ranged from 74.34% in total laterals to 97.44% in sex ratio indicating varied seasonal effect on character expression. High estimates of heritability (>60%) was obtained for all characters. The genetic gain was higher for all the traits except plant height, trunk girth, total laterals, flowering duration and shelling % (>20%) indicating the predominance of additive gene effects.Vegetative and flowering characters like trunk girth, canopy spread both in East-West and North-South direction, canopy area, nuts panicle^{-1}and nuts m^{-2} were significantly positively correlated with nut yield both at genotypic and phenotypic levels. It is evident from both direct and indirect effects of the characters at phenotypic level that canopy spread (East-West), canopy area, trunk girth and nuts panicle^{-1}would be of more value while selecting for yield. Multivariate analysis of tested cashew varieties revealed that crosses between genotypes of cluster V with genotypes of cluster VI may give rise to high yielding segregantsbecause of highest inter-cluster distance (441.034). Intercrossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the nut yield plant^{-1}. The results also indicate that selection of genotypes with high cluster mean values for particular attribute could be used in the hybridization programme for improvement of that character.

Keywords: Cashew, variability, character association, yield attributes, nut yield

1. Introduction

The major constraints of low production of cashewnut are due to inferior genetic stock coupled with poor management practices. Efforts to improve the cashew crop through breeding and agronomic measures were started in the early 1950's. The success of plant breeding depends on significant level of genetic variability in the original population followed by an efficient selection method for fixation of desirable genetic combinations (Pertriniani and Miranda Filho, 1987). The efficiency of breeding methods depends on the genetic mechanism involved in the inheritance of the traits to be improved such as the number of genes that influence it, gene actions and effect, genetic heritability, genetic gain and association with other traits. Cashew is being a highly cross pollinated crop, the seedling progenies are highly heterogeneous in nature. So,

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genetic variability is widely observed among the progenies both at phenotypic and genotypic levels (Samal, 2002). Morphological variability and character associated with high productivity of cashew was reported by Dela Cruz and Fletcher (1997). Cavalcanti (2000) concluded that the characters like plant height, canopy diameter and nut yield were sufficient for selection of clone. Swamy et al. (1990) quantified the variability for various characters and to select the superior clones having comparatively better yield. In the present study, efforts has been taken to estimate the character association and multivariate analysis for vegetative and yield traits in twenty five released cashew varieties of India.

2. Materials and Methods

A multi locational trial was laid out during the year 2008 using clonal planting materials of twenty five released cashew varieties collected from different co-operating centres of All India Coordinated Research Project on Cashew, India (Table 1). The grafted plants were planted at a spacing of 7.5×7.5 m^2 following Randomized Block Design (RBD) having six plants per treatment. The trial was replicated twice. Recommended package of practices were adopted uniformly to raise a good crop. The present study was undertaken during the year 2013-2015 with an objective to study the association among different vegetative, yield attributes, nut yield and multivariate analysis among the 25 released cashew varieties. Data were recorded on various vegetative growth parameters, yield attributing traits and nut yield of different cashew varieties adopting standard procedure as described by Swamy et al., 1998. Statistical procedures were followed for analysis of variance and covariance as stated by Singh and Choudhury, 1985. The simple correlation coefficients for each pair of characters were computed and the path co-efficient (direct and indirect effects) were calculated as per Dewey and Lu (1959).

Table 1: Details of source of collection of cashew varieties used in the experiment

Sl. No.	Name of cashew types	Source
1.	BPP-4, BPP-6, BPP-8	Cashew Research Station (CRS), Bapatla, Andhra Pradesh
2.	Bhubaneswar-1	Cashew Research Station (CRS), Bhubaneswar
3.	Chintamani-1, Ullal-1, Ullal-3, Ullal-4	Cashew Research Station (CRS), Hogalagere, Karnataka
4.	Jhargram-1	Cashew Research Station (CRS), Jharagram, West Bengal
5.	Madakkathara-1, Madakkathara-2, K-22-1, Dhana, Kanaka, Priyanka, Amrutha, UN-50	Cashew Research Station (CRS), Madakkathara, Kerala
6.	Vengurla-1, Vengurla-4, Vengurla-6, Vengurla-7	Regional Fruit Research Station (RFRS), Vengurle, Maharashtra
7.	VRI-3	Regional Research Station (RFRS), Vridhachalam, Tamil Nadu
8.	Bhaskara, NRCC Sel-2	Directorate of Cashew Research Puttur(DCR), Karnataka
9.	Goa-1	ICAR Research Complex for Goa, Ela, Old Goa.

3. Results and Discussion

3.1. Mean performance and variability

The mean performances of the twenty five genotypes with respect to the fifteen vegetative and economic traits revealed following results. The mean plant height among the twenty five genotypes varied from 3.06 m in VRI-3 to 4.35 m in BPP-8 with a mean value of 3.77 m. Trunk girth showed a greater variation ranging from 35.69 cm (Amrutha) to 57.35 cm (Vengurla-7) with a mean value of 45.81 cm.Canopy spread both in East-West and North-South direction varied from 3.53 m to 6.63 and 3.77 m to 6.92 m respectively in genotype Amrutha and Vengurla-7. Sharma et al., 2011; Dasmohapatra and Pattnaik, 2012a, Dadzie et al., 2014 and Tripathy et al., 2015 also recorded greater variability for vegetative traits in cashew.

Similarly, flowering lateral m^{-2} showed a greater variation among the genotypes. It ranges from 12.02 m^{-2} (Ullal-3) to 20.82 m^{-2} (VRI-3) with a mean value of 16.34 m^{-2}. Number of nuts panicle^{-1} ranged from 1.17 (Jhargram-1) to 5.83 (Bhubaneswar-1) with an overall mean of 3.97. Nut weight (g) ranged from 5.37 g (BPP-6) to 10.0 g (Priyanka) with an overall mean of 7.41 g and number of nuts m^{-2} ranged from 7.54 (Jharagram-1) to 30.40 (BPP-4) with a mean value of 21.03. Apple weight among cashew genotypes exhibited grater variation ranging from 30.67 (VRI-3) to 87.42 (Priyanka) with an overall mean of 51.45 g. Sex ratio varied from 0.08 (Ullal-1) to 0.8 (Kanaka) with an average value of 0.28 while flowering duration ranged from 75 days in Ullal-3 to 97.33 days in Chintamani-1 with an overall mean of 88.23 days. Shelling ranged from minimum 25.63% in genotype Priyankato 30.75% in Bhubaneswar-1 with an overall mean of 29.39%. Nut yield plant^{-1} showed a greater variation ranging from 1.31 kg (Jharagram-1) to 5.97 kg (Vengrula-7) with an overall mean of 3.61 kg. Similar variations in vegetative, yield attributing traits and nut yield in cashew were reported by Reddy et al., 1989, Gajbhiye et al., 2015; Hore et al., 2015, Poduval, 2015 and Chandrasekhar et al., 2018.

3.2. Coefficients of variations

Wide difference in mean performance as well as coefficient of variation both at phenotypic (PCV) and genotypic (GCV) levels in most of the characters confirmed existence of genetic variability in the tested cashew genotypes (Table 2 and 3). The estimates of coefficients of error variation (CVe) varied from 2.64% for shelling per cent to 16.21% for nuts m^{-2}.The estimates of PCV varied from 4.7% for shelling percentage to 65.15% for sex ratio. The estimates of GCV showed a similar trend and varied from 4.31% for shelling percentage to 65.29% for sex ratio. Higher magnitude of PCV and GCV shelling % indicates relatively higher contribution of this characters towards genetic variability.

Table 2: ANOVA of nut yield and its components in cashew

Characters	Blocks (3)	Genotypes (24)	Error (72)
Plant height (m)	0.060	0.309	0.043
Trunk girth(cm)	17.074**	71.884**	11.736
Canopy spread (East-West (m)	0.142	1.415	0.187
Canopy spread (North-South) (m)	0.007	1.537	0.200
Canopy area (m^2)	10.361**	107.963**	7.585
Flowering laterals m^{-2}	0.992	14.165**	2.710
Total laterals m^{-2}	5.504**	13.491**	3.327
Nuts panicle^{-1}	0.265	3.425**	0.3810
Nuts m^{-2}	5.181**	76.39**	11.619
Nut weight (g)	0.117	2.89**	0.2010
Apple weight (g)	51.374**	378.527**	23.860
Sex ratio	0.000	0.068	0.002
Flowering duration (days)	10.105**	66.165**	9.8710
Shelling %	0.237	3.813**	0.600
Nut yield (kg plant^{-1})	0.148	3.388**	0.253

**: indicate significance at (p=0.01) levels of probability respectively; Figure in parentheses indicate degrees of freedom for corresponding sources of variation

Table 3: Genetic parameters for nut yield and its component traits in Cashew

Characters	Range	Mean	CV%	PCV	GCV	Heritability	GA% over mean
Plant height (m)	3.06 to 4.35	3.77	5.52	10.41	9.65	85.97	15.75
Trunk girth (cm)	35.69 to 57.35	45.81	7.48	13.09	11.97	83.67	19.27
Canopy spread (East-West) (m)	3.53 to 6.63	4.93	8.78	17.06	15.9	86.77	26.06
Canopy spread (North-South) (m)	3.77 to 6.92	5.03	8.89	17.42	16.24	86.96	26.66
Canopy area (m^2)	11.44 to 39.34	20.42	13.49	35.99	34.7	92.97	58.88
Flowering laterals m^{-2}	12.02 to20.82	16.34	10.07	16.29	14.65	80.87	23.18
Total laterals m^{-2}	14.67 to22.8	18.35	9.94	14.15	12.29	75.34	18.77
Nuts panicle^{-1}	1.17 to 5.83	3.97	15.55	32.95	31.06	88.86	51.53
Nuts m^{-2}	7.54 to 30.4	21.03	16.21	29.38	27.06	84.79	43.85
Nut weight (g)	5.37 to 10	7.41	6.06	16.23	15.66	93.04	26.58
Apple weight (g)	30.67 to 87.42	51.45	9.49	26.74	25.89	93.70	44.10
Sex ratio	0.08 to 0.8	0.28	14.98	66.15	65.29	97.44	113.43
Flowering duration(days)	75.0 to 97.33	88.23	3.56	6.52	6.01	85.08	9.76
Shelling %	25.63 to 30.75	29.39	2.64	4.70	4.31	84.26	6.97
Nut yield (kg plant^{-1})	1.31 to 5.97	3.16	15.90	41.15	39.58	92.53	67.01

3.3. Heritability and genetic advance

Heritability is a measure of the genetic relationship existing between parent and progeny. In other words, it is a measure of the potentiality of an individual to transmit a particular trait to the offspring. The heritability estimate is useful in prediction of yield from generation to generation. The heritability estimates depend upon the amount of genetic variation in the population and the environmental conditions under which the population is evaluated. The heritability estimates ranged from 75.34% in total laterals to 97.44% in sex ratio indicating varied seasonal effect on character expression. High estimates of heritability (>60%) was obtained for all characters indicating predominance of heritable components of variation suggesting effectiveness of selection on the basis of phenotypic expression of the traits (Table 3).

Heritability is one of the factors influencing genetic gain under selection. Heritability estimates along with genetic gain is more reliable in predicting the effect of selection. Expected genetic advance for different characters expressed as percent of population mean ranged from 6.97% in shelling% to 113.43% in sex ratio at 10% selection intensity. High heritability estimates coupled with high genetic advance were observed for all the traits except for plant height, trunk girth, total laterals, flowering duration and shelling %. This indicated the presence of additive gene effects for these characters. This clearly indicated that selection in the desired direction might be quite effective for thesecharacters. Lenka et al., 2001, Dasmohapatra et al., 2012b, Sethi et al., 2016a and Mohapatra et al., 2018 reported similar variations in vegetative and yield contributing traits and nut yield of cashew both at genotypic and phenotypic level.

3.4. Nature of character association

The correlation coefficients provide useful information for choice of characters in a selection program. There were all together 105 sets of estimates both for genotypic and phenotypic correlation (Table 4). Out of 105 sets of phenotypic correlation coefficients, the positive association was observed for 76 sets and negative association in 29 sets. In genotypic correlation coefficients, the positive association was observed for 78 sets and negative association in 27 sets.

The phenotypic correlation recorded highest positive significant association (0.961) between canopy spread in North-South direction and canopy area while the lowest positive significant association (0.453) was found between nuts panicle^{-1} and nut yield. The correlation at genotypic level recorded highest positive significant association (0.988) between canopy spread in East-West direction and canopy spread in North-South direction whereas lowest positive significant association (0.398) was found between trunk girth and total laterals. The negative associations observed for apple weight with nuts panicle^{-1} (-0.431), nuts m^{-2}(-0.452) and flowering duration (-0.403) were found to be significant both at phenotypic and genotypic levels.

3.5. Association among yield component traits

Phenotypic correlation coefficients among the 14 characters (excluding yield) were positive and significant in 13 cases. Positive association though not significant were found in 49 cases and negative association was found in 25 cases. Genotypic correlation coefficient among the 14 characters (excluding yield) were significantly positive in 16 cases while non significant positive association was found in 49 cases. In 26 cases it observed negative association (Table 4). Plant height was significantly positively correlated with trunk girth canopy spread both in East-West and North-South direction and canopy area while it was significantly negatively correlated with nuts panicle^{-1}, nuts m^{-2} and flowering duration both at phenotypic and genotypic level. Similarly, trunk girth was significantly positively correlated with canopy spread (East-West and North-South direction) and canopy area at phenotypic and genotypic level. It also exhibited significant positive correlation with total laterals m^{-2}at genotypic level. Canopy spread in East-West direction exhibited significant positive association with canopy spread in North-South direction and canopy area Both at genotypic and phenotypic level. It showed positive association though not significant with flowering laterals, total laterals, nut weight, apple weight, sex ratio, flowering duration and shelling %. Canopy spread in North-South showed significant positive association with plant height, trunk girth, canopy spread in East-West direction and canopy area at both the level of significance. The association of canopy spread in North-South direction was positive (non significant) with flowering laterals , total laterals , nut weight, apple weight, sex ratio, flowering duration and shelling % while its association was negative (non significant) with nuts panicle^{-1}and nuts m^{-2}. The association of canopy area with different vegetative and yield attributing traits showed similar results as that of canopy spread in both (East-West and North-South) directions. At phenotypic and genotypic levels flowering laterals m^{-2} exhibited significant positive association with total laterals. Nuts panicle^{-1} exhibited positive significant association with nuts m^{-2} and negative significant association with apple weight. Nuts m^{-2} exhibited significant negative association with apple weight while nut weight exhibited positive significant association with apple weight. Apple weight exhibited positive significant association with nut weight but negative significant association with nuts panicle^{-1}, nuts m^{-2} and flowering duration. Sex ratio exhibited both positive and negative associations though not significant with all characters.Flowering duration recorded significantly negative association with apple weight both at phenotypic and genotypic level. Shelling % showed positive association with all the characters except nuts m^{-2}, sex ratio and flowering duration. Similar, correlation among different vegetative and yield attributing traits were also reported by Sena et al., 1994, Reddy et al., 1996 , Lenka et al., 2001 and Sethi et al., 2016b.

3.6. Association of nut yield with component traits

Vegetative and yield attributing characters like trunk girth,

Table 4: Phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among nut yield and its components in Cashew

Characters	PH	TG	CS (E-W)	CS (N-S)	CA	FL	TL	N/P	N/M^2	NW	AW
PH		0.772**	0.719**	0.673**	0.687**	0.035	0.132	-0.249	-0.231	0.178	0.295
TG	0.823**		0.83**	0.84**	0.837**	0.211	0.328	0.124	-0.058	0.078	0.122
CS (E-W)	0.758**	0.92**		0.941**	0.954**	0.116	0.234	-0.193	-0.053	0.242	0.132
CS (N-S)	0.704**	0.90**	0.988**		0.961**	0.137	0.247	-0.175	-0.067	0.227	0.088
CA	0.713**	0.890**	0.984**	0.984**		0.135	0.237	-0.205	-0.070	0.290	0.110
FL	0.051	0.252	0.112	0.127	0.136		0.749**	-0.068	0.000	-0.064	-0.183
TL	0.199	0.398*	0.279	0.260	0.271	0.805**		0.028	-0.014	-0.028	-0.090
N/P	-0.272	-0.135	-0.222	-0.220	-0.236	-0.076	0.036		0.650**	-0.294	-0.431*
N/M^2	-0.277	-0.059	-0.038	-0.061	-0.068	0.038	0.008	0.716**		-0.179	-0.452*
NW	0.190	0.072	0.283	0.263	0.315	-0.067	-0.029	-0.310	-0.239		0.565**
AW	0.359	0.150	0.157	0.099	0.118	-0.239	-0.135	-0.472**	-0.497**	0.595**	
SR	0.071	0.162	0.067	0.063	0.041	-0.022	-0.064	0.059	0.043	0.002	0.163
FD	-0.120	0.086	0.123	0.137	0.133	0.103	0.269	0.363	0.420*	-0.150	-0.470*
S %	0.156	0.065	0.050	0.066	0.103	0.227	0.040	0.001	0.003	0.309	0.072
NY	0.430*	0.571**	0.574**	0.518**	0.553**	0.054	0.135	0.529**	0.536**	0.172	-0.098

Table 4: Continue...

Characters	SR	FD	S %	Correl. with NY
PH	0.064	-0.126	0.123	0.383
TG	0.152	0.085	0.058	0.513**
CS (E-W)	0.050	0.089	0.055	0.515**
CS (N-S)	0.058	0.114	0.065	0.475*
CA	0.034	0.111	0.102	0.512**
FL	-0.015	0.074	0.205	0.058
TL	-0.061	0.234	0.036	0.129
N/P	0.052	0.307	0.001	0.453*
N/M^2	0.045	0.375	-0.008	0.456*
NW	0.004	-0.127	0.284	0.159
AW	0.154	-0.403*	0.083	-0.088
SR		0.073	-0.165	0.213
FD	0.064		-0.088	0.117
S %	-0.188	-0.074		0.119
NY	0.214	0.131	0.152	

* and **: indicate significance at (p=0.05) ($r \geq 0.396$) and (p=0.01) ($r \geq 0.505$) levels probability respectively; PH: Plant height (m); TG: Trunk girth (cm); CS (E-W) (m): Canopy spread (East-West)(m); CS (N-S): Canopy spread (North-South) (m); CA: Canopy area (m^2), FL: Flowering laterals m^{-2}; TL: Total laterals m^{-2}, N/P: Nuts panicle^{-1}, N/M^2: Nuts m^{-2}, AW: Apple weight (g), SR: Sex ratio, FD: Flowering duration (days) , S %: Shelling %, and NY: Nut yield (kg tree^{-1})

canopy spread both in East-West and North-South direction, canopy area, nuts panicle^{-1}and nuts m^{-2} were significantly positively correlated with nut yield both at genotypic and phenotypic levels. Positive but non-significant correlation was observed with all other characters except apple weight with which it was negatively correlated. Though the direction of both genotypic and phenotypic correlation is same, the phenotypic correlation is of higher magnitude as compared to genotypic correlation in all the cases. Parameswaran et al., 1984 and Rao et al., 2002 , Aliyu, 2006 and Sethi et al*.,* 2016b reported that nut panicle^{-1}, number of nuts tree $^{-1}$ and number of hermaphrodite flowers panicle^{-1} were positively correlated with nut yield and could be used as primary components for improving yield.

3.7. Path coefficient analysis

The association between yield and its 14 component traits was further subjected to path analysis to partition into direct and indirect effect of the component traits on nut yield at phenotypic level (Table 5). The pattern of direct and indirect effects was of different magnitude and direction in many cases. Canopy area had the highest positive direct effect (0.526) on yield followed by nuts panicle^{-1} (0.498), canopy spread in East-West direction (0.271), nuts m^{-2} (0.248), nut weight (0.239), trunk girth (0.227), sex ratio (0.161), plant height (0.113), flowering laterals m^{-2} (0.016) and shelling% (0.004), whereas canopy spread in North-South direction (-0.484) recorded highest negative direct effect followed by flowering duration (-0.186), apple weight (-0.105) and total laterals m^{-2} (-0.001).

Table 5: Direct and indirect effects of yield components on yield and its components at the phenotypic level in cashew

Characters	PH	TG	CS (E-W)	CS (N-S)	CA	FL	TL	N/P	N/M^2	NW	AW
PH	0.113	0.175	0.195	-0.326	0.361	0.001	0.000	-0.124	-0.057	0.043	-0.031
TG	0.087	0.227	0.226	-0.408	0.440	0.003	0.000	-0.062	-0.014	0.019	-0.013
CS (E-W)	0.081	0.189	0.271	-0.455	0.502	0.002	0.000	-0.096	-0.013	0.058	-0.014
CS (N-S)	0.076	0.191	0.255	-0.484	0.505	0.002	0.000	-0.087	-0.017	0.054	-0.009
CA	0.077	0.190	0.259	-0.465	0.526	0.002	0.000	-0.102	-0.017	0.069	-0.012
FL	0.004	0.048	0.031	-0.066	0.071	0.016	-0.001	-0.034	0.000	-0.015	0.019
TL	0.015	0.074	0.063	-0.120	0.125	0.012	-0.001	0.014	-0.003	-0.007	0.009
N/P	-0.028	-0.028	-0.052	0.085	-0.108	-0.001	0.000	0.498	0.161	-0.070	0.045
N/M^2	-0.026	-0.013	-0.014	0.032	-0.037	0.000	0.000	0.324	0.248	-0.043	0.048
NW	0.020	0.018	0.066	-0.110	0.152	-0.001	0.000	-0.146	-0.044	0.239	-0.060
AW	0.033	0.028	0.036	-0.043	0.058	-0.003	0.000	-0.215	-0.112	0.135	-0.105
SR	0.007	0.034	0.014	-0.028	0.018	0.000	0.000	0.026	0.011	0.001	-0.016
FD	-0.014	0.019	0.024	-0.055	0.058	0.001	0.000	0.153	0.093	-0.030	0.042
S %	0.014	0.013	0.015	-0.031	0.054	0.003	0.000	0.000	-0.002	0.068	-0.009

Table 5: Continue...

Characters	SR	FD	S %	Correl. with NY
PH	0.010	0.023	0.001	0.383
TG	0.024	-0.016	0.000	0.513
CS (E-W)	0.008	-0.017	0.000	0.515
CS (N-S)	0.009	-0.021	0.000	0.475
CA	0.005	-0.021	0.000	0.512
FL	-0.002	-0.014	0.001	0.058
TL	-0.010	-0.043	0.000	0.129
N/P	0.008	-0.057	0.000	0.453
N/M^2	0.007	-0.070	0.000	0.456
NW	0.001	0.024	0.001	0.159
AW	0.025	0.075	0.000	-0.088
SR	0.161	-0.014	-0.001	0.213
FD	0.012	-0.186	0.000	0.117
S %	-0.027	0.016	0.004	0.119

P (R)= 0.512, R^2 (%)= 73.81; PH: Plant height (m), TG: Trunk girth (cm), CS (E-W) (m): Canopy spread (East-West) (m), CS (N-S): Canopy spread (North-South) (m), CA: Canopy area (m^2), FL: Flowering laterals m^{-2}, TL: Total laterals m^{-2}, N/P: Nuts panicle^{-1}, N/M^2: Nuts m^{-2}, AW: Apple weight (g), SR: Sex ratio, FD: Flowering duration (days), S%: Shelling %

Canopy area had the highest positive direct effect (r=0.526) on yield where as the correlation between the two characters was 0.512. The high magnitude of correlation coefficient was due to the positive indirect effect via plant height, trunk girth, canopy spread (East-West) and flowering laterals. Nuts panicle^{-1} had the second highest direct positive effect (0.498) on yield but the magnitude of correlation with yield was positive (r=0.453). The association of canopy spread (North-South) with yield was significantly highest (r=0.515), but its direct effect on yield was found to be small (0.271). This small direct effect was enhanced by positive indirect effect via characters like plant height, trunk girth, canopy area, flowering laterals m^{-2} and nut weight. In such situations, the indirect causal factors are to be considered simultaneously for selection.

A low to moderate level of direct positive effect on yield was observed for nuts m^{-2}, nut weight, trunk girth, sex ratio, plant height, and shelling %. The correlation coefficient for these characters was almost equal to their direct effect, the correlation explained true relationship and a direct selection through these traits will be effective. A negative correlation was also observed between yield and apple weight (r=-0.088) where as a low degree of negative direct effect (-0.105) was observed for this character on yield. The low degree of negative direct effect was due to nullifying effects of positive indirect effect via other characters.

The residual effect at phenotypic level was very low (0.512) indicating the 14 characters taken together accounted for about 73% of the variability in the yield, whereas same other components which were not considered have accounted for 27% of the variation on yield.

Thus, it is evident from both direct and indirect effects of the characters at phenotypic level that canopy spread (East-West), canopy area, trunk girth and nuts panicle^{-1} would be of more value while selecting for yield. Also the indirect causal factors should be considered simultaneously for selection of yield.

A direct selection for yield through canopy spread will be more effective. Aliyu, 2006 found the relationships between cashew nut yield and different yield attributing characters and observed strong significant correlation with these traits. Anitha et al., 1991, Lenka et al., 1999, Manoj et al., 1994, Swarnapiria and Manivannan, 1999 and Sethi et al., 2016 reported similar positive direct effect of vegetative and yield attributing traits on nut yield of cashew.

3.8. Multivariate analysis of genetic divergence

Simultaneous variations in all the fifteen characters for twenty five cashew genotypes were tested for assessing the nature of genetic divergence among them following Mahalanobis D^2 statistic. The aggregate effect of all the fifteen characters tested by Wilk's criterion indicated highly significant differences among the genotypes (Table 6). On the basis of genetic diversity as measured by Mahalanobis values, all the twenty five cashew genotypes were grouped into six clusters following Tocher's method of which three were multi variety clusters and three were single variety clusters. The cluster I consisted of seventeen genotypes, cluster II consisted of three genotypes III included two varieties while Cluster IV, V and VI consisted of one genotypes each.

Table 6: Intra-(diagonal) and inter -cluster average d2 among 25 cashew genotypes

Cluster	I (17)	II (3)	III (2)	IV (1)	V (1)	VI (1)	Genotypes in cluster
I	76.402	124.501	114.273	345.643	424.447	169.176	Chintamani-1, Vengurla-1, Ullal-1, Bhubaneswar-1, Vengurla-4, NRCC Sel.-2, Goa-1, Amrutha, Vengurla-6, VRI-3, Ullal-4, Madakkathara-2, Madakkathara-1, Bhaskara, K22-1, BPP-6, BPP-8
II		94.134	167.000	379.723	327.732	240.667	UN-50, Ulla-3, Jharagram-1
III			119.445	201.512	272.497	117.145	Dhana, BPP-4
IV				0.000	239.348	437.645	Kanaka
V					0.000	441.034	Priyanka
VI						0.000	Vengurla-7

From the average intra and from inter-cluster distance presented in Table 6, it is evident that the lowest intra-cluster distance of 94.134 was associated with cluster II, while it was the highest for cluster III (D^2=119.445). Average inter-cluster distance varied from 114.273 (between cluster I and III) to 441.034 (cluster V and VI).Cluster I was the largest having seventeen genotypes characterized by lower values for canopy spread (East-West and North-South), nuts panicle^{-1}, nut weight, plant height and sex ratio with moderate values for all other traits. Cluster II was distinguished for its lowest values for sex ratio, nuts panicle^{-1}, and nut yield. Cluster III exhibit extreme value for nuts m^{-2}, small plant height and nuts panicle^{-1}. Cluster IV was a monotypic cluster and had the distinction of having small canopy area, nut weight and sex ratio. Cluster V genotype recorded larger trunk girth, nut and apple weight. Cluster VI recorded higher values for nine characters. Relative contribution of different characters to total divergence (Table 7) revealed that sex ratio had the highest contribution to divergence (27.28%) followed by nut yield (13.76%), nut weight (11.14%), apple weight (10.09%) and flowering duration (7.47%).

Table 7: Cluster means of 15 characters in 25 cashew genotypes

Characters	Clusters					
	I (17)	II (3)	III (2)	IV (1)	V (1)	VI (1)
PH	3.69	4.02	3.63	4.26	3.70	4.32
TG	44.62	46.09	47.76	51.03	44.50	57.35
CS (E-W)	4.75	5.14	5.06	4.92	5.32	6.63
CS (N-S)	4.87	5.08	5.36	4.86	5.38	6.92
CA	18.96	21.18	21.74	18.90	22.95	39.34
FL	16.35	16.30	16.40	17.35	14.03	17.50
TL	18.31	18.39	18.55	18.29	17.03	19.83
N/P	4.37	2.16	4.39	4.02	2.28	3.45
N/M^2	22.51	12.73	26.22	17.40	11.42	23.79
NW	7.18	7.59	7.24	6.18	10.00	9.67
AW	47.40	61.64	50.42	56.5	87.42	50.67
SR	0.24	0.13	0.43	0.8	0.61	0.28
FD	89.58	82.67	87.92	82.33	88.33	88.33
S %	29.53	29.44	27.83	30.27	27.94	30.45
NY	3.17	2.02	3.63	3.63	2.23	5.97

The bold figures indicates minimum and maximum values for each character

Greater the distance between two clusters, wider the genetic diversity among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. Avoidance of selection of parents from genetically homogeneous clusters should be preferred to maintain relatively broad genetic base. So, it is expected that crosses between genotypes of cluster V with genotypes of cluster VI may give rise to high yielding segregants because of highest inter-cluster distance (441.034) (Table 8). Intercrossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the seed yield per plant. The results also indicate that selection of genotypes with high cluster mean values for particular attribute could be used in the hybridization programme for improvement of that character.These morphological characters need to be substantiated further with molecular markers for confirming the genetic differences among the genotypes. Aliyu and Awopetu, 2007 and Sethi et al., 2016c reported that the contribution of characters to divergence depends on the number of characters studied and the influence of the environment on the expression of characters.

Table 8: Contribution of yield and its components to genetic divergence

Characters	Averaged^2	% contribution	Percentage of total rank
PH	5.521	3.830	6.578
TG	2.870	1.990	7.886
CS (E-W)	3.748	2.600	7.322
CS (N-S)	1.453	1.010	9.064
CA	4.350	3.020	8.225
FL	3.250	2.250	8.100
TL	1.657	1.150	9.000
N/P	6.193	4.290	6.756
N/M^2	4.979	3.450	6.861
NW	16.070	11.140	4.808
AW	14.552	10.090	4.908
SR	39.341	27.280	4.028
FD	10.768	7.470	5.722
S %	9.611	6.660	6.150
NY	19.839	13.760	4.592

4. Conclusion

The investigation that the cashew varieties tested in the experiment exhibited lot of variability among the vegetative and yield attributing traits of cashew. The results indicate that selection of genotypes with high cluster mean values for particular attribute could be used in the hybridization programme for improvement of that character.These morphological characters need to be substantiated further with molecular markers for confirming the genetic differences among the genotypes.

5. Future Research

It is suggested to go for hybridization programme in order to develop suitable cashew types such as high yield, suitable for high density planting , resistant /tolerant to disease and pest etc.

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