

Varietal Character Analysis and Evaluation of Inflorescence Blight Tolerance in Cashew (*Anacardium occidentale L.*) at Eluwankulama Seed Garden

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ABSTRACT

The study was conducted at Cashew Seed Garden, Eluwankulama to analyze the varietal characters and evaluate the inflorescence blight tolerance in 35 cashew genotypes. A Non hierarchical cluster analysis was done based on 25 varietal characters. Genotypes were grouped under three clusters and the clones of cluster I (SLCC-N1, SLCC-N5, SLCC-N6, SLCC-N13, SLCC-N14, SLCC-N23, SLCC-M1 and SLCC-M7) and cluster II (SLCC-N21, SLCC-M6 and SLCC-M12) were found to be useful for use in hybridization to obtain maximum heterosis for varietal improvement.

Inflorescence Blight (die-back) is one of the major diseases in cashew cultivation. A study was carried out to identify the tolerant clones and their tolerant level against the inflorescence blight. Twenty five centimeters long undamaged healthy inflorescences were selected for data collection from all clones. Results revealed that clones had a significant effect on the infection of inflorescence blight. SLCC-N3, SLCC-N14, SLCC-N16, SLCC-M3 and SLCC-M8 clones had a higher tolerance against the inflorescence blight over others and SLCC-N6, SLCC-N15, SLCC-N20, SLCC-M4, SLCC-M10, SLCC-M12 had a lower tolerance. Therefore, SLCC-N3, SLCC-N14, SLCC-N16, SLCC-M3 and SLCC-M8 clones can be used as parent material for breeding inflorescence blight tolerant progenies in future.

KEY WORDS: *Anacardium occidentale L.*, Cashew, Inflorescence Blight tolerance, Varietal Characters

INTRODUCTION

Cashew (*Anacardium occidentale L.*) which belongs to family anacardiaceae, has gained the status of one of the most important commercial crops in Sri Lanka. It has been identified as a low input plantation crop which can survive even in the driest parts of the country (Jayasekera et al., 2000).

The world demand for cashew is rising annually (Anon, 2003), but the growers are still unable to meet the demand. Therefore, there is a higher potential and opportunity to develop and improve the cashew cultivation in Sri Lanka, which would provide higher income to cashew growers.

In the past, several other varieties have been cultivated, such as Kondachchi, Mannar, Batticaloa, Ulal, Vital and several indigenous types. Surprisingly, 39% of the total extent is covered by the indigenous types while mixed varieties cover approximately 8%. Some of these varieties are old heterogeneous populations of trees and are poor or low yielding varieties, and they have originated from unknown pedigree stocks or poor quality seeds (Jayasekera and Kodikara, 2003).

At present, the proper maintenance and reestablishment of cashew plantations are not practiced efficiently due to poor productivity of cashew plantations. Some of the major constraints responsible for poor productivity are unorganized orchards, poor cultural methods, pests, old heterogeneous populations, low yielding varieties, poor quality seeds, poor extension services and multiplication of plants from unknown pedigree stocks (Jayasekera and Kodikara, 2003).

Therefore, development of cashew sector demands new varieties with better performances through breeding programmes. For this purpose, superior clones have to be selected. The selection should be based on the varietal characters; tree and branches, leaf characters, flowering and inflorescence, cashew apple, nut characters and kernel characters that specially affect the yield of a particular variety (Mandal, 1997). The economically important product of cashew is the kernel. Yield of cashew mainly based on the kernel weight (seed weight) (Ratnasiri, 2003). Not only seed weight but also mean nut weight plays significant effect on yield of cashew (Jayasekera, 2003). Even though, it would be very much beneficial to determine the relationship between the varietal characters and the yield (seed weight and nut weight), a proper varietal analysis has not yet been done.

Die-back and inflorescence blight in cashew occurs as a secondary infection due to the damages caused by tea mosquito bug *Helopeltis anatonii*. These disease conditions occur when the feeding punctures of sucking insect pests are infected by fungal pathogens such as *Colletotrichum gloeosporioides*, *Botrydiplodia sp.*, *Phomopsis anacardii* and *Pellicularia sp.* The initial symptom is the appearance of water soaked lesions on the surfaces of inflorescence branches, shoots and also immature nuts and apples. Gummy exudation may occur in lesions. After two three days, they become brown and enlarged in size. The affected parts get dried up and become black showing scorching appearance. When the shoots are damaged, they start

drying up from tip downwards and have the name die back (Ranaweera and Wijetunga, 2003).

Inflorescence blight has been a major disease problem in Sri Lankan cashew cultivation which severely affects the cashew production. To cope up with the problem, a selection of cashew varieties which are tolerant to inflorescence blight is necessary.

Therefore, varietal analysis and biological studies of existing cashew clones / varieties are of much importance for future cashew breeding programmes that would aim at better performing varieties for Sri Lankan conditions (Jayasekera and Kodikara, 2003). These studies will pave the way to produce high yielding hybrid varieties by crossing suitable parent material and to select the inflorescence blight tolerant varieties from existing cultivars.

MATERIALS AND METHODS

Thirty five cashew clones maintained at cashew seed garden, Eluwankulama were chosen for the study. The duration of the experiments was from February to June 2006. Selected cashew clones were SLCC-N1, SLCC-N2, SLCC-N3, SLCC-N4, SLCC-N5, SLCC-N6, SLCC-N7, SLCC-N8, SLCC-N9, SLCC-N10, SLCC-N11, SLCC-N12, SLCC-N13, SLCC-N14, SLCC-N15, SLCC-N16, SLCC-N17, SLCC-N18, SLCC-N19, SLCC-N20, SLCC-N21, SLCC-N22, SLCC-N23, SLCC-M1, SLCC-M2, SLCC-M3, SLCC-M4, SLCC-M5, SLCC-M6, SLCC-M7, SLCC-M8, SLCC-M9, SLCC-M10, SLCC-M11 and SLCC-M12. All these clones were established in year 2000. SLCC-N4, SLCC-N16, SLCC-N19, SLCC-N22 and SLCC-M11 clones were planted at 21.8 × 21.8 feet spacing and others were planted at 23.4 × 23.4 feet. All the management practices were carried out according to the recommendations the Sri Lanka Cashew Corporation. The experiments were conducted under field conditions.

Study was based on two major aspects. They were analysis of varietal characters and evaluation of inflorescence blight tolerance in cashew clones.

Analysis of varietal characters of cashew clones

Observations were taken from 20 cashew plants of each clone. All the clones except SLCC-N3 and SLCC-N7 were taken for data collection. Data were collected on main character categories namely tree and branches, leaf characters, flowering and inflorescence, cashew apple, nut characters and kernel characters. Data for twenty five characters of the main categories were selected. The characters are as follows. Tree height (m), tree spread (m), branching habit, internodal length, number of leaves per twig, season of flowering, secondary flowering, compactness of inflorescence, sex ratio, inflorescence size, ease of peeling of cashew apple, size of apple, weight of apple, width of nut (cm), length of nut

(cm), nut thickness (cm), weight of nut (gm), shelling percentage, seed weight (gm), attachment of peel and kernel, kernel quality, kernel length (cm), kernel width (cm), kernel thickness (cm) and breakage percentage. All these characters were measured as described by Jayasekera (2001).

Variability among the clones were identified using mean values of the different characters and high performing clones were selected using the measurements of seed weight, nut weight and breakage percentage. To identify the correlation on characters; seed weight, nut weight, breakage percentage, etc. correlation matrix analysis was used. Cluster analysis was done for group the clones according to the character variations and genetic distances were studied. Clones with high similarity were clustered in one group and divergent were grouped in another. Data were analyzed using cluster analysis following the method suggested by Everitt (1994) to access the genetic divergence. The correlation matrix for varietal characters was taken using SPSS software package.

Evaluation of the inflorescence blight tolerance in cashew clones

Healthy and undamaged inflorescences 25cm in length were randomly selected from each clone. Two inflorescences per plant and six plants for each clone were taken to measure the disease severity. Lengths of the blighted patches were measured using a tape (cm) every two weeks for three months. Mean separation was done to find out the level of severities of the infection of inflorescence blight by using the SAS computer software package.

RESULTS AND DISCUSSION

Analysis of varietal characters of cashew clones

The results indicate that the characters; sex ratio, nut weight, shelling percentage, seed weight, breakage percentage and kernel quality had the variation among these clones. Clones SLCC-N19 and SLCC-M9 had the high seed weight (8) (Annex 1). The highest nut weight (9) was recorded by SLCC-N1, SLCC-N5, SLCC-N6, SLCC-N14, SLCC-N23, SLCC-M1, SLCC-M3, SLCC-M7 and SLCC-M12 clones. The lowest breakage percentage was observed in SLCC-N23 clone and the overall breakage percentage ranged from 5% to 60%. High variation could be seen among the characters; nut weight, seed weight, breakage percentage.

If the breeder's preference is towards only the economically important characters; seed weight, nut weight and breakage percentage, the above clones can be suggested as better parental clones.

Correlation matrix for the twenty five variables showed that (Annex 2) seed weight had significantly positive correlation with nut weight and kernel length. The characters; apple size, nut width, nut length, nut thickness, seed weight and kernel length had a significantly positive correlation and breakage

percentage had a significantly negative correlation with the character nut weight. Brakeage percentage had a significantly positive correlation with sex and kernel quality and significantly negative correlation with nut width, nut length, nut thickness and nut weight.

These correlations suggested that when selecting the parental clones, it is necessary to consider, the improved characteristics of not only the seed weight, nut weight and breakage percentage but also other physical parameters of plant. When hybridizing the clones, to produce new high performing cashew clones have to consider characters; nut weight, breakage percentage, apple size, nut width, nut length, nut thickness, seed weight, sex ratio, kernel quality and kernel length.

Genetic divergence among the 33 cashew clones studied was assessed using cluster analysis. Through cluster analysis, clones were grouped into clusters according to the character variations. The Euclidean cluster analysis grouped the 33 cashew clones into three clusters (Table1).

Tables 1 - Clones belong to separate clusters:

Cluster I	Cluster II	Cluster III
SLCC-N1	SLCC-N21	SLCC-N2
SLCC-N5	SLCC-M6	SLCC-N8
SLCC-N6	SLCC-M12	SLCC-N9
SLCC-N13		SLCC-N10
SLCC-N14		SLCC-N15
SLCC-N23		SLCC-N16
SLCC-M1		SLCC-N17
SLCC-M7		SLCC-N20
		SLCC-N22
		SLCC-M2
		SLCC-M4
		SLCC-M5
		SLCC-M8
		SLCC-M10
		SLCC-M11

Final cluster centers explained each factor contribution to the cluster formation (Table2). To form cluster 1, characters; tree spread, apple size, nut width, nut length, nut thickness, nut weight, seed weight, kernel length, kernel width and kernel thickness contributed more than other characters. And internodal length, number of leaves per twig, inflorescence size, sex ratio, apple weight, shelling percentage, attachment of peel to kernel, breakage percentage and kernel quantity characters contributed more on cluster II. The formation of cluster III was due to the main contribution of tree height, branching pattern and compactness of inflorescence and easy of peeling of cashew apple.

The intra-cluster distances (diagonal values) of the clusters explained that intra-cluster distance was highest between cluster I and cluster II and lowest between cluster I and cluster III (Table.3).

Table 2 - Final Cluster Centers:

Character	Cluster		
	I	II	III
TH (m)	3.54	3.69	3.76
TS (m)	5.15	4.68	4.81
BP	2	2	2.2
IL	5	5.33	4.99
NOL	15.47	16.06	15.62
SF	5.5	5.5	5.48
SEF	0	0	0
IS	5.12	5.6	5.19
COM	3	3	3.11
SEX	3.15	4.43	3.19
EP	3.88	3	4.09
AS	7	6.33	6.13
AW	7.88	8	7.6
NWI (cm)	2.85	2.58	2.59
NL (cm)	3.96	3.55	3.61
NT (cm)	2.09	1.87	1.9
NW (gm)	8.75	7	6.33
SH	6.56	7	6.6
SW	6.5	5.67	5.53
ATT	3.75	4.33	3.65
KL (cm)	3.04	2.68	2.86
KWI (cm)	1.79	1.63	1.72
KT (cm)	1.42	1.14	1.38
BRA	10	49.67	19.85
QUA	4.73	10.99	5.89

(TH: tree height, TS: tree spread, BP: branching pattern, IL: internodal length, NOL: number of leaves, SF: season of flowering, SEF: secondary flowering, IS: inflorescence size, COM: compactness of inflorescence, SEX: sex ratio, EP: easy of peeling of cashew apple, AS: apple size, AW: apple weight, NWI: apple width, NL: nut length, NT: nut thickness, NW: nut weight, SH: shelling percentage, ATT: attachment of peel to kernel, KL: kernel length, KWI: kernel width, KT: kernel thickness, BRA: breakage percentage, QUA: kernel quality)

Table -3 Distances between Final Cluster Centers:

Cluster	I	II	III
1		40.264	10.325
2	40.264		30.323
3	10.325	30.323	

This suggests that members of cluster I and cluster II are more divergent. Similarly, the members of cluster I and cluster III are more convergent with respect to the varietal characters studied. This study could group the genotypes into different clusters. The members of genetically distant clusters can be combined in all possible combinations to exploit the heterosis to the maximum (Jayalekshmy and Jhon, 2004). When cluster I (SLCC-N1, SLCC-N5, SLCC-N6, SLCC-N13, SLC-N14, SLCC-N23, SLCC-M1, SLCC-M7) and cluster II (SLCC-N21, SLCC-M6, SLCC-M12) are used as parents for the hybridization,

it can produce a higher heterosis in offsprings for varietal characters than other combinations of cluster I and III and cluster II and III. Members of cluster II and Cluster III can produce a higher heterosis than combination cluster I and III but lower heterosis than combination of cluster I and II.

Evaluation of the inflorescence blight tolerance

The results indicate that severity of infection of inflorescence blight had a significant variation ($P>0.05$) between clones (Table 4).

Table 4 - Mean severity value for inflorescence blight in Cashew Clones:

Clone	Mean	Clone	Mean
SLCC-N20	95.000 ^a	SLCC-N22	81.667 ^{abc}
SLCC-N15	94.667 ^a	SLCC-M11	80.667 ^{abc}
SLCC-M4	94.667 ^a	SLCC-N9	76.333 ^{bc}
SLCC-M10	94.333 ^a	SLCC-M6	71.000 ^{cd}
SLCC-M12	94.000 ^a	SLCC-M7	63.333 ^{de}
SLCC-N6	93.333 ^a	SLCC-N17	60.667 ^{de}
SLCC-N8	89.000 ^{ab}	SLCC-N12	55.750 ^{ef}
SLCC-N10	89.000 ^{ab}	SLCC-N21	47.333 ^{fg}
SLCC-M1	88.333 ^{ab}	SLCC-N2	37.000 ^{gh}
SLCC-N23	87.667 ^{ab}	SLCC-N11	34.667 ^{gh}
SLCC-M2	87.333 ^{ab}	SLCC-N18	27.667 ^{hi}
SLCC-M5	86.667 ^{ab}	SLCC-N1	17.000 ^{ij}
SLCC-N7	86.000 ^{ab}	SLCC-M8	13.667 ^j
SLCC-N13	86.000 ^{ab}	SLCC-N16	8.000 ^j
SLCC-N4	85.000 ^{abc}	SLCC-M3	8.000 ^j
SLCC-M9	84.000 ^{abc}	SLCC-N3	4.000 ^j
SLCC-N5	83.667 ^{abc}	SLCC-N14	4.000 ^j
SLCC-N19	82.667 ^{abc}		

Severity mean in column having a same letters are not significantly difference by PDIFF 5% (CV- 23.04, $R^2 - 0.8219$)

The higher tolerance against the inflorescence blight was observed in SLCC-N1, SLCC-N3, SLCC-N14, SLCC-N16, SLCC-M3 and SLCC-M8 clones over others. The clones; SLCC-N6, SLCC-N15, SLCC-N20, SLCC-M4, SLCC-M10, SLCC-M12, SLCC-N4, SLCC-N5, SLCC-N7, SLCC-N8, SLCC-N10, SLCC-N13, SLCC-N19, SLCC-N23, SLCC-M1, SLCC-M2, SLCC-M5 and SLCC-M9 clones had a lower tolerance while Others showed medium tolerance level.

CONCLUSIONS

The suitable parental combinations for obtaining superior cashew clones for the development of cashew sector are the crossing between SLCC-N1, SLCC-N5, SLCC-N6, SLCC-N13, SLCC-N14, SLCC-N23, SLCC-M1, SLCC-M7 clones and SLCC-N21, SLCC-M6, SLCC-M12 clones, which gives a higher heterosis in varietal characters than other combinations. The inflorescence blight (die back) tolerance is higher in SLCC-N1, SLCC-N3, SLCC-N14, SLCC-N16, SLCC-M3 and SLCC-M8 clones.

ACKNOWLEDGEMENTS

Authors gratefully acknowledge invaluable support given by all the staff members of Cashew Seed Garden, Eluwanukulama to carry out this task successfully. Sincere thanks are extended to Miss. Auchitya Dissanayake Research Assistant, Genetic and Plant Breeding Division, Coconut Research Institute, Lunuwila for the valuable guidance given for the in statistical analysis.

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Annex 1- Variability in varietal characters of cashew clones:

CLONE	TH	TS	BP	IL	NOL	SF	SEF	IS	COM	SEX	EP	AS	AW	NWI	NL	NT	NW	SH	SW	ATT	KL	KWI	KT	BRA	QUA
SLCC-N1	3.03	4.66	2.00	5.00	16.05	5.50	0	5.00	3.00	3.00	5.00	7.00	8.00	2.84	4.23	2.33	9.00	5.00	5.00	3.13	1.74	1.5410.00	4.73		
SLCC-N2	3.23	5.06	2.00	5.10	15.15	5.50	0	5.30	3.00	3.00	3.00	7.00	8.00	2.61	3.81	1.90	7.00	6.00	5.00	3.10	1.90	1.1030.00	7.54		
SLCC-N4	4.08	6.22	2.00	7.00	15.83	5.30	0	5.00	3.00	3.00	****	5.00	8.00	2.69	4.21	2.17	7.00	5.00	5.00	3.00	1.60	1.1810.00	3.82		
SLCC-N5	3.75	5.68	2.00	5.00	14.80	5.50	0	5.00	3.00	3.00	5.00	7.00	7.00	3.10	3.90	1.90	9.00	7.00	7.00	4.00	2.80	1.80	1.1010.00	4.76	
SLCC-N6	3.48	5.20	2.00	5.00	15.00	5.30	0	5.00	3.00	3.00	3.00	7.00	8.00	2.80	4.10	1.80	9.00	6.00	7.00	4.00	3.50	2.00	1.4010.00	4.86	
SLCC-N8	3.50	4.85	2.00	5.00	15.90	5.50	0	5.00	3.00	3.00	3.00	5.00	7.00	2.30	3.10	1.60	5.00	8.00	5.00	3.00	2.60	1.60	1.5020.00	5.61	
SLCC-N9	3.99	5.78	2.00	5.00	15.95	5.73	0	5.60	3.00	4.20	5.00	7.00	8.00	2.80	3.80	1.90	5.00	7.00	5.00	4.00	2.90	1.90	1.3015.00	5.02	
SLCC-N10	3.71	5.39	2.00	5.00	15.26	5.30	0	5.00	3.00	3.00	3.00	7.00	8.00	2.66	3.70	2.10	7.00	7.00	5.00	5.00	2.70	1.70	1.1020.00	6.10	
SLCC-N11	3.23	4.13	2.00	7.00	****	5.50	0	5.00	3.00	3.00	4.00	7.00	8.00	2.68	3.64	2.00	7.00	7.00	7.00	3.00	3.10	1.70	1.2010.00	4.97	
SLCC-N12	***	5.29	2.00	5.50	16.00	5.70	0	3.00	3.00	3.00	2.68	6.26	8.00	2.30	3.20	1.80	5.00	7.00	5.00	4.00	2.60	1.30	1.3020.00	****	
SLCC-N13	4.00	5.89	2.00	5.00	15.32	5.50	0	5.42	3.00	3.42	3.00	7.00	8.00	2.80	3.80	2.10	7.00	8.50	5.00	4.00	2.90	1.70	1.3010.00	4.47	
SLCC-N14	3.82	5.29	2.00	5.00	15.29	5.70	0	5.00	3.00	3.00	4.00	7.00	8.00	2.80	4.10	1.90	9.00	7.00	7.00	4.00	3.10	1.80	1.7010.00	4.90	
SLCC-N15	4.11	5.49	2.00	5.00	15.74	5.70	0	5.11	3.00	3.00	5.00	7.00	8.00	2.80	3.60	2.20	7.00	6.00	5.00	5.00	3.00	1.80	1.6020.00	6.12	
SLCC-N16	4.13	5.95	2.00	5.00	15.50	5.50	0	5.00	3.00	3.00	3.00	7.00	7.00	2.61	3.51	1.79	7.00	7.00	5.00	3.00	3.01	1.61	1.2815.00	4.90	
SLCC-N17	3.48	4.90	2.00	5.00	14.75	5.30	0	5.00	5.00	3.00	5.00	7.00	8.00	2.80	3.50	1.80	5.00	7.00	7.00	3.00	2.50	1.70	1.1020.00	5.97	
SLCC-N18	3.23	3.49	2.00	4.16	15.68	5.50	**	5.90	3.00	3.00	3.00	5.00	8.00	2.31	3.06	1.79	5.00	7.00	5.00	4.00	2.62	1.70	1.1835.00	8.24	
SLCC-N19	3.69	5.21	2.00	5.00	15.61	5.50	0	6.26	3.00	3.42	6.00	5.00	8.00	2.47	3.46	1.63	7.00	****	8.00	3.00	3.36	1.72	1.0840.00	9.61	
SLCC-N20	3.38	3.83	2.00	5.00	16.33	5.50	0	4.41	2.65	2.65	2.65	6.18	8.00	2.70	3.60	2.00	7.00	6.00	5.00	2.80	2.80	1.70	1.3020.00	5.81	
SLCC-N21	3.65	4.84	2.00	6.00	16.60	5.30	0	6.80	3.00	3.30	3.00	7.00	8.00	2.54	3.81	2.03	7.00	8.00	5.00	3.00	2.78	1.72	1.1240.00	9.23	
SLCC-N22	4.08	5.31	2.00	5.00	16.44	5.50	0	6.00	3.00	4.00	6.00	5.00	8.00	2.42	3.13	2.08	7.00	7.00	7.00	3.00	2.76	1.58	3.0220.00	6.24	
SLCC-N23	3.58	4.55	2.00	5.00	15.50	5.50	0	5.00	3.00	3.00	3.00	7.00	8.00	3.10	3.90	2.20	9.00	7.00	7.00	3.00	3.20	1.70	1.305.00	3.96	
SLCC-M1	3.18	4.80	2.00	5.00	16.10	5.50	0	5.00	3.00	3.00	5.00	7.00	8.00	3.02	3.83	2.70	9.00	6.00	7.00	3.00	2.80	1.80	1.6015.00	5.60	
SLCC-M2	4.00	4.61	2.00	5.00	15.28	5.30	0	5.00	3.00	3.00	5.00	3.00	5.00	2.36	3.90	1.30	7.00	5.00	5.00	5.00	2.60	1.70	1.3020.00	5.64	
SLCC-M3	3.93	4.15	2.00	4.57	12.21	5.50	**	6.23	3.00	3.92	3.00	7.00	8.00	2.66	4.14	2.05	9.00	8.00	7.00	3.00	3.33	1.83	1.3410.00	4.98	
SLCC-M4	4.07	4.11	2.00	7.00	15.94	5.50	0	5.00	3.00	3.00	3.00	7.00	8.00	2.70	3.60	2.00	5.00	7.00	5.00	3.00	2.70	1.70	1.2020.00	5.60	
SLCC-M5	3.63	3.94	2.00	5.00	15.50	5.50	0	5.00	3.00	3.00	3.00	7.00	8.00	2.50	4.13	2.10	7.00	7.00	5.00	5.00	2.60	1.70	1.1020.00	6.20	
SLCC-M6	3.53	4.13	2.00	5.00	15.79	5.70	0	5.00	3.00	5.00	3.00	5.00	8.00	2.39	3.05	1.72	5.00	8.00	5.00	5.00	2.61	1.44	1.1260.00	12.58	
SLCC-M7	3.45	5.15	2.00	5.00	15.70	5.50	0	5.50	3.00	3.74	3.00	7.00	8.00	2.30	3.79	1.80	9.00	6.00	7.00	3.00	2.90	1.80	1.4010.00	4.56	
SLCC-M8	3.58	3.08	2.00	5.78	15.50	5.50	0	5.56	3.00	3.22	6.00	7.00	8.00	2.04	3.56	1.84	7.00	7.00	7.00	3.00	3.63	1.73	1.0722.80	6.71	
SLCC-M9	3.54	4.58	2.00	4.60	17.60	5.30	0	5.00	3.00	3.00	3.00	5.00	8.00	2.34	3.46	1.60	5.00	****	8.00	3.00	2.64	1.66	1.1037.00	8.68	
SLCC-M10	4.03	5.53	2.00	5.00	15.55	5.50	0	5.00	3.00	3.30	3.00	7.00	8.00	3.09	3.84	1.90	7.00	5.00	7.00	4.00	3.30	1.80	1.2020.00	6.08	
SLCC-M11	3.41	4.29	5.00	2.00	15.47	5.30	0	5.88	3.00	3.53	5.65	2.82	7.00	2.44	3.35	2.00	5.00	7.00	5.00	3.00	2.68	1.70	1.4615.00	4.78	
SLCC-M12	3.90	5.08	2.00	5.00	15.80	5.50	0	5.00	3.00	5.00	3.00	7.00	8.00	2.81	3.80	1.85	9.00	5.00	7.00	5.00	2.66	1.74	1.18	49.00	11.15
MEAN	3.67	4.86	2.09	5.11	15.60	5.48	0	5.21	3.05	3.29	3.84	6.28	7.79	2.63	3.68	1.94	7.00	6.66	5.97	3.66	2.91	1.71	1.33	20.87	6.23
SD	0.32	0.74	0.52	0.86	0.83	0.13	0	0.64	0.36	0.56	1.16	1.19	0.60	0.26	0.33	0.25	1.50	0.98	1.10	0.82	0.29	0.13	0.35	12.58	2.06

(TH: tree height (m), TS: tree spread (m), BP: branching pattern, IL: internodal length, NOL: number of leaves, SF: season of flowering, SEF: secondary flowering, IS: inflorescence size, COM: compactness of inflorescence, SEX: sex ratio, EP: easy of peeling of cashew apple, AS: apple size, AW: apple weight, NWI: nut width (cm), NL: nut length (cm), NT: nut thickness (cm), NW: nut weight (gm), SH: shelling percentage, SW: seed weight, ATT: attachment of peel to kernel, KL: kernel length (cm), KWI: kernel width (cm), KT: kernel thickness (cm), BRA: breakage percentage, OUA: kernel

Annex 2 - Correlation matrix for varietal characters in cashew:

	TH	TS	BP	IL	NOL	SF	SEF	IS	COM	SEX	EP	AS	AW
TH	1.000												
TS	0.508**	1.000											
BP	-0.150	-0.139	1.000										
IL	0.200	0.092	-0.652**	1.000									
NOL	-0.141	0.028	-0.028	0.156	1.000								
SF	0.136	0.045	-0.257	0.070	-0.010	1.000	(a)						
SEF	(a)	(a)	(a)	(a)	(a)	(a)	(a)	(a)					
IS	0.073	-0.117	0.188	-0.197	-0.170	-0.251	(a)	1.000					
COM	-0.078	0.052	-0.025	-0.019	-0.211	-0.256	(a)	-0.020	1.000				
SEX	0.227	0.039	0.076	-0.170	-0.080	0.297	(a)	0.282	-0.057	1.000			
EP	0.022	0.014	0.285	-0.182	0.013	-0.005	(a)	0.310	0.211	0.033	1.000		
AS	0.005	0.157	0.520**	0.407*	-0.207	0.303	(a)	-0.124	0.109	-0.084	-0.286	1.000	
AW	-0.186	-0.040	-0.236	0.230	0.108	0.277	(a)	0.049	0.051	0.143	-0.218	0.574**	1.000
NWI	0.124	0.428*	-0.130	0.082	-0.205	0.070	(a)	-0.127	0.106	-0.102	-0.042	0.503**	0.175
NL	0.097	0.234	-0.180	0.219	-0.347	-0.176	(a)	0.035	-0.089	-0.184	-0.058	0.440*	0.037
NT	-0.150	0.070	0.046	0.101	-0.008	0.102	(a)	0.034	-0.104	-0.123	0.090	0.446**	0.494**
NW	-0.041	0.177	-0.239	0.064	-0.339	-0.010	(a)	0.088	-0.235	-0.005	0.025	0.451**	0.069
SH	0.028	-0.175	0.064	-0.083	-0.203	0.180	(a)	0.286	0.084	0.119	-0.159	0.061	0.145
SW	-0.067	-0.020	-0.158	-0.003	-0.107	-0.099	(a)	0.160	0.191	0.112	0.252	0.167	0.226
ATT	0.139	0.102	-0.144	-0.124	-0.041	0.240	(a)	-0.259	-0.109	0.244	-0.055	0.035	-0.151
KL	0.024	0.021	-0.139	0.163	-0.343	0.088	(a)	0.235	-0.233	-0.098	0.175	0.357*	0.259
KWI	-0.104	0.069	-0.020	-0.123	-0.324	-0.142	(a)	0.409*	-0.016	-0.094	0.135	0.378	0.078
KT	0.175	0.174	0.069	-0.150	0.144	0.173	(a)	0.128	-0.112	0.134	0.361*1	-0.165*	0.007
BRA	-0.068	-0.246	-0.084	-0.058	0.335	0.057	(a)	0.173	-0.010	0.512**	-0.127	-0.255	0.108
QUA	-0.100	-0.258	-0.128	-0.052	0.286	0.108	(a)	0.223	-0.016	0.546**	-0.118	-0.174	0.171

	NWI	NL	NT	NW	SH	SW	ATT	KL	KWI	KT	BRA	QUA
NWI	1.000											
NL	0.545**	1.000										
NT	0.532**	0.364*	1.000									
NW	0.485**	0.706**	0.388*	1.000								
SH	-0.253	-0.405	-0.057	-0.347	1.000							
SW	0.164	0.11	-0.07	0.415*	-0.108	1.000						
ATT	0.124	0.178	-0.047	0.101	-0.243	-0.315	1.000					
KL	0.185	0.426*	0.138	0.508**	-0.161	0.402*	-0.208	1.000				
KWI	0.442*	0.590**	0.171	0.495	-0.262	0.277	-0.021	0.490**	1.000			
KT	-0.017	-0.174	0.253	0.155	-0.008	0.107	-0.089	-0.032	-0.074	1.000		
BRA	-0.377*	-0.488**	-0.373*	-0.374*	0.082	-0.03	0.208	-0.31	-0.297	-0.243	1.000	
QUA	-0.339	-0.458**	-0.332	-0.279	0.091	0.07	0.236	-0.245	-0.319	-0.222	0.988**	1.000

** Correlation is significant at the 0.01 level (2-tailed).

* Correlation is significant at the 0.05 level (2-tailed).

(TH: tree height (m), TS: tree spread (m), BP: branching pattern, IL: internodal length, NOL: number of leaves, SF: season of flowering, SEF: secondary flowering, IS: inflorescence size, COM: compactness of inflorescence, SEX: sex ratio, EP: easy of peeling of cashew apple, AS: apple size, AW: apple weight, NWI: nut width (cm), NL: nut length (cm), NT: nut thickness (cm), NW: nut weight (gm), SH: shelling percentage, SW: seed weight, ATT: attachment of peel to kernel, KL: kernel length (cm), KWI: kernel width (cm), KT: kernel thickness (cm), BRA: breakage percentage, QUA: kernel quality)