

## Assessment of the Diversity in Fruit Yield and Fruit Components among Sri Lanka Tall Coconut Accessions Conserved *Ex-Situ*

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### Abstract

Characterization of conserved coconut germplasm has been undertaken globally for identification of important features of different accessions for them to be effectively used in coconut breeding. One hundred and fifty seven accessions comprising of local and exotic material have been conserved in *ex-situ* field genebanks of Coconut Research Institute in Sri Lanka. The objective of this study is to quantitatively characterize nut yield and fruit components by weights among Sri Lanka Tall (*Typica*) coconut accessions. Twenty local tall coconut accessions were characterized for nut yield and fruit components following Bioversity International descriptors for coconut. Bunch wise nut yield was recorded in all the coconut phenotypes in the six most mature bunches in 25 randomly selected palms from each accession. Sampled nuts were scored for weights of fresh nut, husked nut, split nut and kernel and the weights of husk, water and shell of each nut were derived from the scored data. Analysis of variance by general linear models procedure and mean separation by Duncan's multiple range test were performed in SAS v8 and principal component analysis and cluster analysis using squared Euclidean distances were performed in Minitab V17. General linear models procedure revealed significant differences for nut yield and all the fruit components at 5% probability level. Walahapitiya recorded the highest average nut yield followed by the Razeena with statistically equal performances. Clovis recorded the highest values for most of the parameters for fruit component analysis followed by the accession Margaret, grouping together in Dendogram and the scatter plot. The highest per nut kernel producer, Clovis, was followed by Margaret with statistically equal performances and this is important because kernel is the main economically important component followed by the husk. Results revealed that there is no significant correlation between nut yield and all the fruit components in tall accessions indicating the importance of taking these two parameters separately to formulate germplasm conservation strategies.

**Keywords:** Coconut, Germplasm, Fruit Component Analysis, Characterization, Multivariate Discrimination, Sri Lanka Tall, fruit yield

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## Introduction

The Coconut palm, *Cocos nucifera* L. is the most important palm of the wet tropics and extensively grown palm tree worldwide. It is a diploid species with a chromosome number  $2n = 32$  and belongs to the family Arecaceae under monocotyledons. Every part of the plant is useful and, in many cases, human life in certain parts of the world would be impossible in its absence. Hence, it acts as an important fruit tree in the tropical regions and the fruit can be made into a variety of foods and beverages.

Conservation of coconut germplasm has been undertaken globally in view of its economic importance. Coconut genetic resources have been traditionally collected and conserved in major coconut producing countries with the objective of using these to improve the genetic makeup of their existing cultivars. Selected germplasm are generally used as planting material to improve the coconut productivity, test material to determine the phenotypic and genotypic characters of value and population base for breeding superior hybrids/varieties (Baudouin and Santos, 2005). Currently coconut germplasm is conserved as accessions and there are 24 institutes managing *ex-situ* coconut field genebanks globally, totalling to more than 1500 accessions. These conserved germplasm is used for enhancing breeding strategies, used as national repository, facilitates materials for Germplasm exchange and used for characterizing and evaluating important traits.

Characterization of coconut germplasm can be done in several ways; Morphological characterization, Biochemical Characterization and Molecular Characterization. Morphometric characterization can be done by using stem, leaf and inflorescence characters and nut yield and fruit components also can be used for further characterization. Literature revealed the availability of a number of publications for morphometric characterization using stem, leaf and inflorescence characters (Sankaran *et al.*, 2012; Perera *et al.*, 2009; Perera and Ekanayake, 2009) but, only a very few publications deal with nut yield and fruit characters (Perera *et al.*, 2014; Harries, 1981). Different components of the fruit

provide major economically important produce offered by the coconut palm such as kernel, liquid endosperm, husk and shell. Furthermore, producing high quality fruit is a key breeding objective and overall breeding focus on quality traits includes; husk, shell and kernel proportions; kernel oil content and fatty acid composition; and coconut water levels and composition (Johnson *et al.*, 2014). Therefore, the quantitative evaluation of each of these components by weight is a highly important aspect of morphological characterization as it directly deals with the yielding capacity of the coconut palm. Components of the fruit combined with the nut yield of the palm provide the actual yield of the coconut palm in terms of the total kernel, husk, water or shell produced by a given palm (Perera *et al.*, 2014).

Coconut in Sri Lanka is currently classified into 15 different coconut forms grouped under three varieties, namely *Typica*, *Nana* and *Aurantiaca*. The Coconut Research Institute of Sri Lanka (CRISL) initiated a systematic collection and conservation of coconut germplasm on 1984 (Wickremaratne, 1984). Currently, 157 accessions comprising of local and exotic material collected and have been conserved in the field genebanks of coconut at the CRISL (CGRD database). And also, coconut germplasm has been effectively utilized in breeding programs such as production of Brown Dwarf hybrids (Kumara *et al.*, 2014 and Dissanayake *et al.*, 2012) and San Ramon hybrids (Perera *et al.*, 2010). Further, these conserved germplasm display considerable diversity for morphological characters indicating the potential of them to be utilized in coconut breeding and the effectiveness of sampling in the conservation process. The objective of this paper is to quantitatively characterize nut yield and fruit components in tall coconut accessions at Pottukulama Research Station in Sri Lanka.

## Materials and methods

Twenty coconut accessions belonging to the tall coconut variety (Table 1) conserved in Pottukulama *ex-situ* field gene bank were characterized for nut yield and fruit components following Bioversity IPGRI Descriptors for

coconut (1995). All the accessions are categorized under Sri Lanka Tall variety (Figures 1 and 2) collected randomly covering different geographical locations except Clovis and Margaret were collected bias sampling method. The plants were 25-30 years of age at the time of data recording and were managed with average standard management practices for coconut. Bunch wise nut yield was recorded in all the coconut phenotypes in the 6 most mature bunches in 25 randomly selected palms from each accession. A total of 40 nuts from each coconut phenotype were sampled as 2 nuts from a palm. Sampled nuts were subjected to fruit component analysis and weights of fresh nut (FW), husked nut (HNW), split nut (SNW) and kernel (KW) were recorded and the fruit components husk weight (HW), water weight (WW) and shell weight (SW) of each nut were derived from the scored data. The data were analyzed using analysis of variance and general linear models procedure followed by mean separation procedures Duncan's multiple range test and least squares using statistical software package SAS version 8 and Minitab version 17 used for principal component analysis, distance matrix, correlation matrix, cluster analysis and dendrogram based on squared Euclidean distances.



**Figure 1.** Nuts of Sri Lanka Tall coconut



**Figure 2.** Shape of the crown in Sri Lanka Tall coconut

## Results and discussion

### Nut yield

General linear models procedure revealed significant differences ( $P = 0.006$ ) at 5% probability level for scored nut yield. The average number of nut yield of the six most mature bunches in the studied coconut phenotypes varied from 28.6 to 46.2. Walahapitiya (acc no: 22) recorded the highest average nut yield followed by Razeena (acc no: 11) with statistically equal performances for mean separation procedures of Duncan's multiple range test (Table 2). Further that is proven by recording the highest average number of fruits per bunch in Walahapitiya (acc no: 22) and Razeena (acc no: 11) indicating the possibility of utilization of these two varieties for future coconut breeding programs.

### Fruit Component Analysis

#### Analysis of Variance

General linear models procedure revealed statistically significant differences at 5% probability level among all of the quantitative traits scored. Clovis (acc no: 4) revealed the highest values for most of the parameters followed by Margaret (acc no: 7) for mean separation procedures Duncan's multiple range test (Table 3). The edible part of the coconut fruit (coconut meat and coconut water) is the endosperm tissue which gives the economic value to the fruit mainly (Yong *et al.*, 2009). The

**Table 1.** Accession Names and code according to the CGRD database and their origin

Accession name	Accession no/ code	Origin
Moorcock	CRI SLT13	Sri Lanka Tall
Palugaswewa	CRI SLT15	Sri Lanka Tall
Pitiyakanda	CRI SLT16	Sri Lanka Tall
Clovis	CRI SNRT01	Sri Lanka Tall having San Ramon origin
Namalwatta	CRI SLT14	Sri Lanka Tall
St. Anne's	CRI SLT19	Sri Lanka Tall
Margaret	CRI SLT12	Sri Lanka Tall having San Ramon origin
Kasagala	CRI SLT07	Sri Lanka Tall
Debarayaya	CRI SLT03	Sri Lanka Tall
Razeena	CRI SLT17	Sri Lanka Tall
Ambakelle sp	CRI SLT50	Sri Lanka Tall
Melsiripura	CRI SLT10	Sri Lanka Tall
Mangalaeliya	CRI SLT11	Sri Lanka Tall
Goyambokka	CRI SLT05	Sri Lanka Tall
Goluwapokuna	CRI SLT04	Sri Lanka Tall
Keenakelle	CRI SLT08	Sri Lanka Tall
Maliboda	CRI SLT09	Sri Lanka Tall
Horakelle	CRI SLT06	Sri Lanka Tall
Walahapitiya	CRI SLT20	Sri Lanka Tall
Wellawa	CRI SLT21	Sri Lanka Tall

**Table 2.** Average nut yield in each coconut accession

Acc no	Accession name	Average nut yield	Average no of Fruits per bunch
1	Moorock	38.3 <sup>abcde</sup>	6.4
2	Palugaswewa	41.6 <sup>abc</sup>	6.9
3	Pitiyakanda	39.3 <sup>abcd</sup>	6.6
4	Clovis	38.8 <sup>abcde</sup>	6.5
5	Namalwatta	38.3 <sup>abcde</sup>	6.4
6	St. Anne's	42.7 <sup>ab</sup>	7.1
7	Margret	33.6 <sup>bcde</sup>	5.6
8	Kasagala	39.3 <sup>abcd</sup>	6.6
9	Debarayaya	32.8 <sup>bcde</sup>	5.5
11	Razeena	<b>45.9<sup>a</sup></b>	<b>7.6</b>
12	Ambakelle sp	42.1 <sup>ab</sup>	7.0
13	Malsiripura	40.5 <sup>abcd</sup>	6.8
14	Mangalaeliya	40.1 <sup>abcd</sup>	6.7
15	Goyambokka	35.7 <sup>abcde</sup>	5.9
17	Goluwapokuna	29.9 <sup>de</sup>	5.0
18	Keenakelle	35.6 <sup>abcde</sup>	5.9
20	Maliboda	28.6 <sup>e</sup>	4.8
21	Horakelle	40.3 <sup>abcd</sup>	6.7
22	Walahapitiya	<b>46.2<sup>a</sup></b>	<b>7.7</b>
23	Wellawa	31.1 <sup>cde</sup>	5.2

Means with the same letter are not significantly different ( $P \leq 0.05$ ).

**Table 3.** Mean weights of different fruit components in each coconut accession

Acc no	FNW	HNW	HW	KW	SNW	SW	WW
1	1586.47 <sup>bcd</sup>	666.75 <sup>efgh</sup>	938.24 <sup>abc</sup>	315.78 <sup>defg</sup>	488.58 <sup>gh</sup>	185.33 <sup>cde</sup>	178.17 <sup>bcd</sup>
2	1548.83 <sup>cdefg</sup>	610.47 <sup>hi</sup>	944.24 <sup>ab</sup>	286.83 <sup>fg</sup>	465.62 <sup>ih</sup>	163.61 <sup>de</sup>	141.24 <sup>defg</sup>
3	1299.24 <sup>hi</sup>	520.59 <sup>j</sup>	746.77 <sup>de</sup>	271.04 <sup>g</sup>	422.88 <sup>i</sup>	154.17 <sup>e</sup>	101.36 <sup>g</sup>
4	<b>1852.55<sup>a</sup></b>	<b>996.95<sup>a</sup></b>	849.82 <sup>bcd</sup>	<b>410.90<sup>a</sup></b>	<b>690.11<sup>a</sup></b>	<b>295.89<sup>a</sup></b>	<b>306.84<sup>a</sup></b>
5	1761.36 <sup>abc</sup>	808.95 <sup>c</sup>	933.03 <sup>abcd</sup>	392.16 <sup>ab</sup>	618.18 <sup>bc</sup>	218.79 <sup>bc</sup>	190.05 <sup>bc</sup>
6	1391.39 <sup>ghi</sup>	594.81 <sup>hij</sup>	807.25 <sup>bcd</sup>	297.95 <sup>efg</sup>	473.83 <sup>ih</sup>	190.18 <sup>cde</sup>	120.97 <sup>fg</sup>
7	1740.80 <sup>abcd</sup>	<b>914.08<sup>b</sup></b>	863.76 <sup>bcd</sup>	<b>407.52<sup>a</sup></b>	<b>652.72<sup>ab</sup></b>	<b>246.80<sup>b</sup></b>	<b>268.72<sup>a</sup></b>
8	1513.46 <sup>defgh</sup>	680.82 <sup>efgh</sup>	838.62 <sup>bcd</sup>	366.59 <sup>abcd</sup>	540.53 <sup>defg</sup>	204.59 <sup>cd</sup>	140.29 <sup>defg</sup>
9	1634.91 <sup>abcde</sup>	741.27 <sup>cde</sup>	853.30 <sup>bcd</sup>	351.85 <sup>bcd</sup>	560.93 <sup>de</sup>	205.10 <sup>cd</sup>	206.48 <sup>b</sup>
11	1623.90 <sup>bcd</sup>	753.30 <sup>cde</sup>	857.82 <sup>bcd</sup>	364.85 <sup>abcd</sup>	571.10 <sup>cd</sup>	203.89 <sup>cd</sup>	182.35 <sup>bcd</sup>
12	1404.33 <sup>fghi</sup>	632.08 <sup>ghi</sup>	754.26 <sup>cde</sup>	308.53 <sup>efg</sup>	483.41 <sup>gh</sup>	187.16 <sup>cde</sup>	148.67 <sup>cdef</sup>
13	1286.48 <sup>i</sup>	659.92 <sup>efghi</sup>	630.16 <sup>e</sup>	332.32 <sup>cdef</sup>	509.59 <sup>efgh</sup>	182.07 <sup>cde</sup>	150.33 <sup>cdef</sup>
14	1475.38 <sup>efghi</sup>	634.00 <sup>ghi</sup>	835.26 <sup>bcd</sup>	330.79 <sup>cdef</sup>	493.98 <sup>fgh</sup>	184.21 <sup>cde</sup>	140.03 <sup>defg</sup>
15	<b>1811.07<sup>ab</sup></b>	789.88 <sup>cd</sup>	<b>1108.48<sup>a</sup></b>	371.05 <sup>abc</sup>	586.53 <sup>cd</sup>	220.43 <sup>bc</sup>	203.35 <sup>b</sup>
17	1391.11 <sup>ghi</sup>	582.64 <sup>ji</sup>	825.00 <sup>bcd</sup>	292.70 <sup>fg</sup>	470.73 <sup>ih</sup>	197.38 <sup>cde</sup>	116.92 <sup>fg</sup>
18	1551.13 <sup>cdefg</sup>	666.44 <sup>efghi</sup>	911.78 <sup>bcd</sup>	305.00 <sup>efg</sup>	498.19 <sup>fgh</sup>	195.10 <sup>cde</sup>	162.22 <sup>bcd</sup>
20	1633.05 <sup>abcde</sup>	715.28 <sup>defg</sup>	929.32 <sup>abcd</sup>	334.58 <sup>cdef</sup>	538.18 <sup>defg</sup>	194.77 <sup>cde</sup>	177.10 <sup>bcd</sup>
22	1686.65 <sup>abcde</sup>	732.06 <sup>cdef</sup>	937.67 <sup>abc</sup>	362.80 <sup>abcd</sup>	549.47 <sup>def</sup>	201.25 <sup>cd</sup>	182.58 <sup>bcd</sup>
23	1596.18 <sup>bcd</sup>	638.63 <sup>fghi</sup>	<b>981.49<sup>ab</sup></b>	307.37 <sup>efg</sup>	493.28 <sup>fgh</sup>	188.72 <sup>cde</sup>	150.76 <sup>cdef</sup>

Means with the same letter in each column are not significantly different ( $P \leq 0.05$ ).

**Table 4.** Principal Component Analysis: FNW, HW, HNW, WW, SNW, SW, KW, And NY for Eigen analysis of the Correlation Matrix

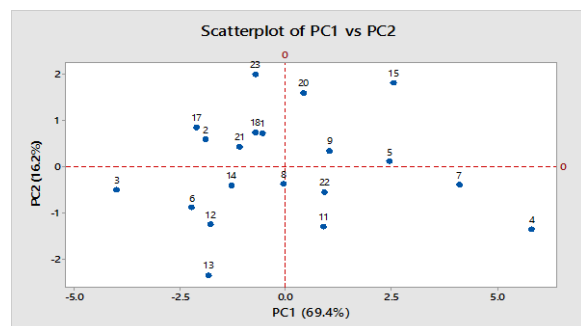
<b>Eigen value</b>	5.5508	1.2931	0.8479	0.1707	0.1109	0.0172	0.0084	0.0011
<b>Proportion</b>	0.694	0.162	0.106	0.021	0.014	0.002	0.001	0
<b>Cumulative</b>	0.694	0.855	0.961	0.983	0.997	0.999	1	1
<b>Variable</b>	<b>PC1</b>	<b>PC2</b>	<b>PC3</b>	<b>PC4</b>	<b>PC5</b>	<b>PC6</b>	<b>PC7</b>	<b>PC8</b>
<b>FNW</b>	0.385	0.279	-0.271	-0.087	-0.167	0.606	-0.532	-0.123
<b>HW</b>	0.165	0.695	-0.509	0.004	0.17	-0.345	0.278	0.079
<b>HNW</b>	0.419	-0.115	0.054	-0.086	-0.17	0.039	0.495	-0.725
<b>WW</b>	0.403	-0.085	0.113	-0.521	-0.493	-0.429	-0.133	0.318
<b>SNW</b>	0.416	-0.123	0.053	0.262	-0.003	0.399	0.486	0.587
<b>SW</b>	0.393	-0.125	0.187	-0.314	0.817	-0.066	-0.156	-0.003
<b>KW</b>	0.395	-0.178	-0.042	0.724	-0.027	-0.406	-0.34	-0.08
<b>NY</b>	-0.052	-0.597	-0.782	-0.15	0.061	-0.012	0.032	0.031

highest average per nut kernel producer, Clovis, was followed by Margaret with statistically equal performances and this fact is vital as kernel is the main economically important fruit component followed by the husk. Further, the highest average husk weight was recorded in Goyambokka (acc no: 15) followed by Wellawa (acc no: 23), with statistically significant differences between them.

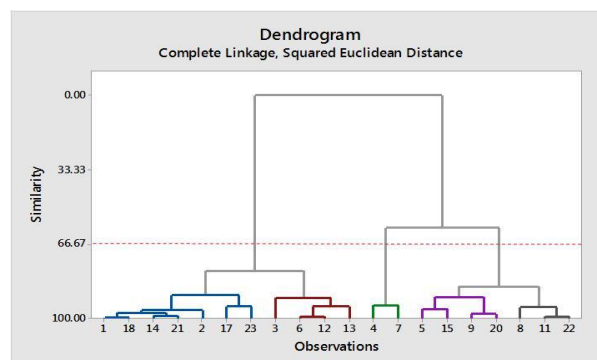
### Multivariate Discrimination

Principal component Analysis was used to describe the variation in the data set. The first three principal components (PC1, PC2 and PC3) accounted for 69.4%, 16.2% and 10.6% of the variation respectively accumulating to a total of 96.1% variability among the coconut accessions evaluated (Table 4). All traits except Nut Yield (NY) showed high positive loadings for the first principal component while husk weight recorded the lowest positive loading of 0.165 for PC1. But in contrast, husk weight had high positive correlation of 0.695 for PC2 and all the other characters except Fresh nut weight and Husk weight were negatively correlated with PC2.

PC scatter plot (Figure 3) and the Dendrogram (Figure 4) clearly indicated the grouping of accessions by their similarity levels. According to the PC scatter plot, the accessions were organized into several distinct groups which were further proved by the Phenetic tree by forming of major three groups of accessions at the 66.6% similarity level. Both plots revealed that Clovis (acc no: 4) and Margaret (acc no: 7) grouped together indicating the relative genetic similarity of the accessions Margaret and Clovis which has a history of an ancestry with the variety San Ramon (SNRT).



**Figure 3.** Scatter plot of PC1 Vs PC2



**Figure 4.** Phenetic tree drawn using Euclidean distances

### Distance matrix and Correlation matrix

Pair-wise distance matrix (Table: 5) revealed the highest distance between Clovis (acc no: 4) and Pitiyakanda (acc no: 3) and the lowest distance between the accession Goyambokka (acc no: 15) and St. Annes' (acc no: 6) among all accessions.

Pearson correlation coefficients among the quantitative traits are presented in Table 6. Highly strong positive correlations ( $>0.75$ ) were observed between many of the fruit components but, results revealed that there is no significant correlation between Nut Yield (NY) and the other fruit components. Therefore, nut yield cannot be taken as a predictor for fruit components in the studied tall accessions of coconut. Further, Kernel weight (KW) showed strong positive correlation with all the other fruit components except Husk Weight (HW).

### Conclusion

Nut yield and the fruit components of all tall accessions at Pottukulama genebank were quantitatively characterized in this research. Accordingly, Walapitiya and Razeena reported the highest values for nut yield and grouped together in scatter plot and the dendrogram. Further, these two accessions reported comparatively high values for fruit components as well. Clovis and Margaret scored the highest values for fruit component analysis and grouped together in scatter plot and the dendrogram. Further evidence for this was given in the distance matrix by showing minimum distance (157.6) between these two accessions. Clovis is a San Ramon variety. The results identified



**Table 5.** Pair- wise distance matrix among the accessions based on the scored morphological traits

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1		88.5	392.1	515.8	273.4	253.5	371.3	133.3	151.2	158.1	263.1	431.8	160.4	330.3	250.8	50.1	87.1	72.8	143.4	60.5
2	88.5		336.3	601.0	352.8	212.4	456.4	161.0	228.4	232.5	242.6	417.6	144.9	395.9	204.5	84.0	168.1	54.5	223.1	80.3
3	392.1	336.3		834.8	629.5	150.6	686.7	336.0	460.4	460.1	178.7	218.2	250.5	719.0	152.8	352.4	455.5	341.4	514.3	408.9
4	515.8	601.0	<b>834.8</b>		275.1	693.9	157.6	525.0	388.9	389.9	658.2	747.3	599.5	374.5	702.2	532.0	435.8	570.2	389.8	544.8
5	273.4	352.8	629.5	275.1		483.6	157.1	302.8	179.8	175.9	467.5	598.1	380.6	187.8	487.3	297.1	189.2	322.0	132.4	289.7
6	253.5	212.4	150.6	693.9	483.6		544.4	188.5	317.8	315.7	73.1	223.6	106.1	575.1	27.2	209.7	310.9	204.8	370.0	275.2
7	371.3	456.4	686.7	157.6	157.1	544.4		372.4	241.5	239.7	511.1	608.3	448.7	301.6	552.7	384.7	291.5	423.6	252.6	404.2
8	133.3	161.0	336.0	525.0	302.8	188.5	372.4		153.7	142.4	184.0	332.4	92.1	406.8	193.2	99.3	148.4	114.9	199.1	167.4
9	151.2	228.4	460.4	388.9	179.8	317.8	241.5	153.7		36.2	294.2	429.6	217.0	315.9	324.2	155.7	90.9	194.9	104.3	196.0
10	158.1	232.5	460.1	389.9	175.9	315.7	239.7	142.4	36.2		293.1	425.2	214.8	316.7	322.9	158.8	95.1	194.8	106.0	200.1
11	263.1	242.6	178.7	658.2	467.5	73.1	511.1	184.0	294.2	293.1		177.0	111.0	578.4	96.4	219.2	307.6	228.9	363.3	297.8
12	431.8	417.6	218.2	747.3	598.1	223.6	608.3	332.4	429.6	425.2	177.0		280.7	729.8	243.8	388.1	463.2	401.2	513.7	469.9
13	160.4	144.9	250.5	599.5	380.6	106.1	448.7	92.1	217.0	214.8	111.0	280.7		476.6	112.4	118.1	209.5	121.4	266.4	191.7
14	330.3	395.9	719.0	374.5	187.8	575.1	301.6	406.8	315.9	316.7	578.4	729.8	476.6		572.1	368.8	272.8	380.6	224.4	319.0
15	250.8	204.5	152.8	702.2	487.3	<b>27.2</b>	552.7	193.2	324.2	322.9	96.4	243.8	112.4	572.1		207.8	311.4	198.8	371.6	267.6
16	50.1	84.0	352.4	532.0	297.1	209.7	384.7	99.3	155.7	158.8	219.2	388.1	118.1	368.8	207.8		110.2	56.3	172.8	88.8
17	87.1	168.1	455.5	435.8	189.2	310.9	291.5	148.4	90.9	95.1	307.6	463.2	209.5	272.8	311.4	110.2		139.5	67.2	116.0
18	72.8	54.5	341.4	570.2	322.0	204.8	423.6	114.9	194.9	194.8	228.9	401.2	121.4	380.6	198.8	56.3	139.5		194.9	74.7
19	143.4	223.1	514.3	389.8	132.4	370.0	252.6	199.1	104.3	106.0	363.3	513.7	266.4	224.4	371.6	172.8	67.2	194.9		162.7
20	60.5	80.3	408.9	544.8	289.7	275.2	404.2	167.4	196.0	200.1	297.8	469.9	191.7	319.0	267.6	88.8	116.0	74.7	162.7	

**Table 6.** Correlation matrix among the measured variables

	FNW	HW	HNW	WW	SNW	SW	KW
<b>HW</b>	0.711						
	(0.000)						
<b>HNW</b>	0.845	0.254					
	(0.000)	(0.28)					
<b>WW</b>	0.819	0.236	0.971				
	(0.000)	(0.317)	(0.000)				
<b>SNW</b>	0.831	0.245	0.986	0.924			
	(0.000)	(0.297)	(0.000)	(0.000)			
<b>SW</b>	0.743	0.182	0.93	0.896	0.921		
	(0.000)	(0.444)	(0.000)	(0.000)	(0.000)		
<b>KW</b>	0.777	0.220	0.930	0.840	0.966	0.843	
	(0.000)	(0.351)	(0.000)	(0.000)	(0.000)	(0.000)	
<b>NY</b>	-0.147	-0.246	-0.068	-0.117	-0.068	-0.129	0.032
	(0.537)	(0.296)	(0.775)	(0.624)	(0.777)	(0.589)	(0.894)

Margaret as the closest accession with Clovis indicating an exotic San Ramon origin, yet within the variety tall. Finally, results revealed diversity of nut yield and fruit components among tall accessions indicating the potential of them to be utilized in breeding programmes. The study also unveiled certain duplications among accessions with respect to fruit components which will help in formulating future conservation strategies.

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