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Phenotypic Characterization of Selected Traits in 'Saba' Banana (*Musa balbisiana*), Chico (*Manilkara zapota*) and Pummelo (*Citrus maxima*) for Crop Improvement

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Phenotypic characteristics of 'Saba' banana, chico and pummelo were assessed for variability, clustering patterns and character association of 67 saba clones, 71 chico and 73 pummelo genotypes collected mainly from Luzon. Characters were analyzed for agglomerative clustering and correlation analyses. Five clusters for saba, chico and pummelo genotypes were arbitrarily formed a highly branched dendrogram for each species was generated. In 'Saba', 22 grouped in Clusters 1, 24, 18, 1 and 2 in Clusters II, III, IV and V, respectively. In chico, 67 genotypes clustered in Cluster I, while 1 each belongs to Clusters II, III, IV and V. In pummelo, 37, 4, 29, 2 and 1 genotypes grouped, respectively, in Clusters I, II, III, IV and V. High degree of association between characters indicated dependency of certain characters on others, suggesting that evaluation of traits can be reduced to save time, effort and resources during peak of evaluation periods. Eighteen saba clones of Cluster III, while in Chico, CH7-IPB in Cluster II and 41 accessions from Clusters I and II of pummelo could be used in varietal improvement due to high total soluble solids (TSS) and edible portion, heavy fruit weight and size, and few number of seeds for chico and pummelo.

Key Words: agglomerate clustering, chico, correlation analysis, dendrogram, pummelo, saba, traits analyses, variability

Abbreviations: EP – edible portion, TSS – total soluble solids

INTRODUCTION

The potential of a crop to respond positively to a breeding program depends upon the variability found within members of the population. This variability, which is usually heritable, could be used for variety development which, in turn, is the basis for selection of desirable genotypes (Brown and Caligari 2008). Prior to utilization of germplasm in a breeding program, evaluation of their phenotypic traits to determine extent of variability is important for a knowledge of the population's genetic base. These characteristics may include yield, resistance to diseases and insects, heat and frost tolerance (Chrispeels and Sadova 2002). For perennial fruit crops, fruit size and shape, total soluble solids, percent edible portion, and other traits that could contribute to improved adaptation to the environment need to be evaluated (Coronel 1986; Charrier et al. 2001).

As a tropical country, the Philippines is blessed with several nutritious, delicious and juicy fruits. Banana (*Musa balbisiana*), a triploid hybrid (BBB) cultivar, traces its origin to the Philippines (Lim 2012). 'Saba', the most popular cooking and processing cultivar in the country, can be made into snack foods like "turon", banana cue, and banana chips. This cultivar is very similar to 'Cardaba', which is more popular in the Visayas and Mindanao. It is highly resistant to banana bunchy top virus (BBTV), Sigatoka leaf spot, and moderately resistant to nematodes (Dela Cruz et al. 2008). In 2017, production area of 'Saba' in the country was 185,279 ha with a total production volume of 2,520,010.28 MT. The Davao Region is the highest producer (582,529 MT) during the last 10 yr (HVCDP 2013).

'Saba' banana is commonly propagated using suckers. However, tissue culture via meristem culture is becoming a popular propagation method due to efficiency in the production of seedlings, uniformity of resulting plants, precocious flowering and freedom from insect pests and diseases. Within the natural 'Saba' population, variation in plant stature, bunch and fruit sizes including disease resistance exists between clones. Selection of desirable clones and subsequent tissue culture production of their planting materials can be done (PCAARRD 2013). Evaluation and characterization of desirable selections can be done for exploitation in crop improvement (Pillay and Tenkouano 2011; Chai, nd.).

On the other hand, chico or sapodilla or naseberry (*Manilkara zapota* Linn. Van Royen), a member of the family Sapotaceae, is one of the most interesting and prolific tropical fruits with a delightful taste. Chico originated from Southern Mexico and Central America (Coronel 2011). It was introduced in the Philippines during the Spanish colonial period and is presently cultivated in many places in the country (Morton 1987). Chico is a good source of the gum chicle of commerce which is used in manufacturing chewing gum (Coronel 1986). Generally, ripe chico is merely cut in half and the flesh is scooped with a spoon and eaten fresh. It is an ideal dessert fruit as the skin, which is not eaten, remains firm enough to serve as a "shell". Chico is a popular fruit during Christmas as it is also usually a component of the collection of round fruits which is a Filipino tradition during New Year. This period coincides with the peak of fruiting season (November to January), which is usually extended. The average national production volume of chico was 6,103 MT from 2012 to 2014 (PSA 2015). ‘Pineras’ and ‘Ponderosa’ are the two main varieties grown in the country. Others such as ‘Sao Manila’ and ‘Gonzales’ (Coronel 2011) and ‘Mapino’ (Magdalita et al. 2001) are also grown on a limited scale. In addition, chico trees grown from seeds also produce marketable fruits but they are variable in terms of tree and fruit characteristics. This variation can be exploited for variety development but before this can be realized, there is a need for evaluation and characterization of existing fruiting trees.

‘Suha’ (*Citrus maxima* Burm.) (Merr.), also known as pummelo or lukban, is a member of the family Rutaceae and is found throughout the tropics. Pummelo originated from Southeast Asia and was introduced in many tropical and subtropical countries during the pre-historic period in the Philippines where it is now commonly grown in many home gardens and commercial orchards (Coronel 2011). The fresh fruit is a good source of vitamin C, iron and calcium. In the Philippines, pummelo is eaten as a dessert with salt, while the leaves are used for aromatic baths (Galvez-Tan and Maraña Galvez-Tan 2008). It is widely grown in the country since it is well adapted to local soil and climatic conditions (HVCDP 2013). From 2012 to 2014, the average national production of pummelo was 30,158 MT and the highest production volume was recorded in the Davao Region (PSA 2015). The pink-fleshed ‘Magallanes’ and the white-fleshed ‘Sunwuilluk’ are the two common varieties grown in the country. The peak of fruiting season is from November to February. Pummelo trees grown from seeds are known to be variable in terms of tree and fruit characteristics. This natural variation can be exploited in the selection of trees with superior traits for variety development. Before this could be realized, however, evaluation and characterization need to be done first.

Traditionally, plant breeders have selected fruit crops based on their visible and measurable traits, such as prolificacy, fruit size and shape, taste and edible portion (Jiang 2013). Characterization and evaluation based on phenotypic traits of the plants is a quick, easy and practical guide in selection of parents for use in hybridization (Biodiversity International 2007). Cluster analysis is a method used to determine the patterns and relationships between objects in the data set and to group objects into homogenous and well-defined groups where observations within each cluster are similar to one another, and where the complete set of clusters contains all individuals belonging to it (Everitt et al. 2011). Clustering the different genotypes belonging to the three different fruit crop species and determining the association of a particular character in relation to the other traits will contribute to identification of good parents for use in a structured breeding program.

The objectives of the study were to: i) characterize the selected phenotypic traits of different genotypes of three fruit crop species, ii) categorize or group different genotypes in the different fruit species using agglomerative cluster analysis, and iii) find out the correlation of the different quantitative characters of the different fruit species.

MATERIALS AND METHODS

Phenotypic evaluation of different fruit species was conducted at the Institute of Plant Breeding, College of Agriculture and Food Science, University of the Philippines Los Baños. Fruits of two different fruit species, namely, chico and pummelo, were collected from different areas of Luzon (specified in Tables 1 and 2), and evaluated for various phenotypic characters. Mature bunches of ‘Saba’ banana were harvested from tissue-cultured selections grown in Tranca, Bay, Laguna and ripe fruits were used for evaluation of fruit qualities. Physiologically mature fruits of ‘Saba’ banana, chico and pummelo were harvested for evaluation of fruit qualities. Specifically, ‘Saba’ bananas were harvested when the fingers have no more angularity or 20–24 wk after shooting. For chico fruits, the index of maturity or time of harvest is when the peel or skin appeared yellowish after scratching it with the fingernails, or 85 d after fruit set. Further, pummelo fruits were harvested when the sepal

Table 1. Chico genotypes with their corresponding codes and their places of collection.

Chico	Location
60	College, Los Baños, Laguna
61	College, Los Baños, Laguna
62	College, Los Baños, Laguna
63	College, Los Baños, Laguna
64	College, Los Baños, Laguna
65	College, Los Baños, Laguna
66	College, Los Baños, Laguna
58	College, Los Baños, Laguna
67	College, Los Baños, Laguna
59	College, Los Baños, Laguna
68	College, Los Baños, Laguna
69	College, Los Baños, Laguna
Ch1-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch2-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch3-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch4-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch5-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch6-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch8-IPB	Institute of Plant Breeding, UPLB, College, Laguna
Ch1-Mainit	Mainit Bay, Laguna
Ch2-Mainit	Mainit Bay, Laguna
Ch3-Mainit	Mainit Bay, Laguna
Ch4-Mainit	Mainit Bay, Laguna
Ch6-Mainit	Mainit Bay, Laguna
Ch7-Mainit	Mainit Bay, Laguna
Ch8-Mainit	Mainit Bay, Laguna
Ch9-Mainit	Mainit Bay, Laguna
Ch10-Mainit	Mainit Bay, Laguna
Ch11-Mainit	Mainit Bay, Laguna
Ch12-Mainit	Mainit Bay, Laguna
Ch13-Mainit	Mainit Bay, Laguna
Ch14-Mainit	Mainit Bay, Laguna
Ch1-BK	Bagong Kalsada, Los Baños, Laguna
Ch2-BK	Bagong Kalsada, Los Baños, Laguna
Ch28-IPB	Institute of Plant Breeding, UPLB, College, Laguna
CH1-SPC	San Pablo City, Laguna
CH3-LBC	College, Los Baños, Laguna
CH4-ST	Sto. Tomas, Batangas
CH10-CA	Calamba City, Laguna
CH3-CA	Calamba City, Laguna
CH22XSM	Institute of Plant Breeding, UPLB, College, Laguna
CH2-SPC	San Pablo City, Laguna
CH2-CA	Calamba City, Laguna
CH4-CA	Calamba City, Laguna
CH5-CA	Calamba City, Laguna
CH6-CA	Calamba City, Laguna
CH7-CA	Calamba City, Laguna
CH8-CA	Calamba City, Laguna
CH9-CA	Calamba City, Laguna
CH1-TA	Tanauan, Batangas
CH1-GE	Grove, Batong Malake, Los Baños, Laguna
CH2-GE	Grove, Batong Malake, Los Baños, Laguna
CH3-GE	Grove, Batong Malake, Los Baños, Laguna
CH1-PCARRD	PCARRD, Los Baños, Laguna
CH2-PCARRD	PCARRD, Los Baños, Laguna
CH4-PCARRD	PCARRD, Los Baños, Laguna
CH4-KN	Kalookan, Talisay, Batangas
CH3-KN	Kalookan, Talisay, Batangas
CH2-KN	Kalookan, Talisay, Batangas
CH5-KN	Kalookan, Talisay, Batangas
CH1-KN	Kalookan, Talisay, Batangas
CH5-BY	Paciano, Bay, Laguna
CH4-BY	Paciano, Bay, Laguna
CH3-BY	Paciano, Bay, Laguna
CH2-BY	Paciano, Bay, Laguna
CH1-BY	Paciano, Bay, Laguna
CH28-TY	Talisay, Batangas
CH7-IPB	Institute of Plant Breeding, UPLB, College, Laguna
CH5-Mainit	Mainit, Bay, Laguma
CH28 x SM	Institute of Plant Breeding, UPLB, College, Laguna
CH1-CA	Calamba City, Laguna

remnant located between the apex of the fruit and the peduncle started to disappear or when the fruit turns shiny starting from the bottom going to the apex, or 8 mo after fruit setting.

Sixty-seven 'Saba' clones were grouped into clusters based on selected traits such as: finger weight, finger length, finger width, finger thickness, skin weight, bunch weight, number of hands, number of fingers, and bunch length. Seventy-one chico genotypes were clustered based on fruit weight, fruit length, fruit width, TSS, seed number, edible portion (EP), seed weight, skin weight, seed length, seed width, and seed thickness. In addition, 73 pummelo accessions were grouped based on fruit weight, fruit length, fruit width, TSS, number of seeds, EP, rind thickness, rind length, vesicle weight, vesicle number, and rag weight. The weight of the fruit, skin, bunch, seed, vesicle, rind and rag were determined using a triple beam balance (OHAUS Triple Beam 700/800 Series, USA) while bunch weight was determined using a top-loading balance (Fujisun Top Loading Balance, Japan). The finger length, fruit length, width, seed length, width and thickness, rind thickness, rind length were measured using a Vernier caliper (Mitutuyo, Japan), while bunch length was measured using a meterstick. A hand-held refractometer (Atago Handheld Refractometer, Japan) was used to measure the TSS, while edible portion (%) was determined by dividing the edible portion by the total fruit weight and then multiplied by 100.

STATISTICAL ANALYSIS

A total of 30 ripe fruit samples for each genotype of chico and pummelo were used for evaluation of the different fruit characteristics. For 'Saba' banana, a total of 75 fingers taken from 5–6 hands replicated thrice with 25 fruit samples per replicate were used for each of the 67 'Saba' clones. Samples for chico and pummelo were harvested randomly from one tree per genotype and harvested fruits were replicated thrice with 10 fruit samples per replicate. Data for the different quantitative characters were analyzed using the Statistical Tool for Agricultural Research (STAR) (IRRI 2014) software. Descriptive

Table 2. Pummelo genotypes with their corresponding code and their places of collection.

Genotype	Location
Suha B-1	Lamot II, Calauan, Laguna
Suha Pink B-6	Lamot II, Calauan, Laguna
Suha PM12	Talisay, Batangas
Suha PM15	Talisay, Batangas
Suha White B-2	Lamot II, Calauan, Laguna
Suha White B-3	Lamot II, Calauan, Laguna
Suha White B-4	Lamot II, Calauan, Laguna
Suha White B-5	Lamot II, Calauan, Laguna
Suha1	Lamot II, Calauan, Laguna
Suha11	Davao City (Larry Laroy)
Suha13-Tree4	Lamot, Calauan, Laguna
Suha14-2	Tagaytay City, Cavite
Suha15-2	Natunin- Mountain Province
Suha18-2	Davao City (Larry Laroy)
Suha19-4	Tagaytay City, Cavite
Suha20-1	Umali Subdivision, Los Baños, Laguna
Suha-2011-SH1	Silang, Cavite (Toto Paner)
Suha21-1	Mabacan, Calauan, Laguna
Suha23-1	Ibaan, Batangas
Suha25-1	San Pablo City, Laguna
Suha26-1	Silang, Cavite
Suha29-2	Calauan, Laguna
Suha30-1	Batong Malake, Los Baños, Laguna
Suha31-1	Batong Malake, Los Baños, Laguna
Suha32-5	Tagaytay City, Cavite
Suha33-2	Umali Subdivision, Los Baños, Laguna
Suha34-1	Tagaytay City, Cavite
Suha36-1	Raymundo, Los Baños, Laguna
Suha37-3	Tagaytay City, Cavite
Suha5	Banaue, Ifugao
Suha6	NFA Aquian View, Banaue, Ifugao
Suha8	Los Baños, Laguna
Suha9	Talisay, Batangas
Suha-B	Talisay, Batangas
Suha-Dr Salazar	Los Baños, Laguna
Suha-Kalabaw-3	Dolores, Quezon
Suha-S-E	Los Baños, Laguna
Suha CM1	Malvar, Batangas
Suha10	Boas, Marinduque
Suha3	Babaue, Ifugao
Suha4	Lagawe, Ifugao
Suha PM10	Talisay, Batangas
Suha PM11	Talisay, Batangas
Suha PM13	Talisay, Batangas
Suha PM14	Talisay, Batangas
Suha PM16	Talisay, Batangas
Suha PM17	Talisay, Batangas
Suha PM18	Talisay, Batangas
Suha PM2	Talisay, Batangas
Suha PM20	Talisay, Batangas
Suha PM3	Talisay, Batangas
Suha PM4	Talisay, Batangas
Suha PM5	Talisay, Batangas
Suha PM6	Talisay, Batangas
Suha PM7	Talisay, Batangas
Suha PM8	Talisay, Batangas
Suha PM9	Talisay, Batangas
Suha SH4	Talisay, Batangas
Suha12	Calauan, Laguna
Suha17-1	Davao City (Larry Laroy)
Suha1-LC	Talisay, Batangas
Suha2	Davao City (Larry Laroy)
Suha24-2	Mabacan, Calauan, Laguna (Dory Ilagan)
Suha27-2	Silang, Cavite
Suha35-1	Talisay, Batangas
Suha7	Tagaytay City, Cavite
Suha-A	Talisay, Batangas
Suha-Kalabaw-1	Dolores, Quezon
Suha-Kalabaw-2	Dolores, Quezon
Suha-SH-C	Talisay, Batangas
Suha16-1	Natunin, Mountain Province
Suha28-3	Natunin, Mountain Province
Suha22	Nueva Vizcaya

statistics such as the mean and standard deviation were determined. Agglomerative cluster analysis was performed using the complete and average clustering method. The Euclidian value, as the distance determinant method to assess the level of similarity between fruit crop species in order to group them in a dendrogram, was also determined. Correlation of fruit traits per fruit species was analyzed using Pearson's r coefficient at α = 5%.

RESULTS AND DISCUSSION

The mean and standard deviation, clustering of the different genotypes including the association of selected characters were presented for each crop species as follows:

'Saba' Banana

Dendrogram resulting from the clustering of 67 'Saba' clones utilizing complete clustering method and Euclidian distance as a dissimilarity measure is presented in Figure 1. The dendrogram was grouped into 5 clusters and was cut at 6 Euclidian distance. Examples of the 'Saba' clones used for evaluation of the different traits are presented in Figure 1 showing the bunch length, number of hands, fruit length, the cross and longitudinal sections of the ripe fruits. The fingers evaluated came from long bunches almost 1 m long with more than 100 fingers in each bunch. In addition, fingers were almost 30.5 cm long with firm and sweet flesh.

The Agglomerative Cluster Analysis grouped 67 'Saba' banana clones into 5 clusters (Table 3). Cluster I comprised 22 members with 'Saba' clones, namely, 90-1, 86-1, 83-1, 82-1, 65-1, 39-1, 34-1, 30-1, 29-1, 27-1, 26-1, 22-1, 20-1, 19-1, 18-1, 17-1, 16-1, 15-1, 14-1, 13-1, 11-1 and 4-1. This cluster has the second highest number of members of 22 clones. Members of this cluster have a long bunch measuring an average of 60.32 cm with 10 hands in a bunch. Cluster II has 24 members with 'Saba' clones consisting of the following: 89-2, 81-1, 80-1, 78-1, 76-1, 75-

Table 3. Distribution of 67 'Saba' banana clones in the five different clusters.

Cluster	'Saba' Banana Clones	Cluster Size
I	90-1, 86-1, 83-1, 82-1, 65-1, 39-1, 34-1, 30-1, 29-1, 27-1, 26-1, 22-1, 20-1, 19-1, 18-1, 17-1, 16-1, 15-1, 14-1, 13-1, 11-1, 4-1	22
II	89-2, 81-1, 80-1, 78-1, 76-1, 75-1, 71-1, 68-1, 57-1, 48-2, 46-1, 45-1, 42-2, 38-1, 37-1, 36-1, 35-1, 33-1, 28-2, 25-1, 24-1, 23-1, 21-1, 9-1	24
III	87-1, 84-1, 74-2, 72-1, 69-1, 63-1, 61-1, 58-1, 41-3, 32-2, 31-3, 12-1, 10-1, 8-1, 7-1, 6-1, 5-1, 1-B	18
IV	44-1	1
V	43-1, 40-1	2

1, 71-1, 68-1, 57-1, 48-2, 46-1, 45-1, 42-2, 38-1, 37-1, 36-1, 35-1, 33-1, 28-2, 25-1, 24-1, 23-1, 21-1 and 9-1. This cluster has the highest number of members of 24 clones. The members of this cluster have also a long bunch averaging 50.33 cm with nine hands in a bunch. For Cluster III, the 'Saba' clones 87-1, 84-1, 74-2, 72-1, 69-1, 63-1, 61-1, 58-1, 41-3, 32-2, 31-3, 12-1, 10-1, 8-1, 7-1, 6-1, 5-1 and 1-B are clustered together. This cluster has the third highest number of members of 18 clones. Members of this cluster have the longest bunch averaging 74 cm with 10 hands in a bunch. 'Saba' clone 44-1 is the only member of Cluster IV. This cluster has only one member which is the lowest among the five clusters. The lone member of this cluster has the shortest bunch and the lowest number of hands at three in a bunch. In addition, two 'Saba' clones were grouped in Cluster V, namely, 43-1 and 40-1. This cluster has only two members which is second to the lowest among the five clusters. Members of this cluster have medium bunch length averaging 40 cm with six hands in a bunch.

The mean and standard deviation of the various quantitative traits of the 'Saba' clones belonging to a specific cluster are presented in Table 4. The characteristics of the five different clusters of 'Saba' clones are as follows:

Cluster I. Twenty-two 'Saba' clones grouped in Cluster I. These clones have a mean bunch weight of 21.25 kg and a bunch length of 60.32 cm. The mean number of hands is 10, while the mean number of fingers in a bunch is 152. Fingers are medium in size with a mean weight of 132.19 g. The mean finger length of the 22 'Saba' clones is 11.32 cm, finger width is 4.72 cm, while the finger thickness is 3.31 cm. The mean skin weight is 21.25 g. This cluster has members whose bunch characteristics are very similar to the popular 'Saba' cultivars grown by farmers. These are characterized by big bunches with 8–16 hands having 12–20 fingers per hand, while the fingers are short and stubby and highly angular; the skin is thick and yellow when ripe, and the pulp is creamy white and fine-textured (BPI, nd.). This result suggests that majority of the members of this cluster can be multiplied for planting by banana growers in the country.

Cluster II. Out of the 67 'Saba' clones, 24 clones belong to Cluster II. Clones in this cluster have a mean bunch weight of 14.70 kg and a bunch length of 50.33 cm. The mean number of hands is 9, while the mean number of fingers is 131. Fingers of the 'Saba' clones belonging to Cluster II have a mean weight of 95.23 g, which are smaller than the fingers of the other 'Saba' clones in Clusters I, III, IV and V. The mean finger length is 9.99 cm, finger width is 4.22 cm, while the finger thickness is 3.15 cm. Mean skin weight is 38.22 g. This result suggests that the members have a bit shorter bunch length and lower bunch weight plus lesser number of fingers than the members of Cluster I. However, these clones are

Fig. 1. Phenotypic characteristics of samples of 'Saba' banana clones used for the evaluation of different traits.

Table 4. Distribution of 67 'Saba' banana clones in the five different clusters.

Cluster	Statistics	Fruit Characters								
		Finger Weight (g)	Finger Length (cm)	Finger Width (cm)	Finger Thickness (cm)	Skin Weight (g)	Bunch Weight (kg)	No. of Hands	No. of Fingers	Bunch Length (cm)
I	Mean	132.19	11.32	4.72	3.31	52.21	21.25	10	152	60.32
	SD	22.49	1.16	0.27	0.31	8.00	3.43	2.85	27.71	7.15
II	Mean	95.23	9.99	4.22	3.15	38.22	14.70	9	131	50.33
	SD	12.99	0.84	0.29	0.35	7.87	3.59	2.04	31.90	9.21
III	Mean	162.06	12.82	5.14	3.93	65.48	29.68	10	178	74.00
	SD	33.19	.93	0.36	0.35	11.56	4.11	1.23	37.79	10.40
IV	Mean	120.85	12.75	7.80	1.00	43.75	6.00	3	41	34.00
	SD	12.20	0.92	0.32	0.33	8.20	4.25	2.5	25.10	8.51
V	Mean	118.08	13.70	4.38	0.88	39.00	11.25	6	75	40.00
	SD	33.57	2.51	0.54	0.14	10.97	7.42	0.71	41.01	16.97

equally acceptable in terms of fruit qualities, suggesting that they can also be grown for commercial production. Compared with the 'Saba'/'Cardaba' of Cagayan Valley, the member cultivars of this cluster have lower number of hands up to 16 with 12–20 fingers per hand (CAGAYANDEORO.DA.GOV.PH, 2013).

Cluster III. Eighteen 'Saba'clones grouped in Cluster III. The clones belonging to this cluster have the highest mean bunch weight of 29.68 kg and bunch length of 74 cm among the five clusters. The mean number of hands is 10 while the mean number of fingers is 178. Fingers of 'Saba' clones in this cluster have the largest fingers among the five clusters with weight of 162.06 g. This result suggests that genotypes in this cluster which have special phenotypic properties like being large-fruited could be intended for specialty purposes and for curiosity.

Cluster IV. Only one 'Saba' clone 44-1 belongs to Cluster-IV. Clone 44-1 has the lowest mean number of hands at 3 and number of fingers at 41. Fingers are quite big with a mean finger weight of 120.85 g, which are second in size to those clones in Cluster III. Mean finger length is 12.75 cm, finger width is 7.80 cm, while finger thickness is 1.00 cm. The mean skin weight is 43.75 g. While the lone member of this cluster has the lowest number of hands, the fingers are big, indicating that the finger size could substitute for bunch weight. Since there is only one genotype member of this group, this lone member can be multiplied by micropropagation for planting by banana growers. This strategy was also done in Taiwan where the lone selection 'GCTCV-218' later released as 'Formosana', a high-yielding and resistant variety to *Fusarium*, was multiplied in tissue culture to over two million plantlets and distributed to banana growers (Yan Tang 2015).

Cluster V. Cluster V is composed of 'Saba' clones 43-1 and 40-1. These clones have a mean bunch weight of 11.25 kg and a bunch length of 40 cm. The mean number of hands is 6, while the mean number of fingers in a bunch is 75. Fingers like those in Cluster IV are also quite big with a mean finger weight of 118.08 g. The mean finger length is 13.70 cm, finger width is 4.38 cm, while finger thickness is 80 cm. Two clones in this cluster have a mean skin weight of 39.00 g. While the two members of this cluster have moderately heavy bunches and shorter bunch compared to the members of Clusters III and IV, they still have an acceptable bunch length of 40 cm long, and a bunch weight of 11.25 kg with 75 fingers in each bunch. This medium bunch length and the bunch weight of the members of this cluster appeared to be the most common type characteristic which is popular for cultivation by backyard growers in many places in the country.

The matrix showed the different degrees of correlation among the selected traits in 'Saba' banana (Table 5). Bunch weight is strongly correlated with bunch length (r=0.800; p=0.00), skin weight (r=0.730; p=0.00), finger weight (r=0.7164; p=0.00) and number of fingers (r=0.715; p=0.00). Similar result has been reported in banana that bunch weight is correlated with hand number, number of fingers and stem diameter (Nodals 1980). In addition, fruit weight has been reported to be correlated with fruit width, flesh thickness and peel weight in sweetsop (*Annona squamosa* Linn.) (Magdalita and Valencia 2004). Also, bunch weight is moderately correlated with finger length (r=0.5675; p=0.00) and finger thickness (r=0.593; p=0.00). However, bunch weight has moderate correlation with the number of hands (r=0.446; p=0.00) and finger width (r=0.4001; p=0.00). Similarly, the number of hands has moderate correlation with the number of fingers

Table 5. Correlation matrix of 9 quantitative characters of 'Saba' clones.

	FW	FL	FWd	FT	SW	BW	No. H	No. F	BL
Finger weight (FW)	1.0000								
Finger length (FL)	0.8001*	1.0000							
Finger width (FWd)	0.6547*	0.6057*	1.0000						
Finger thickness (FT)	0.4555*	0.2057	0.1719	1.0000					
Skin weight (SW)	0.8973*	0.6780*	0.6456*	0.521*	1.0000				
Bunch weight (BW)	0.7164*	0.5675*	0.4001*	0.593*	0.730*	1.0000			
No. of hands (No. H)	0.0908	-0.0531	-0.1489	0.191	0.208	0.446*	1.0000		
No. of fingers (No. F)	0.2421*	0.1589	0.0701	0.452*	0.351*	0.715*	0.4505*	1.0000	
Bunch length (BL)	0.5258*	0.4808*	0.3165*	0.582*	0.625*	0.800*	0.4279*	0.7077*	1.0000

* Significant at α=5%

(r=0.4505; p=0.00) and bunch length (r=0.4279; p=0.00). On the other hand, bunch length is strongly correlated with number of fingers (r=0.7077; p=0.00). It is moderately correlated with skin weight (r=0.625; p=0.00), finger thickness (r=0.582; p=0.00) and finger weight (r=0.5258; p=0.00). In addition, finger weight is strongly correlated with skin weight (r=0.8973; p=0.00), finger length (r=0.8001; p=0.00) but moderately correlated with finger width (r=0.6547). However, finger weight has moderate correlation with finger thickness (r=04555; p=0.00).

Chico

The chico genotypes evaluated were clustered using the average clustering method and Euclidian distance as the distance determinant method to assess the level of similarity between the genotypes in order to group them accordingly in a dendrogram. Phenotypic characteristics such as fruit size, fruit shape, fruit length, fruit width, flesh color and seed color are presented in Figure 3. The dendrogram was automatically cut at a Euclidian distance between 5 and 6 (Fig. 4) and was based on fruit weight, fruit length, fruit width, TSS, seed number, EP, seed weight, skin weight, seed length, seed width and seed thickness. The cluster number, the chico genotypes belonging to each cluster, and the cluster size in terms of the number of members are indicated in Table 4. Out of 71 chico genotypes, 67 were grouped together in Cluster I. The 4 remaining clusters, namely, II, III, IV and V, each contained only one member. The mean and standard deviation of the quantitative traits of the chico genotypes belonging to the five different clusters are presented in Table 6.

The mean and standard deviation of the various quantitative traits of the different chico genotypes belonging to a specific cluster are presented in Table 7. The characteristics of the five different clusters of chico genotypes are as follows:

Cluster I. The 67 chico genotypes clustered in Cluster I are group of individuals having small fruits with a mean fruit weight of 105.66 g. These genotypes have a mean fruit length of 62.02 mm and a fruit width of 53.15 mm. The mean TSS is 19.91% Brix while the mean % EP is 83.33%. This cluster of chico genotypes has the lowest mean number of seeds at 3 among the five clusters, with mean seed weight of 14.41 g. The mean for seed length is 20.71 mm, seed width is 11.45 mm, while seed thickness is 5.89 mm.

Table 6. Distribution of 71 chico genotypes in the five different clusters.

Cluster	Chico Genotypes	Cluster Size
I	60, 61, 62, 63, 64, 65, 66, 58, 67, 59, 68, 69, Ch1-IPB, Ch2-IPB, Ch3-IPB, Ch4-IPB, Ch5-IPB, Ch6-IPB, Ch8-IPB, Ch1-Mainit, Ch2-Mainit, Ch3-Mainit, Ch4-Mainit, Ch6-Mainit, Ch7-Mainit, Ch8-Mainit, Ch9-Mainit, Ch10-Mainit, Ch11-Mainit, Ch12-Mainit, Ch13-Mainit, Ch14-Mainit, Ch1-BK, Ch2-BK, Ch28-IPB, CH1-SPC, CH3-LBC, CH4-ST, CH10-CA, CH3-CA, CH22Xsm, CH2-SPC, CH2-CA, CH4-CA, CH5-CA, CH6-CA, CH7-CA, CH8-CA, CH9-CA, CH1-TA, CH1-GE, CH2-GE CH3-GE, CH1-PCARRD, CH2-PCARRD, CH4-PCARRD, CH4-KN, CH3-KN, CH2-KN, CH5-KN, CH1-KN, CH5-BY, CH4-BY, CH3-BY, CH2-BY, CH1-BY and CH28-TY	67
II	Ch7-IPB	1
III	Ch5-Mainit	1
IV	CH28 x SM	1
V	CH1-CA	1

Cluster II. Only one chico genotype CH7-IPB belongs to Cluster-II. This genotype has the highest TSS, highest EP, the thinnest skin and the smallest seeds. It has the highest TSS among the 71 genotypes evaluated, hence, it is the sweetest among them. It has also a few number of seeds at 3. CH7-IPB has a mean fruit weight of 132 g, mean fruit length of 69 mm, and mean fruit width of 56.53

Table 7. Mean and standard deviation of selected quantitative characters of chico genotypes belonging to the five clusters.

Cluster	Statistics	Fruit Characters										
		Fruit Weight (g)	Fruit Length (mm)	Fruit Width (mm)	TSS (% Brix)	Seed No.	EP (%)	Seed wt (g)	Skin Weight (g)	Seed Length (mm)	Seed Width (mm)	Seed Thickness (mm)
I	Mean	105.6	62.02	53.15	19.91	2.62	83.33	1.88	14.41	20.71	11.4	5.89
	SD	40.43	10.81	7.76	6.52	0.88	8.26	0.99	8.77	1.56	1.09	0.88
II	Mean	132.0	69.00	56.53	24.56	2.66	95.15	2.16	3.86	2.14	1.10	0.59
	SD	32.50	8.20	6.20	2.50	0.75	7.90	0.89	8.50	1.79	1.06	0.85
III	Mean	138.8	76.40	59.10	17.00	4.00	72.69	2.90	15.00	23.30	11.8	7.20
	SD	30.20	7.10	5.20	2.80	0.79	6.20	0.85	7.75	1.29	1.32	0.88
IV	Mean	157.8	75.20	65.40	16.00	3.00	89.70	3.90	12.60	27.20	14.1	12.20
	SD	28.20	7.30	4.50	2.30	0.69	5.90	0.78	6.56	1.87	1.45	0.79
V	Mean	178.9	69.50	67.72	17.62	3.80	83.22	3.62	23.40	20.30	14.5	18.32
	SD	25.20	5.12	3.20	2.80	0.58	6.10	0.74	5.78	1.34	1.50	0.75

mm. The mean seed weight is 2.16 g, seed length is 2.14 mm, seed width is 1.10 mm, while seed thickness is 0.59 mm. The mean skin weight is 3.86 g.

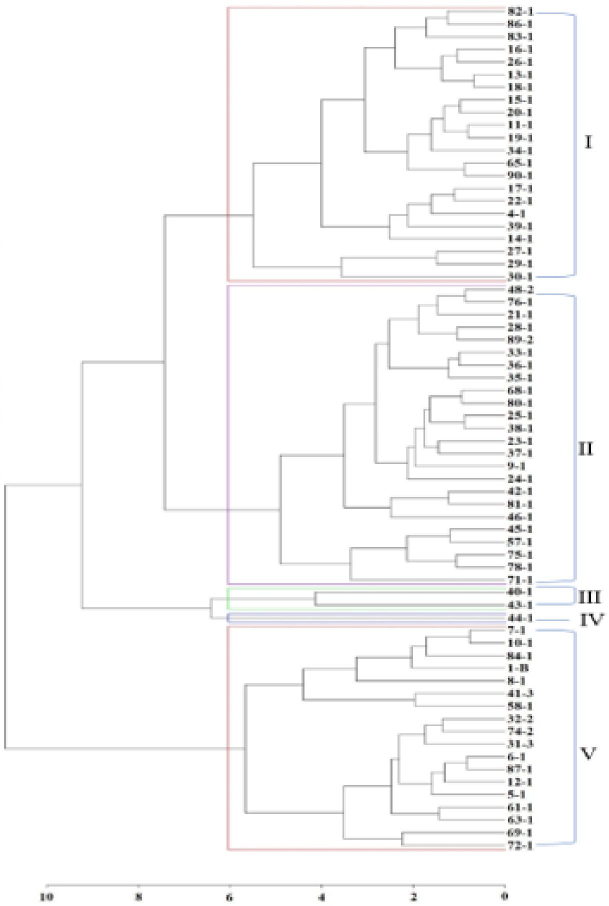

Fig. 2. Dendrogram of 67 'Saba' banana clones based on nine quantitative characters cut at 6 Euclidian distance.

Cluster III. This cluster also has only one member genotype CH5-Mainit. It has a mean fruit weight of 138.80 g, fruit length of 76.40 mm and fruit width of 59.10 mm. The mean TSS is 17.0 % Brix. This cluster has the lowest EP of 72.69% among the five clusters. The reason for this is the high non-edible part with a mean skin weight of 15 g, skin thickness of 7.20 mm, and more number of seeds at 4.0 compared to the others. The mean seed weight is 2.90 g, seed length is 23.30 mm, seed width is 11.80 mm and thickness is 7.20 mm.

Cluster IV. This cluster is composed of one member genotype that is a hybrid between CH28 selection and Sao Manila (CH28x Sao Manila). It has a mean fruit weight of 157.80 g, fruit length of 75.20 mm, and mean fruit width of 65.40 mm. CH28x Sao Manila has the lowest TSS of 16.0 % Brix among the five clusters evaluated. The mean % EP is relatively high at 89.70%. It has a mean seed number of 3.0 and a seed weight of 3.90 g. Mean seed length is 27.20 mm, seed width is 14.10 mm and seed thickness is 12.30 mm; mean skin thickness is 12.20 mm while the mean skin weight is 12.60 g.

Cluster V. Likewise, this cluster is composed of only

Fig. 3. Phenotypic characteristics of different chico genotypes used for the evaluation of various traits.

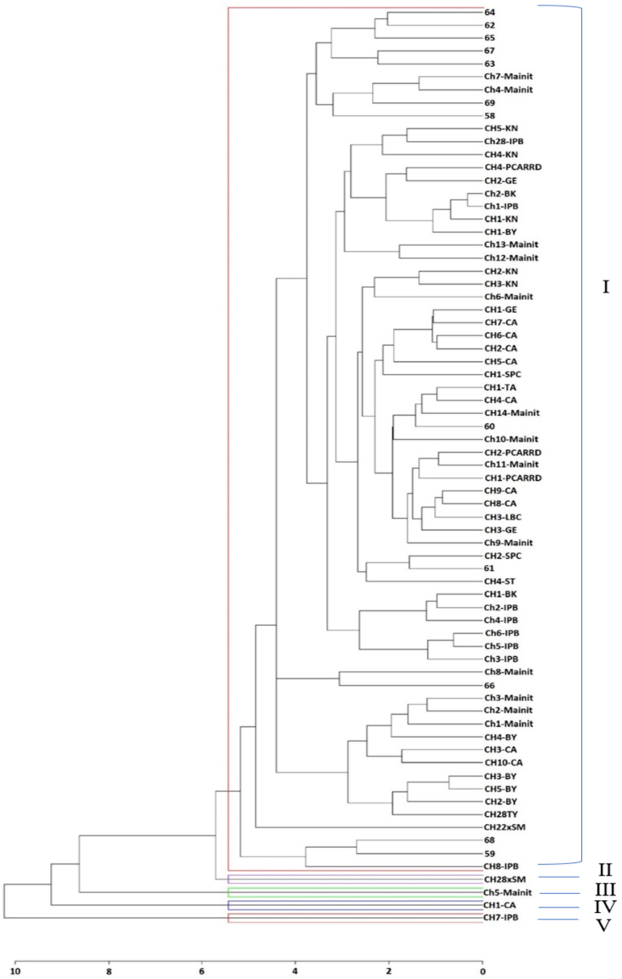

Fig. 4. Dendrogram of 71 chico genotypes based on 11 quantitative characters cut between 5 and 6 Euclidean distance.

one member genotype CH1-CA. This cluster has the biggest fruit with mean fruit weight of 178.95 g among the five clusters. The mean fruit length is 69.50 mm while the fruit width is 67.72 mm. It has a mean TSS of 17.62 % Brix and % EP of 83.22%. Mean seed number is 4. Mean seed weight is 3.62 g, seed length is 20.30 mm and seed width is 14.50 mm, seed thickness is 18.32 mm, while mean skin weight is 23.40 g.

The matrix showed different levels of correlation among the selected traits of the 71 chico genotypes evaluated (Table 8). Fruit weight, which is the most important trait considered in the selection of elite genotypes, has a strong correlation with fruit width (r=0.840; p=0.00). It is moderately correlated with fruit length (r=0.598; p=0.00) and skin weight (r=0.516; p=0.00). Similar results were obtained in avocado (*Persea americana* Mill.) where fruit weight is correlated with fruit width and seed weight (Magdalita and Valencia 2004). On the other hand, fruit width is moderately correlated with seed number (r=0.5514; p=0.00) and skin weight (r=0.5817; p=0.00). TSS and EP have very weak correlation with other selected traits evaluated. This result suggests that these two traits in chico are indeed distinct varietal characteristics that are independent of other characters, suggesting that they should be evaluated independently. The same result was obtained in rambutan (*Nephelium lappaceum* Linn.) (Magdalita and Valencia 2004). Moderate negative correlation existed between EP and skin weight (r=−0.6364; p=0.00). Seed length and seed width have strong correlation (r=0.7016; p=0.00), while seed width is moderately correlated with seed thickness (r= 0.6151; p=0.00).

Pummelo

The phenotypic characteristics such as fruit shape, skin color, vesicle color, and skin thickness of the 73 pummelo genotypes evaluated are presented in Figure 5. These pummelo genotypes were clustered using the average clustering method and Euclidian distance as a measure of similarity/dissimilarity. The dendrogram was cut at Euclidian distance between 5 and 6 based on fruit weight, fruit length, fruit width, TSS, number of seeds, edible portion, rind thickness, rind length, rind width, vesicle weight, vesicle number, and rag weight (Fig. 6). The cluster number, pummelo genotypes and the cluster size are indicated in Table 9. Thirty-seven (37) pummelo genotypes clustered together in Cluster I. Cluster II has four members and Cluster III has 29 members. Cluster IV and Cluster V have three and one member, respectively. The mean and standard deviation of the quantitative traits of the different pummelo genotypes belonging to the different clusters are presented in Table 10.

Cluster I. Thirty-seven pummelo genotypes grouped together in Cluster I (Table 7). The members of this cluster are genotypes with small fruits with a mean fruit weight of 0.75 kg. The mean fruit length is 13.13 cm, while fruit width is 12.13 cm. This cluster has the highest

Fig. 5. Phenotypic characteristics of pummelo genotypes used for the evaluation of different traits.

Table 8. Correlation matrix of 11 quantitative characters of 71 chico genotypes.

	FW	FL	FWd	TSS	SNo	EP	SW	SkW	SL	SWd	SdT
Fruit weight (FW)	1.00										
Fruit length (FL)	0.598*	1.000									
Fruit width (FWd)	0.840*	0.4143*	1.000								
TSS	-0.185	-0.0491*	-0.272*	1.000							
Seed no. (SNo)	0.465*	0.1498	0.551*	-0.2412*	1.000						
Edible portion (EP)	0.204	0.1737	0.054	-0.0637	-0.005	1.000					
Seed wt. (SW)	0.289	0.2325	0.303*	-0.1008	0.457	-0.1740	1.000				
Skin weight (SkW)	0.516*	0.3219*	0.582*	-0.1850	0.314*	-0.6364*	0.151	1.000			
Seed length (SL)	0.124	0.2469*	0.034	-0.2624*	0.036	-0.0760	0.121	0.182	1.00		
Seed width (SWd)	0.271*	0.0565	0.343*	-0.3729*	0.221	-0.1688	0.118	0.395*	0.702*	1.00	
Seed thickness (SdT)	0.344*	0.1833	0.360*	-0.2643*	0.492*	-0.0522	0.229	0.309*	0.427*	0.615*	1.00

* Significant at α=5%

mean EP of 59.05% among the five clusters and a mean TSS of 9.63% Brix. The mean rind thickness is 10.54 cm, rind length is 86.94 mm, and rind weight is 50.82 g. Members of this cluster have the least number of vesicles of 11 among the five clusters with mean vesicle weight of 0.47 kg. The mean number of seeds is 39, while the mean weight of rags is 0.17 kg.

Cluster II. Cluster II is composed of 4 members. The members of this cluster are genotypes with small fruits also having a mean fruit weight of 0.71 kg. The mean fruit length is 13.92 cm, while fruit width is 12.23 cm. This cluster has the highest mean TSS of 10.20% Brix among the five clusters and a mean % EP of 53.91%. Genotypes under this cluster has mean rind weight of 67.58 g and with mean rind thickness of 9.81 mm and rind length of 80.41 mm. Members of this cluster have a mean vesicle weight of 0.80 kg with mean vesicle number of 12. This cluster is the least seeded among the five clusters with mean seed number of 15, while the mean weight of rags is 0.15 kg.

Cluster III. This cluster is composed of 4 members. The members of this cluster are genotypes with also small fruits with a mean fruit weight of 1.58 kg. The mean fruit length is 15.90 cm, while fruit width is 17.45 cm. This cluster has a mean TSS of 9.60% Brix, and a mean % EP of 50.70%. This cluster has a mean rind thickness of 20.54 mm, rind length of 94.50 mm and rind weight of 66.54 g. Members of this cluster have a mean vesicle weight of 0.81 kg with mean vesicle number of 12. This cluster has a mean seed number of 17, while the mean weight of rags is 0.67 kg, which is the highest among the five clusters.

Cluster IV. Cluster IV is composed of two members. The members of this cluster are genotypes with medium-sized fruits with a mean fruit weight of 1.55 kg. The mean fruit length is 13.57 cm, while fruit width is 15.35 cm. This cluster has a mean TSS of 9.07 % Brix, and a mean %EP of 55.88 %. This cluster has a mean rind thickness of 10.38 mm, rind length of 83.20 mm, and rind weight of 85.78 g. Members of this cluster have a mean vesicle weight of 0.97 kg with mean vesicle number of 16. This cluster has the highest mean seed number of 120.0 among the five clusters. However, the same cluster has

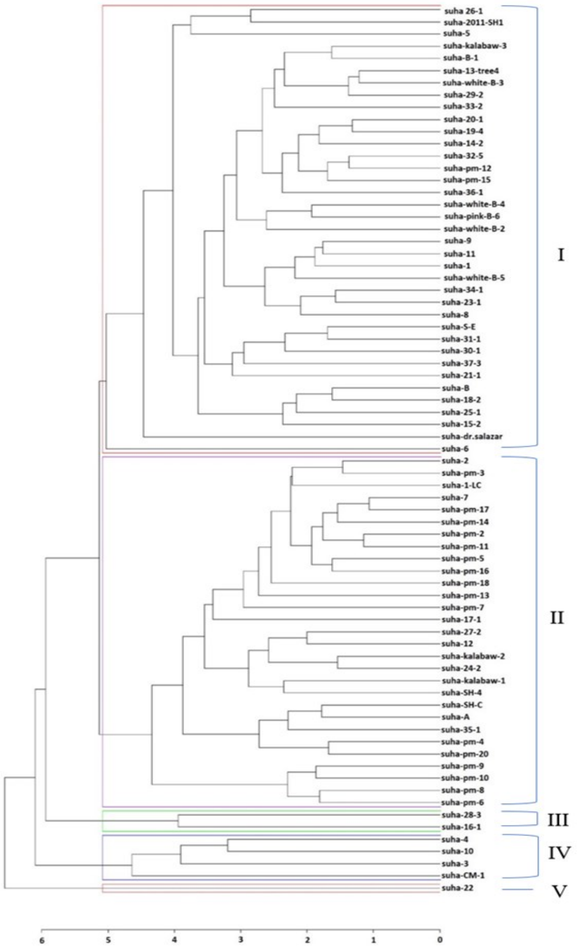

Fig. 6. Dendrogram of 73 pummelo genotypes based on 12 quantitative characters cut at 5 Euclidean distance.

Table 9. Distribution of 71 chico genotypes in the five different clusters.

Cluster	Pummelo Genotypes	Cluster Size
I	Suha B-1, Suha Pink B-6, Suha PM12, Suha PM15, Suha White B-2, Suha White B-3, Suha White B-4, Suha White B-5, Suha1, Suha11, Suha13-Tree4, Suha14-2, Suha15-2, Suha18-2, Suha19-4, Suha20-1, Suha-2011-SH1, Suha21-1, Suha23-1, Suha25-1, Suha26-1, Suha29-2, Suha30-1, Suha31-1, Suha32-5, Suha33-2, Suha34-1, Suha36-1, Suha37-3, Suha5, Suha6, Suha8, Suha9, Suha-B, Suha-Dr Salazar, Suha-Kalabaw-3 and Suha-S-E	37
II	Suha CM1, Suha10, Suha3 and Suha4	4
III	Suha PM10, Suha PM11, Suha PM13, Suha PM14, Suha PM16, Suha PM17, Suha PM18, Suha PM2, Suha PM20, Suha PM3, Suha PM4 Suha, PM5 Suha, PM6 Suha PM7, Suha PM8, Suha PM9, Suha SH4, Suha12, Suha17-1, Suha1-LC, Suha2, Suha24-2, Suha27-2, Suha35-1, Suha7, Suha-A, Suha-Kalabaw-1, Suha-Kalabaw-2 and Suha-SH-C	29
IV	Suha16-1 and Suha28-3	2
V	Suha22	1

the lowest mean weight of rags, which is 0.12 kg, among the five clusters.

Cluster V. This cluster has only one member, Suha 22, which has the biggest fruit among the five clusters with mean weight of 2.23 kg. The mean fruit length is 18.10 cm, while fruit width is 17.80 cm. This cluster has a mean TSS of 9.80 % Brix. However, this cluster has the lowest %EP among the five clusters at 47.63%.

This cluster has a mean rind thickness of 17.70 mm, rind length of 140.07 mm and rind weight of 100.86 g. The mean vesicle weight is 1.23 kg, while the vesicle number is 14. This cluster has a mean seed number of 58, while the mean weight of rags is 0.18 kg.

Table 11 shows the correlation matrices of the different phenotypic traits of pummelo genotypes. This shows that fruit weight is very strongly correlated with fruit width (r=0.937; p=0.00), and strongly correlated with fruit length (r=0.7536; p=0.00), rind thickness (r=0.7294; p=0.00) and vesicle weight (r=0.8656; p=0.00). Fruit weight is moderately correlated with rind length (r= 0.5536; p=0.00) and weight of rags (r=0.6527; p=0.00). Fruit length is strongly correlated with fruit width (r=0.7659; p=0.00) and moderately correlated with weight of rags (r=0.5791; p=0.00), rind thickness (r=0.5741; p=0.00), rind length (r=0.5731; p=0.00) and vesicle weight (r=0.5718; p=0.00). Fruit width is strongly correlated with rind thickness (r=0.7874; p=0.00), vesicle weight (0.7788; p=0.00) but moderately correlated with the weight of rags (r=0.6959; p=0.00). However, TSS has negligible to weak correlation with EP, rind thickness, rind width and weight of rags, implying that TSS is an independent trait that needs to be evaluated by itself. A moderate negative correlation existed between EP and rind thickness (r=–0.5084; p=0.00). In addition, rind thickness is moderately correlated with vesicle weight (r=0.5356; p=0.00), and rind length is also moderately correlated with vesicle weight (r=0.5991; p=0.00).

Each dendrogram generated for 'Saba' banana (Fig. 2), chico (Fig. 4) and pummelo (Fig. 6) showed a highly branched structure. This result suggests that there is a considerable degree of variability and divergence within the population of each fruit crop species. This variability can be attributed to the genetic differences of each genotype considering that each tree bearing the fruit samples evaluated came from seeds. Being open-pollinated, considerable variability is expected to occur due to cross-pollination within each fruit species that was expressed in the resulting progeny trees used as sources

Table 10. Mean and standard deviation of selected quantitative characters of pummelo genotypes belonging to the five clusters.

Cluster	Statistics	Fruit Characters											
		Fruit Weight (kg)	Fruit Length (cm)	Fruit Width (cm)	TSS (% Brix)	No. of Seeds	EP (%)	Rind Thickness (cm)	Rind Length (mm)	Rind Weight (g)	Vesicle Weight (kg)	Vesicle No.	Rag Weight (kg)
I	Mean	0.75	13.13	12.13	9.63	38.9	59.0	10.54	86.94	50.82	0.47	10.82	0.17
	SD	0.22	1.81	1.38	1.58	30.1	8.67	3.47	11.45	26.71	0.16	1.15	0.17
II	Mean	0.71	13.92	12.23	10.20	14.4	53.9	9.81	80.41	67.6	0.80	11.50	0.15
	SD	0.07	1.41	1.39	0.98	14.8	15.8	5.56	3.27	21.25	0.16	0.89	0.24
III	Mean	1.58	15.90	17.45	9.60	16.2	50.7	20.54	94.50	66.54	0.81	11.97	0.67
	SD	0.37	1.79	1.64	1.39	16.1	7.42	4.21	9.97	19.11	0.20	0.88	0.48
IV	Mean	1.55	13.57	15.35	9.07	120	55.9	10.38	83.20	85.78	0.97	15.50	0.12
	SD	0.49	1.52	1.77	0.11	36.8	3.43	0.95	13.15	26.17	0.25	2.12	0.04
V	Mean	2.23	18.10	17.80	9.80	58.0	47.6	17.70	140.1	100.9	1.23	13.33	0.18
	SD	0.35	1.65	1.54	1.35	18.2	5.76	3.56	8.76	20.12	0.27	1.90	0.45

Table 11. Correlation matrix of 11 quantitative characters of 71 pummelo genotypes.

	FW	FL	FWd	TSS	NoS	EP	RT	RL	RW	VW	VN	RgW
Fruit weight (FW)	1.0000											
Fruit length (FL)	0.7536*	1.0000										
Fruit width (FWd)	0.9372*	0.7659*	1.0000									
Total soluble solids (TSS)	-0.066	0.0042	-0.03	1.0000								
No. of seeds (NoS)	-0.080	-0.197	-0.200	0.0190	1.0000							
Edible portion (EP)	-0.378*	-0.396*	-0.478*	0.0199	0.1650	1.0000						
Rind thickness (RT)	0.7294*	0.5741*	0.7874*	0.0168	-0.354*	-0.508*	1.0000					
Rind length (RL)	0.5536*	0.5731*	0.4263*	-0.283*	-0.039	-0.007	0.3175*	1.0000				
Rind weight (RW)	-0.012	0.0437	-0.048	0.0896	-0.075	-0.006	-0.1342	-0.028	1.0000			
Vesicle weight (VW)	0.8656*	0.5718*	0.7788*	-0.138	0.1444	-0.120	0.5356*	0.5991*	-0.202	1.0000		
Vesicle number (VN)	0.4485*	0.1795	0.4317*	-0.211	0.2565*	-0.152	0.1364	0.1252	0.0459	0.442*	1.0000	
Rag weight (RgW)	0.6527*	0.5791*	0.6959*	0.0991	-0.346*	-0.205	0.4965*	0.2117	0.2021	0.476*	0.1688	1.0000

* Significant at α=5%

of the fruit samples evaluated. Similar observations were recorded for jackfruit (*Atrocarpus heterophyllus* Lamk.) genotypes in Eastern Visayas (Dayap 2000) and in Batangas (Magdalita et al. 2011), and genotypes of rambutan, sweetsop (*Annona squamosa* Linn.) and avocado (*Persea americana* Mill.) (Magdalita and Valencia 2004). A similar dendrogram that also suggests high genetic variability of samples for different horticultural traits was generated for 22 pineapple hybrids and cultivars (Ines et al. 2009). Morphological and RAPD markers effectively revealed this high degree of variability in pineapple (*Ananas comosus* L. Merr.) (Ines et al. 2009).

However, the variability observed among the population of 'Saba' banana, chico and pummelo genotypes cannot be solely attributed to the genetic differences but also to environmental conditions such as temperature, solar radiation, humidity, wind, soil moisture content, etc. Therefore, the interaction of the genotype and the environment can contribute to the total variability.

In reality, a dendrogram with a cophenetic correlation value of 1 would give a good grouping of the samples in a given population. Low values would mean a low correlation between the dendrogram and the original similarities or dissimilarities. The cophenetic coefficient gives a measure of how well the original data match the hierarchical clustering through comparisons of the resemblance values from the similarity or dissimilarity matrix with those implied from the dendrogram. For a dendrogram to be a reasonably good reflection of the matrix of association, values of 0.85 or higher are desirable (Stuessy 2009). In the present study, the cophenetic correlation coefficient obtained for chico was 0.89. Since this value is close to 0.85, it indicates that the dissimilarities or similarities of the data are well represented in the dendrogram that was generated. However, the cophenetic correlation coefficient obtained in 'Saba' banana and pummelo were 0.569 and 0.715, respectively. These values were relatively lower than the desirable value of 0.85, indicating that the dissimilarities or similarities of the data may not be well represented in the dendrogram that was generated. Nevertheless, a low cophenetic correlation coefficient does not mean that the dendrogram is not an acceptable representation of the dissimilarities and similarities of the data, rather it may indicate that distortion has taken place during the clustering analysis (Stuessy 2009).

The agglomerative clustering method demonstrated that it can efficiently cluster the 67 'Saba' clones, and the 71 chico and 73 pummelo genotypes as shown by the dendrogram. However, a decision has to be done on how many variables will be used to group the different genotypes. In this study, depending on the fruit crop species, a set of three important fruit traits were used to group the genotypes into five clusters. In 'Saba' banana, bunch weight, bunch length and finger size were used. In chico and pummelo, fruit weight, TSS and EP were used as basis for clustering. However, classifying the 67, 71 and 73 'Saba' banana, chico and pummelo genotypes, respectively, into five groups each is a procedure that could be very subjective. This can happen because there is no definite algorithm that can be used in deciding at what specific coefficient distance the dendrogram should be cut (Brown 1991).

In some cases, *a priori* knowledge can facilitate in determining the number of clusters to be formed. For instance, Cena (1995) used the three populations of cacao (*Theobrama cacao* Linn.), namely, Ferastero, Criollo and Trinitario, as basis in grouping the University of Southern Mindanao Agricultural Research Center (USMARC) cacao collections and found that most of the studied clones with known varietal group fall in the same cluster. One common practice in clustering is to examine the tree generated and then, designate similarity and difference level above which the individuals are considered grouped.

SUMMARY AND CONCLUSION

This study was conducted to characterize selected phenotypic traits of different genotypes of `Saba' banana, chico and pummelo, group different genotypes, and find out the correlation of various quantitative characters of fruit crop species. A highly branched dendrogram for three each fruit species was generated indicating a considerable degree of variability in all traits of each fruit crop species within a population evaluated. Hence, there is a wide window for selection of unique genotypes evaluated by cluster analysis which can be the basis for selecting specific genotypes for developing a new variety or selecting parents for use in hybridization.

Based on the phenotypic traits of genotypes grouped in cluster, potential outstanding clones have been identified. This includes 28 `Saba' banana clones (Cluster III) evaluated to have big fingers and more number of fingers per bunch, and potential parents for crop improvement such as CH7-IPB chico genotype (Cluster II) which was evaluated to have the highest TSS, highest EP, thinnest skin, small and few number of seeds 37 pummelo genotypes (Cluster I) evaluated to have high EP, and four other genotypes from Cluster II with relatively high EP and had the highest TSS evaluated among the five clusters were included.

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