

Characterization of some Nigerian pawpaw (*Carica papaya* L.) accessions using pomological traits

KELVIN C. UDUMA¹, RICHMOND E. EDUGBO² and GODSON E. NWOFIA^{1*}

¹Department of Crop and Horticultural Science, Michael Okpara University of Agriculture, Umudike, Abia State, Nigeria.

²Department of Applied Biology, Federal University of Technology, Babura, Jigawa State, Nigeria

Abstract

Genetic diversity assessment is fundamental for crop improvement, particularly in underutilized tropical species like papaya (*Carica papaya* L.). This study evaluated 60 papaya accessions collected from southern Nigeria using pomological traits. Significant genotypic differences ($p < 0.01$) were observed across all traits measured. Fruit length ranged from 23.10 to 31.53 cm (mean = 26.92 cm), while fruit pulp diameter varied between 8.13 and 14.53 cm. Fruit circumference spanned 30.10 to 38.53 cm, and fruit weight exhibited the highest variability, ranging from 0.73 to 2.78 kg (mean = 1.63 kg; CV = 50.90%). Seed number varied widely, from 298 to 945 seeds per fruit, with a mean of 609.00. Fruit shapes were diverse, with elliptic and reniform shapes most common (13.33% each), followed by elongated and plum-shaped (11.67% each), and less frequent shapes like pear, lengthened cylindrical, and globular (1.67% each). Mature fruit skin colour was predominantly green (62.71%), followed by yellowish-green (25.42%) and yellow (11.86%). Fruit flesh colour was mainly deep yellow to orange (33.33%), light yellow (26.67%), bright yellow (23.33%), and reddish-orange (16.67%). This diversity has potential implications for breeding programs. Correlation analysis revealed a strong positive association between fruit length and circumference ($r = 0.97$), suggesting simultaneous improvement potential. Cluster and heatmap analyses grouped accessions into five distinct clusters, indicating substantial genetic divergence. Accessions such as IMNO01 (high fruit weight) and ASUN02 (low seed number) were identified as promising for breeding programs targeting larger fruit size and improved edible yield. The findings provide a foundation for selecting elite genotypes and enhancing papaya breeding efforts in Nigeria.

Keywords: characterization, cluster analysis, fruit trait, genetic diversity.

Introduction

Pawpaw (*Carica papaya* L.), belonging to the family Caricaceae, is a widely cultivated tropical fruit crop valued for its nutritional, medicinal, and economic importance (Adinde et al., 2024; FAOSTAT, 2023). The crop is renowned for its high content of vitamins, antioxidants, and digestive enzymes such as papain, making it a significant component of diets and agro-industries across tropical regions (Alara et al., 2020; Khatun et al., 2023). In Nigeria, pawpaw cultivation plays a vital role in food security and rural livelihoods; however, its full genetic potential remains underutilized due to limited characterization, selection and improvement efforts (Adinde et al., 2024).

Nigeria is the third-largest producer globally, with an annual output of 765,000 tonnes (Aikpokpodion, 2012). However, in spite of its extensive cultivation area (92,500 ha), Nigeria records one of the lowest yields worldwide (8.3 t/ha), thus, highlighting a critical need for genetic improvement of local germplasm. Genetic diversity assessment is fundamental for such improvement, as it offers a reservoir of variations in traits for breeding programs targeting enhanced yield, fruit quality, nutritional content, and resilience to environmental stresses.

Genetic characterization using morphological and pomological traits remains a fundamental approach in identifying intra-specific variations, which is essential for crop improvement programmes (Olawaju et al., 2023). Morphological traits provide an accessible entry point for assessing genetic diversity, reflecting both genetic and environmental influences. Fruit traits size, shape, flesh color, and seed characteristics are particularly relevant for papaya, given their economic and nutritional implications. Morphological diversity in fruit traits is a practical target for selection, as it influences consumer preference and

market value. Pomological traits, such as fruit size, shape, weight, pulp thickness, and seed characteristics, are critical indicators of fruit quality and yield potential and directly influence market acceptance and breeding targets (Aikpokpodion, 2012). Comprehensive evaluation of these traits among diverse *C. papaya* accessions can provide valuable insights for selection of superior genotypes, genetic resource conservation, and enhancement of breeding programmes geared toward pawpaw improvement.

Southern Nigeria, the focus of this study, is a key papaya-growing regions, characterized by high rainfall, fertile soil, and dense farming communities. The region likely harbors unique accessions shaped by local selection pressures and farmer preferences, making them ideal for diversity analysis. Recent work on Nigerian pawpaw (*Carica papaya* L.) shows substantial phenotypic diversity in pomological traits fruit length/diameter, shape, flesh color, cavity shape, edible volume, and yield components useful for selection and breeding. A foundational multi-location study evaluating 60 accessions with IBPGR fruit descriptors and multivariate analyses reported highly significant among-accession variation in these fruit traits and grouped accessions accordingly (Aikpokpodion, 2012). Newer collection-based studies from southern Nigeria (30 accessions sampled across Abia, Imo, Rivers, Enugu, and Anambra) likewise document wide variation in fruit morphology (shape/size/pulp color) and fruit yield characteristics, reinforcing the presence of exploitable pomological diversity in local germplasm (Akinrotimi and Nwofia, 2025). Complementary trials indicate that management factors (e.g., manure rate) can modulate expression of fruit-size and quality traits across accessions, underscoring genotype $\times$ environment effects to consider during selection (Olajide et al., 2020). Overall, Nigerian papaya collections present rich, structured

variation in pomological traits, amenable to standardized characterization and data-driven improvement. For Nigerian papaya, such diversity assessment evaluations will be vital in identification of elite genotypes, development of conservation strategies, as well as addressing production challenges. This study therefore aims to assess the genetic diversity among 60 *Carica papaya* accessions collected from southern Nigeria based on key pomological traits.

Materials and Methods

Sixty (60) papaya accessions were obtained from local markets in three states in Nigeria, namely Abia State, Imo State, and Rivers State. The latitude, longitude, and altitude of the collection sites were obtained using a global positioning system (GPS, Etrex Legend, Garmin). The International Board for Plant Genetic Resources (IBPGR, 1988) descriptor list for papaya was used to characterize the sixty (60) pawpaw accessions. Twenty-one descriptors were used for characterization of the fruit, seeds, and pulp following procedures outlined for sampling in the IBPGR descriptor list. Five (5) replicates were taken to represent each accession for quantitative traits such as fruit length, fruit pulp diameter, fruit circumference, fruit weight, and seed number. Qualitative traits, including fruit shape, fruit skin colour, and fruit flesh colour, were determined by careful observation and comparison with the IBPGR descriptor. Mature pawpaw fruits were obtained from the markets of the selected local governments, and measurements were taken of the fruit length and other traits, such as flesh colour, among others..

Data collected for all observed traits was analyzed using a combination of statistical techniques. Analysis of Variance (ANOVA), and correlation analysis was applied to quantitative traits, while Multivariate analysis employed principal component analysis (PCA) to determine the relative importance of traits contributing to variability among the accessions, following the methodology outlined by Jolliffe (2002) for dimensionality reduction and trait prioritization. These statistical analyses were performed using GenStat Discovery Edition 12.1 software (VSN International, 2009) and SAS v.9.1 (SAS Institute Inc., 2006). To explore relationships among the accessions, cluster analysis was conducted using the nearest neighbour method based on Euclidean distances, as implemented in PASW Statistics Release 18 (SPSS Inc., 2009). This approach, rooted in hierarchical clustering techniques (Everitt *et al.*, 2011), will group accessions based on similarity in trait profiles.

Results

The fruit traits of 60 *Carica papaya* accessions, including fruit length (cm), fruit pulp diameter (cm), fruit circumference (cm), fruit weight (kg), and fruit seed number, with all traits showing highly significant differences among accessions ($p < 0.05$) (Table 1). Fruit length ranged from 23.10 cm (ASUS02, ASIN02) to 31.53 cm (RSPH04) with a grand mean of 26.92 cm and a coefficient of variation (CV% = 13.20%). Fruit pulp diameter varied from 8.13 cm (IMNO04) to 14.53 cm (IMOK02) with a grand mean of 11.10 cm (CV% =

20.40%), while fruit circumference ranged from 30.10 cm (ASUS02, ASIN02) to 38.53 cm (RSPH04) with a grand mean of 33.92 cm (CV% = 11.10%). Fruit weight exhibited the highest variability (CV% = 50.90%), ranging from 0.73 kg (IMOK05) to 2.78 kg (IMNO01) with a grand mean of 1.63 kg, reflecting substantial differences in fruit size. Number of Fruit seed also showed high variability (CV% = 54.50%), ranging from 298.00 (ASUN02) to 945.00 (ASIN02) with a grand mean of 609.00, indicating significant variation in seed production

Qualitative horticultural traits of 60 *Carica papaya* Accessions

There was a significant variation in qualitative traits observed among the accessions studied (Table 4.2). Fruit shape (Fig 1) was predominantly elliptic and reniform, each observed in 13.33% of the accessions. Elongated and plum-shaped fruits were recorded in 11.67% of the accessions, respectively. Blossom-end shaped fruits occurred in 10.00% of cases, while oblong and oval shapes were both present in 8.33% of the accessions. Club and oblong blocky types accounted for 6.67% each, with acorn-shaped fruits observed in 5.00% of the accessions. Less frequently occurring shapes included pear shape, lengthened cylindrical, and globular types, each representing 1.67% of the accessions studied. Mature fruit skin colour was mostly green (62.71%), while yellowish-green was found in 25.42% of the accessions. Yellow skin colour was the least common, observed in 11.86% of the samples (Fig. 2). Fruit flesh colour (Fig. 3) was largely deep yellow to orange (33.33%), followed by light yellow (26.67%) and bright yellow (23.33%). Reddish-orange flesh was the least represented, occurring in 16.67% of the accessions.

Cluster Dendrogram and Heat Map (Pomological Traits or Genetic Similarity)

Hierarchical cluster dendrogram showing the relationships among 60 accessions (A1–A60), based on similarity across pomological, features is presented in Fig. 7. The vertical axis (Height) reflects the linkage distance, or dissimilarity, used to merge clusters during the agglomerative process. The dendrogram revealed the formation of five major clusters, indicated by distinct colors: Cluster 1 (Dark Blue, far left), made up of thirteen (13) accessions forms a compact group with relatively low linkage heights, suggesting high internal similarity. Cluster 2 (Yellow), contains six (6) accessions showing moderate similarity and might represent a transitional group between phenotypically distinct accessions. Cluster 3 (Grey, center), made up twelve (12) accessions and includes a broader range of accessions. The greater vertical height within this group implies more phenotypic variability, potentially incorporating intermediate types. Cluster 4 (Red), comprising eight (8) accessions, and is relatively distinct and may represent a genetically unique or phenotypically specialized group. Cluster 5 (Light and Dark Blue, right side): Encompasses twenty-one (21) accessions. Despite the larger size, the shorter linkage heights within this cluster suggest a high degree of homogeneity. These may represent elite selections or landraces with stable traits.

A heatmap visualization illustrating the genetic diversity among various *Carica papaya* (papaya) accessions, based on phenotypic traits including fruit length, fruit weight, fruit seed number, and fruit circumference and fruit pulp diameter is presented in Fig. 8. across accessions

Table 1: Mean Fruit traits of 60 *Carica papaya* Accessions

Accession	Fruit Length (cm)	Fruit Pulp diameter (cm)	Fruit Circumference (cm)	Fruit weight (kg)	Number of Fruit Seeds
RSPH01	30.63	11.33	37.63	1.64	540.00
RSPH02	31.10	12.67	38.10	1.02	694.00
RSPH03	30.73	11.70	37.73	2.27	632.00
RSPH04	31.53	13.57	38.53	1.27	505.00
RSIK01	30.20	9.70	37.20	1.93	329.00
RSIK02	29.23	10.37	36.23	1.51	476.00
RSIK03	24.10	11.90	31.10	1.28	553.00
RSIK04	24.53	12.77	31.53	1.81	624.00
RSOA01	24.63	10.03	31.63	1.67	595.00
RSOA02	24.90	8.77	31.90	1.22	665.00
RSOA03	27.43	9.20	34.43	1.52	491.00
RSOA04	24.67	12.77	31.67	1.64	434.00
RSOK01	25.23	11.97	32.23	1.22	581.00
RSOK02	27.57	9.70	34.57	1.06	672.00
RSET01	28.03	12.07	35.03	2.04	807.00
RSET02	26.47	10.87	33.47	2.16	404.00
RSEL01	27.77	9.43	34.77	1.74	698.00
RSEL02	26.50	10.43	33.50	2.02	639.00
RSOY01	28.30	11.13	35.30	1.78	719.00
RSOY02	28.67	10.07	35.67	0.85	473.00
ASIK01	29.90	9.83	36.90	1.10	448.00
ASIK02	29.57	11.63	36.57	1.63	629.00
ASIK03	28.13	10.37	35.13	1.67	632.00
ASIK04	27.00	10.33	34.00	1.32	557.00
ASUS01	26.33	13.93	33.33	1.81	709.00
ASUS02	23.10	10.57	30.10	1.75	680.00
ASUS03	26.23	10.43	33.23	2.04	718.00
ASUS04	26.23	10.03	33.23	1.33	345.00
ASUN01	26.00	10.90	33.00	2.21	615.00
ASUN02	28.13	10.90	35.13	1.38	298.00
ASUN03	27.33	11.60	34.33	2.38	499.00
ASUN04	27.10	12.67	34.10	1.60	889.00
ASBD01	24.63	13.07	31.63	1.72	360.00
ASBD02	26.83	11.20	33.83	1.49	766.00
ASBD03	28.37	12.10	35.37	1.74	747.00
ASAS01	27.07	8.73	34.07	1.70	833.00
ASAS02	27.97	11.03	34.90	1.75	595.00
ASAS03	27.23	11.27	34.23	1.11	572.00
ASIN01	28.30	13.23	35.30	1.27	683.00
ASIN02	23.10	8.17	30.10	1.66	945.00
IMNO01	26.50	11.80	33.50	2.78	671.00
IMNO02	25.30	12.57	32.30	1.54	538.00
IMNO03	27.13	12.97	34.13	0.98	667.00
IMNO04	25.13	8.13	32.13	1.75	914.00
IMNO05	23.40	11.63	30.40	1.67	629.00
IMOK01	26.47	8.27	33.47	1.99	474.00
IMOK02	27.30	14.53	34.30	1.16	611.00
IMOK03	26.53	11.30	33.53	1.89	558.00
IMOK04	27.77	12.03	34.77	1.44	739.00
IMOK05	28.27	10.10	35.27	0.73	667.00
IMET01	26.17	12.67	33.17	1.56	387.00
IMET02	26.13	10.47	33.13	1.15	504.00
IMET03	25.97	8.87	32.97	2.29	604.00
IMET04	26.07	10.43	33.07	0.80	737.00
IMET05	24.80	10.63	31.80	1.78	578.00
IMEZ01	26.50	9.60	33.50	2.30	585.00
IMEZ02	25.53	10.47	32.53	1.83	536.00
IMEZ03	27.73	12.67	34.73	1.97	833.00
IMEZ04	26.73	13.33	33.73	1.77	641.00
IMEZ05	25.07	11.10	32.07	2.21	640.00
Grand Mean	26.92	11.10	33.92	1.63	609.00
LSD _(0.05)	5.74	3.67	6.09	1.34	537.10
CV%	13.20	20.40	11.10	50.90	54.50

Note: cm = centimetre, ns = not significant, * =significant at 5%, ** = significant at 1% and *** = significant at 0.01%, Gm = grand mean, LSD = Least Significant Difference, CV% = Coefficient of Variation

Table 2: Frequency Distribution of 3 Qualitative traits assessed in 60 papaya accessions in Southern Nigeria

Character	Description State	% rate
Fruit Shape	1: elliptic	13.33
	2: elongated	11.67
	3: reniform	13.33
	4: plum shape	11.67
	5: club	6.67
	6: oblong	8.33
	7: oval	8.33
	8: blossom-end shape	10.00
	9: oblong blocky	6.67
	10: acorn	5.00
	11: pear shape	1.67
	12: lengthened cylindrical	1.67
	13: globular	1.67
Fruit Skin Colour	1: Yellow	11.86
	2: Yellowish-green	25.42
	3: Green	62.71
Fruit Flesh Colour	1: Deep yellow to orange	33.33
	2: Bright yellow	23.33
	3: Light yellow	26.67
	4: Reddish-orange	16.67

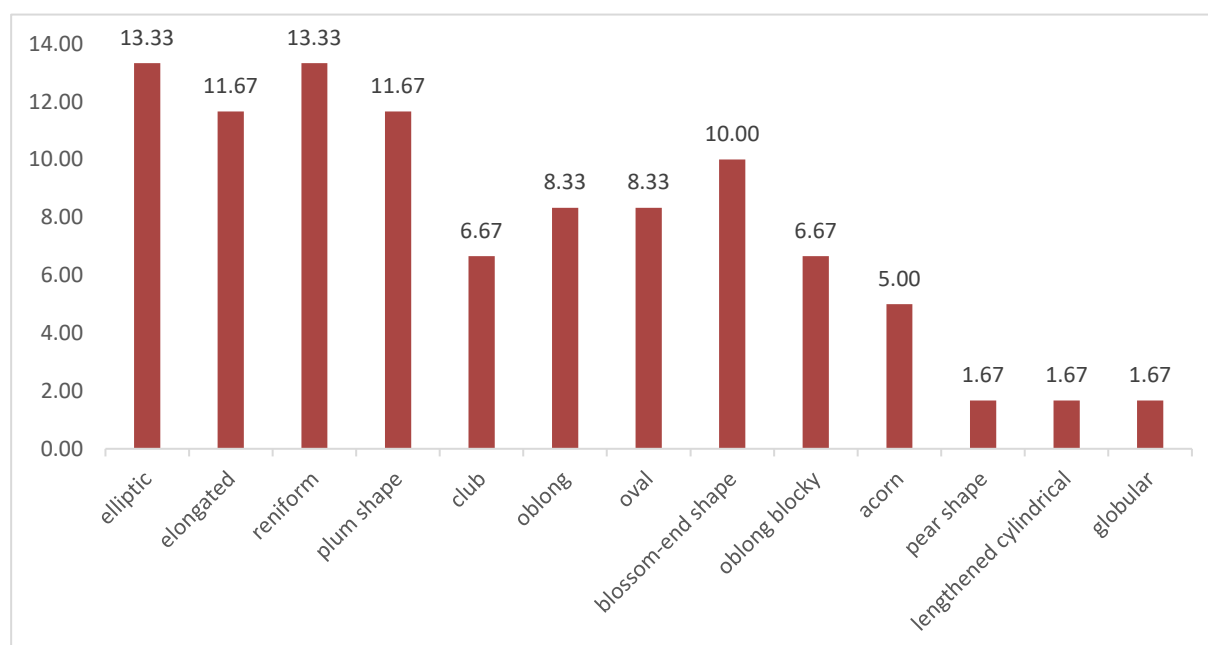


Fig 1: Fruit Shape

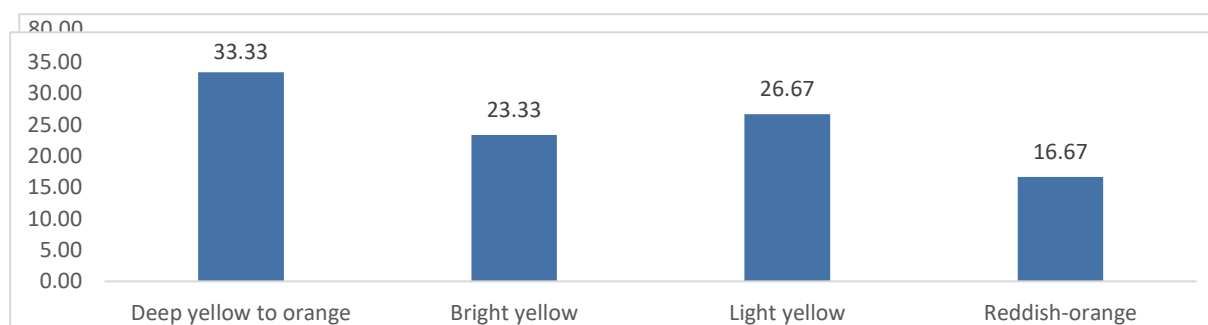


Fig 2: Fruit Skin colour

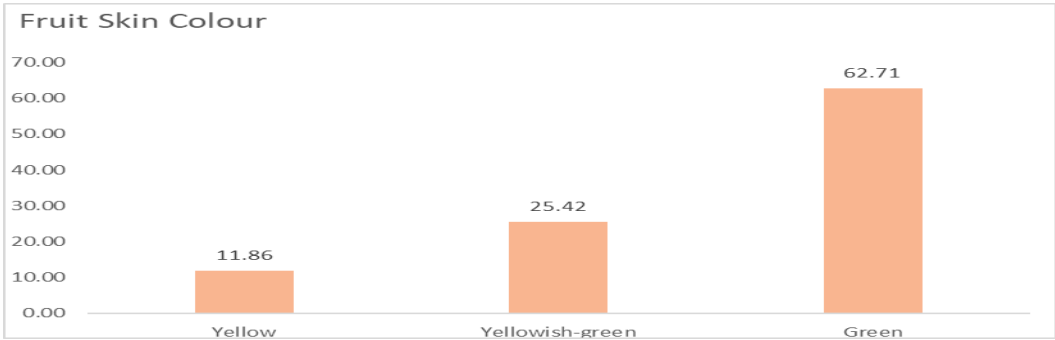


Fig 3: Fruit Flesh colour

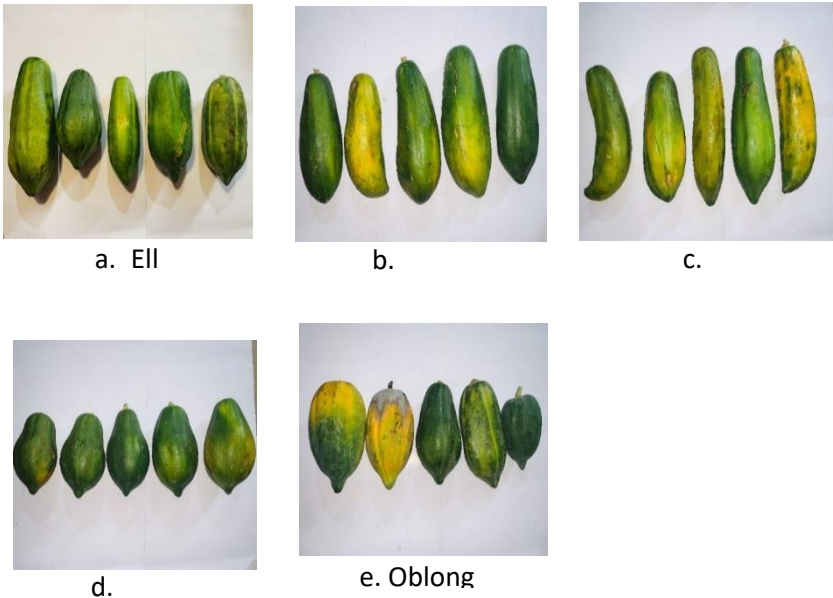


Fig 4: Variation in fruit shapes showing elliptic, elongate, club, oblong and oblong blocky types among papaya accessions in Southern Nigeria.

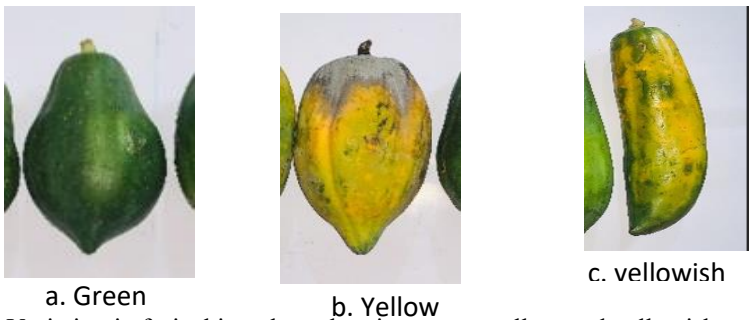


Fig 5: Variation in fruit skin colour showing green, yellow and yellowish green colours among papaya accessions in Southern Nigeria

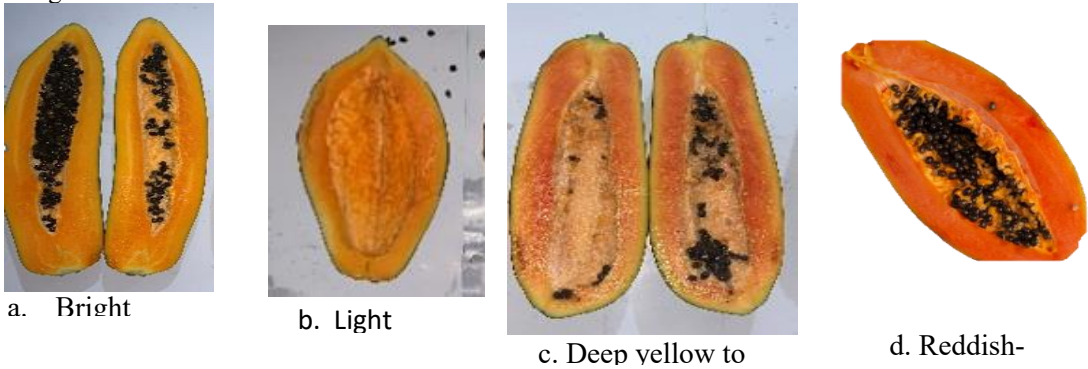


Fig 5: Fig 6. Variation in fruit flesh colour showing bright yellow, light yellow, Deep yellow to green and reddish-orange colours among papaya accessions in Southern Nigeria

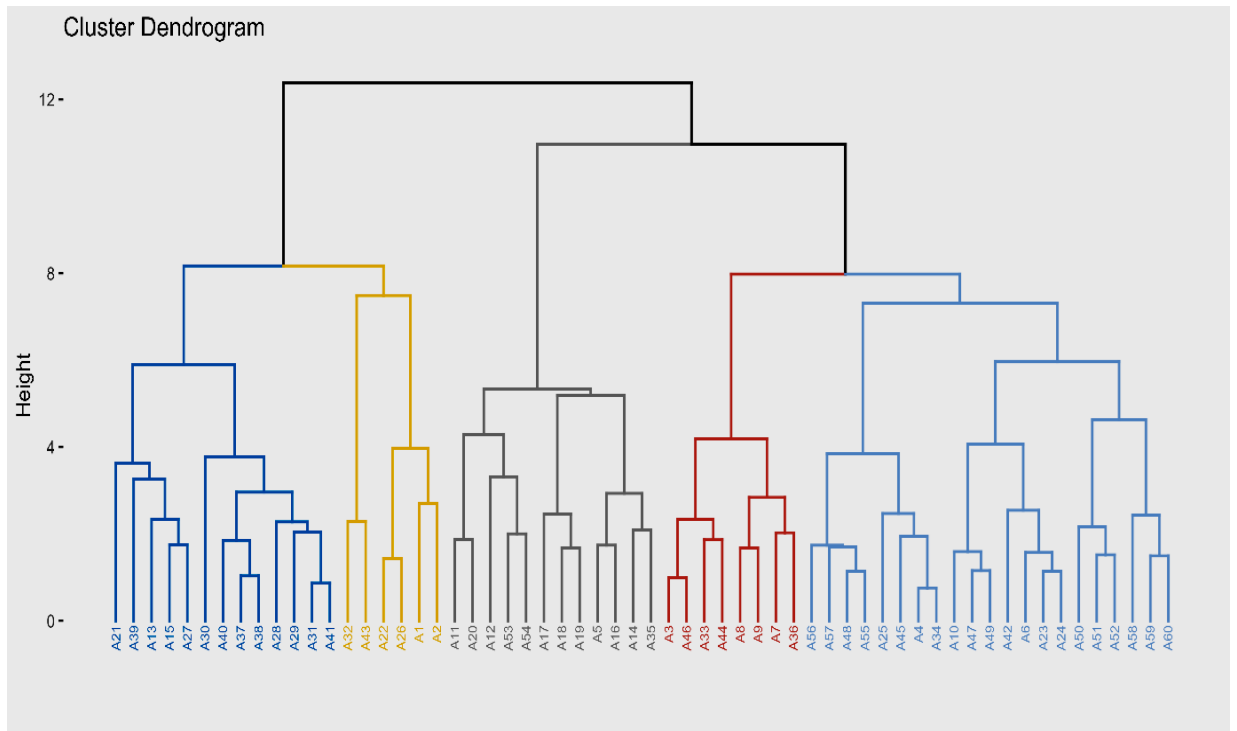


Fig. 7: Cluster Dendrogram (Pomological Traits or Genetic Similarity)

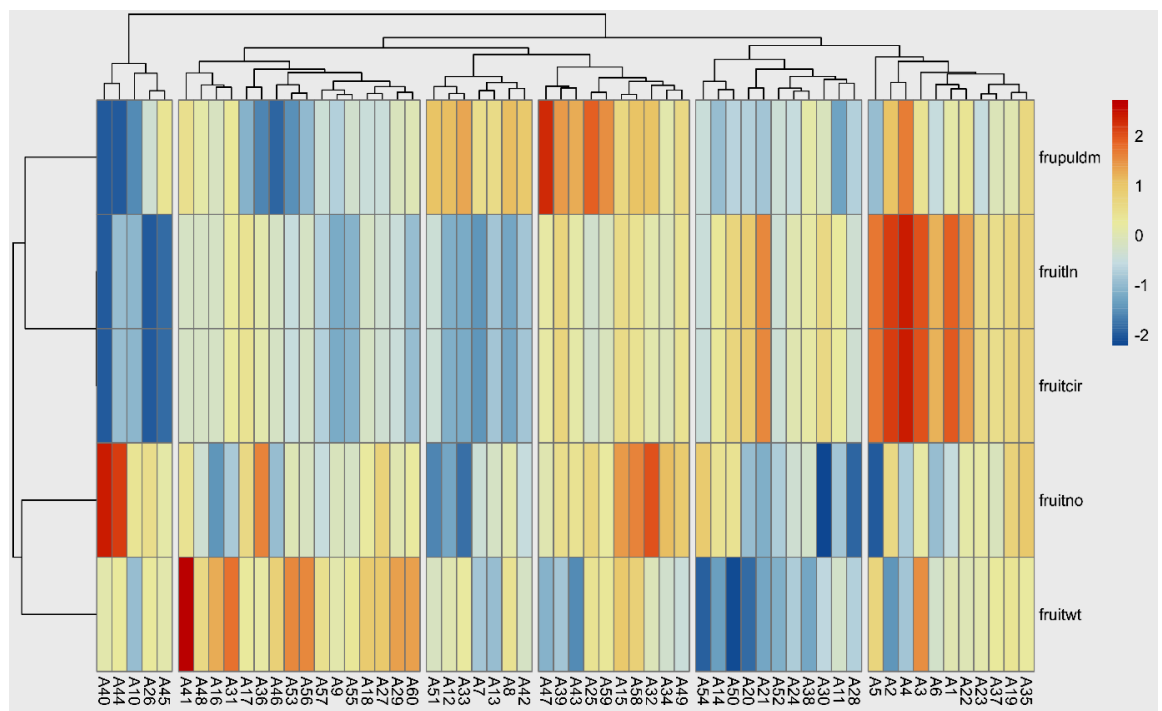


Fig. 8: Fruit traits Heat Map

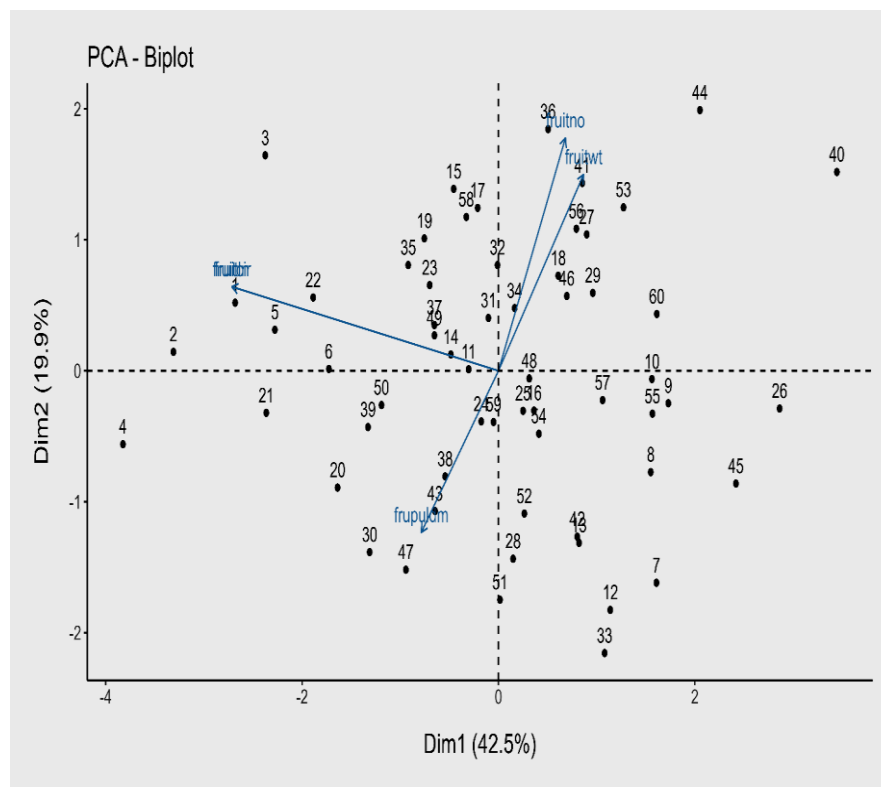


Fig. 9: PCA Biplot of Pomological Traits

The heatmap dendrogram grouped the accessions into six clusters. From left to right, cluster 1 consisting of five accessions indicated high fruit seed number and moderate fruit weight but had shorter fruit with smaller circumference and smaller fruit pulp diameter. Cluster 2 which contained sixteen accessions indicated heavier fruits while cluster 3 indicated higher fruit pulp diameter. Cluster 4 consisting of 10 accessions indicated higher fruit pulp diameter, high fruit seed number and higher pulp diameter but with moderate fruit length, fruit circumference and fruit weight. Cluster 5 with eleven accessions had moderate performance for fruit length, and fruit circumference but had low fruit weight and low fruit pulp diameter. Cluster six also contained eleven accessions and indicated high performance for fruit length and fruit circumference with moderate performance for fruit pulp diameter, fruit seed number and fruit weight

PCA Biplot of Pomological Traits

Principal Component Analysis (PCA) biplot that summarizes the multivariate variation in pomological traits across the fruit samples studied is presented in Fig. 9. The analysis incorporates key variables including fruit weight, fruit length, fruit pulp diameter, fruit circumference. The first principal component (Dim1) accounted for 42.5 % of the total variance, while the second component (Dim2) explained 19.9 %, resulting in a combined explanation of 62.4 % of the overall variation in the dataset. Dim1 primarily reflected fruit size related traits. Variables such as fruit length, fruit circumference and fruit pulp diameter loaded strongly and positively along this axis. Their close clustering indicates a high degree of correlation, suggesting that Dim1 effectively

Discussion

represents a latent dimension corresponding to overall fruit size. Accessions located on the far left of the biplot—are therefore inferred to exhibit larger fruits with higher dimensions. Number of Fruit seeds and fruit weight had high loading along the second PC (Dim 2) axis with accessions located around the far right indicating greater variations for these traits. The spatial arrangement of samples within the biplot revealed significant phenotypic diversity among the fruits. Samples located near the origin (e.g., 14, 24, and 48) likely exhibited intermediate or average values across the measured trait.

Correlation Matrix for Fruit Traits

Correlation matrix delineating the interrelationships among selected fruit traits is shown in fig. 10. A highly salient positive correlation ($r=0.97$) is evident between fruit length and fruit circumference. This substantial coefficient indicates a near-perfect linear relationship, implying that increases in fruit length are almost invariably accompanied by proportional increases in fruit circumference. In contrast, the remaining correlations within the matrix are comparatively subdued. Fruit pulp diameter exhibited weak positive correlations with fruit length ($r=0.08$) and fruit circumference ($r=0.07$). Fruit weight showed weak negative correlations with fruit length ($r=-0.06$) and fruit pulp diameter ($r=-0.08$), alongside a negligible negative correlation with fruit circumference. Number of fruit seed displayed a weak positive correlation with fruit weight ($r=0.11$) and tenuous or imperceptible correlations with the other measured traits.

This study had demonstrated phenotypic variability among the 60 *Carica papaya* accessions collected from southeastern and south-southern Nigeria, particularly in fruit length, pulp diameter, circumference, weight, and number of seeds. This variability is indication of the rich genetic diversity existing within the region's papaya germplasm, and presents valuable opportunities for breeding programs aimed at improving fruit yield, quality, and consumer preferences. These observed variability across all fruit traits were consistent with the findings of Akinrotimi and Nwofia (2025); Odafe and Law-Ogbomo (2021); Olajide *et al* (2020) and Nwofia and Okwu (2012), who reported considerable morphological variation among papaya genotypes in Nigeria and highlighted the genetic potential of indigenous papaya populations for crop improvement. The broad range of fruit weights and numbers of seeds among

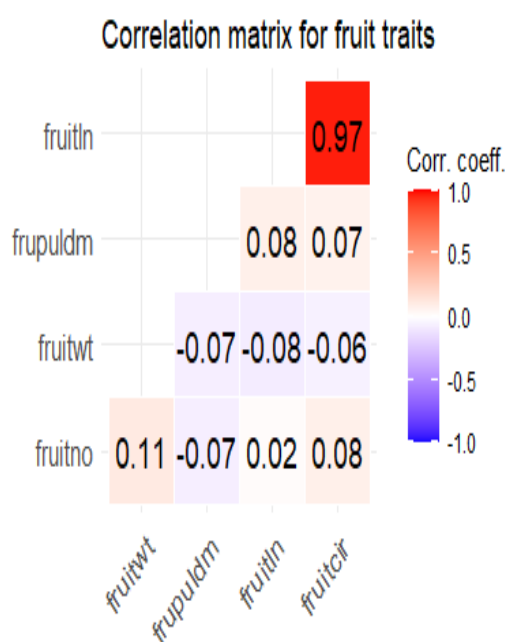


Fig. 10: Correlation Matrix for Fruit Traits

accessions agreed with previous reports by Aikpokpodion (2012), who identified fruit size and seed content as important selection criteria in papaya breeding, given their direct implications for market value and edible portion yield.

This study revealed significant phenotypic variability in fruit shape, skin color, and flesh color among 60 *Carica papaya* accessions from southern Nigeria, underscoring the rich genetic diversity within the region's papaya germplasm. Thirteen distinct fruit shapes were identified, with elliptic and reniform shapes most prevalent (13.33% each), followed by elongated and plum-shaped (11.67% each), while pear-shaped, lengthened cylindrical, and globular shapes were least common (1.67% each). This diversity in fruit shape aligns with previous findings by Ocampo *et al.* (2006) and Siar *et al.* (2011), who noted extensive morphological variation in papaya influenced by genetic and environmental factors. Fruit skin color was predominantly green (62.71%), followed by yellowish-green (25.42%) and yellow (11.86%), consistent with reports by Paull and Duarte (2011) highlighting the commercial preference for green-skinned papayas due to their extended shelf life. Flesh color varied across deep yellow to orange (33.33%), light yellow (26.67%), bright yellow (23.33%), and reddish-orange (16.67%), reflecting potential high carotenoid and lycopene content as noted by Chandrika *et al.* (2003). These variations in fruit traits offer valuable opportunities for breeding programs targeting enhanced nutritional quality, visual appeal, and market-preferred characteristics. The observed diversity, consistent with findings by Akinrotimi and Nwofia (2025) and Olajide *et al.* (2020), suggests that targeted selection and hybridization of accessions with desirable traits, such as deep yellow to orange flesh or elliptic shapes, could address low yields in Nigeria and improve market competitiveness. Future studies integrating molecular markers, as recommended by Ocampo *et al.* (2006), could further elucidate the genetic basis of these traits to support marker-assisted breeding for improved papaya varieties.

The high coefficients of variation (CV) observed for fruit weight and number of seeds further indicated the substantial genetic diversity for these traits, and suggested a scope for selection and improvement. Such high variability is advantageous for breeding, as it facilitated the identification of superior genotypes with desirable agronomic traits. Similar trends was earlier reported by Khatun *et al.* (2023), where high variability in fruit weight and number of seeds among Bangladeshi papaya germplasm provided a basis for selecting high-yielding and consumer-preferred varieties.

Accessions such as IMNO01 (2.78 kg fruit weight), RSPH04 (largest fruit length and circumference), and IMOK02 (highest pulp diameter) emerged as promising candidates for breeding programs targeting improved fruit size, pulp yield, and market quality. Large-fruited varieties with thicker pulp and reduced number of seeds are known to enhance consumer acceptance and processing efficiency, making these traits critical breeding targets (Adinde *et al.*, 2024). Notably, the low number of seed observed in accession ASUN02 (298 seeds) is particularly valuable, given that excessive seed content negatively

affects the edible portion and marketability of papaya fruits.

The cluster dendrogram and heatmap analysis further emphasized the existence of five major phenotypically distinct groups within the studied accessions, reflecting considerable underlying genetic diversity. The formation of genetically distinct clusters is consistent with previous studies by Akinrotimi and Nwofia (2025) and Aikpokpodion (2012), who demonstrated similar clustering patterns in papaya germplasm based on fruit morphological traits. Such clustering provides a practical framework for selecting genetically divergent parental lines, a strategy known to maximize heterosis and genetic gain in hybrid breeding programs (Akinrotimi and Nwofia, 2025).

Principal Component Analysis (PCA) showed that the first two components accounted for 62.4 % of the total phenotypic variation, with fruit size and mass-related traits emerging as major contributors to diversity. These observations were in agreement with Alara *et al.*, (2020) and Aikpokpodion (2012), who emphasized the importance of fruit size parameters in determining genetic diversity in papaya. The identification of accessions such as IMNO01, RSPH04, and ASUN03 in favorable PCA quadrants suggested their utility as elite genetic resources for breeding programs targeting enhanced fruit yield, pulp quality, and nutritional value.

The strong positive correlation between fruit length and fruit circumference aligned with the findings of Olarewaju *et al.* (2023), who reported similar relationships in Nigerian papaya accessions. This suggested that selection for increased fruit length is likely to simultaneously enhanced fruit girth, contributing to overall fruit size improvement. However, the weak or negative correlations observed between fruit weight, pulp diameter, and other fruit dimensions implied the presence of complex genetic interactions, warranting cautious trait integration during breeding to avoid undesirable trade-offs.

The presence of accessions exhibiting both large fruit sizes and lower seed counts (e.g., ASUN03, ASUN02) is particularly valuable for cultivar development, given the global trend towards seedless or low-seeded fruit varieties, which enhance edible yield and market appeal (Singh *et al.*, 2020). Collectively, the genetic diversity detected in this study had provided a robust foundation for pawpaw breeding programs in Nigeria. The identification of superior genotypes with desirable pomological traits holds promise for addressing the low national yield average of 8.3 t/ha reported by FAOSTAT (2023) and improving Nigeria's competitiveness as the third-largest global producer of papaya.

Conclusion

The present study exhibited phenotypic variability among 60 papaya (*Carica papaya* L.) accessions collected from southeastern and south-southern Nigeria based on key fruit traits including length, pulp diameter, circumference, fruit weight, and number of seeds suggesting the presence of considerable genetic diversity within local papaya germplasm. This diversity is crucial genetic improvement, offers opportunities selection and development of cultivars with enhanced fruit size, pulp content, and

reduced seed numbers, which are all traits that corresponds with market demands and consumer preferences. Accessions such as IMNO01 (largest fruit weight), RSPH04 (longest fruit size), IMOK02 (greatest pulp diameter), and ASUN02 (lowest seed count) emerged as promising genetic materials for targeted breeding efforts. . Predominant traits, such as elliptic and reniform shapes, green skin, and deep yellow to orange flesh, alongside less common traits like reddish-orange flesh, offer significant potential for breeding programs aimed at enhancing nutritional quality, market appeal, and yield. The strong positive correlation between fruit length and circumference suggests simultaneous improvement of these traits is feasible, while observed genetic divergence among accessions provided a solid foundation for selecting genetically diverse parental lines to exploit heterosis. The findings aligned with global breeding priorities for papaya improvement, which emphasized fruit yield, quality enhancement, and meeting consumer expectations for larger, fleshier, and low-seeded fruits. These findings are expected to provide baseline data that will support germplasm conservation, facilitate the selection of desirable genotypes, and contribute to ongoing efforts in breeding high-performing pawpaw cultivars adapted to the Nigerian environment.

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