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Variability Studies on Qualitative and Quantitative Traits in *Solanum lycopersicum* (Tomato)

Ajie, V. I[1*] and Olawuyi, O. J[2]
[1]Department of Plant Science and Biotechnology, Rivers State University, Npkolu-Orowuroko, Port-Harcourt, Rivers State, Nigeria.
[2]Genetics and Molecular Biology Unit, Department of Botany, University of Ibadan, Oyo State, Nigeria.

*Corresponding author. Ajie, V. I
Department of Plant Science and Biotechnology, Rivers State University, Npkolu-Orowuroko, Port-Harcourt, Rivers State, Nigeria.
E-mail address: victorajie3@gmail.com
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Abstract
Tomato (Solanum lycopersicum L.) is one of the most economically important vegetable crops worldwide, with a wide array of genetic diversity in morphological traits. Understanding this diversity is crucial for breeding programs aimed at developing improved varieties with desirable traits. The present investigation was undertaken to assess genetic variability using morphological markers among 40 tomato accessions, comprising 30 accessions from the National Center for Genetic Resources and Biotechnology, five from local markets in Ibadan, three varieties from Benue and Oyo States, and two varieties obtained from seed companies. The experiment was conducted using a completely randomized design (CRD) with three replicates. Significant variations ($p < 0.05$) were recorded for several traits, including primary leaf length and width, number of leaves, plant height days to first fruiting, number of inflorescences, and the number of leaves under the first inflorescence. In the principal component analysis, the first three components collectively explained 74.80% of the variation observed among the 40 accessions. Cluster analysis grouped the accessions into two major clusters: cluster I, which contained two sub-clusters comprising 10 accessions, and cluster II, which contained four sub-clusters comprising 30 accessions. This study identified four accessions, namely NGB/00717, NGB/00714, NGB/00696, and NGB/00735b, that exhibited superiority in important vegetative and yield traits. A sufficient level of diversity for future tomato breeding programs was identified.

Introduction
1.1 Background of Study
Systematic genetic diversity analysis is of paramount importance for any effective plant breeding programme. Genetic diversity is a dynamic property of germplasm and its estimation may be based on morphological evaluation, biochemical, or molecular assessment (Bhandari *et al*., 2017). Among the three approaches, morphological characterization offers less costly and readily assessable measurement making them attractive to breeders for a genetic improvement program. The International Plant Genetic Resources Institute (IPGRI, 1996) prepared a standard format for the characterization and preliminary evaluation of data on tomato. The morphological descriptors provide information underlying the conclusions on the genetic variability of tomato accessions.

Tomato (*Solanum lycopersicum* Linn., 2n = 2x = 24) is an annual, self-pollinating crop and ranks among the most significant fruit vegetables globally. In Africa, Nigeria is the second-largest producer, following Egypt, with an annual demand estimated at 2–3 million tonnes (Nassarawa and Sulaiman, 2019; GrowAfrica, 2019). In different countries, genetic diversity studies of tomato have been conducted using morphological traits such as plant height, growth habit, number of branches, days to first flowering, days to first fruit set, fruit weight, corolla colour, hypocotyl colour, number of fruits per plant, etc. (Kaur *et al.,* 2018; Jin *et al*., 2019; Gbadamosi *et al*., 2020; Athinodorou *et al*., 2021). Gbadamosi *et al* (2020) highlighted increased erosion among genetic resources as a major challenge to tomato productivity in Nigeria. Information on genetic variation and relationships among breeding materials is basis for selection as well as for planning crop breeding program (Gopikrishnan *et al*., 2021).
To assess the genetic diversity of crop plants based on morphological traits, basic statistical parameters (Tripathi *et al*., 2022) and multivariate analysis (Azevedo *et al*., 2022) have been used. Principal component analysis (PCA) and cluster analysis are methods used in multivariate analysis. Principal component analysis (PCA) analysis is a multivariate statistical analysis for examining and simplifying complex and large datasets. This analysis transforms the larger number of correlated variables into smaller ones (Ahmed *et al*., 2019). Through the principal component analysis, components or set of components that contribute significant amounts of variation in a population are revealed. In order to determine genetic variation genotype classifications and genetic distance among them the cluster analysis is done. Cluster analysis identifies and classifies objects individuals or variables on the basis of the similarity of the characteristics they possess. It is vital for crop conservation and breeding, as well as understanding crop evolution.
The continuous selection for a limited number of preferred traits has been linked to genetic erosion, which threatens the potential for future advancements in tomato improvement (Gbadamosi *et al*., 2020). Understanding the variability in both qualitative and quantitative traits of *Solanum lycopersicum* is crucial for identifying superior genotypes that can enhance breeding programs and improve crop productivity. This study was therefore aimed at examining the diversity among 40 tomato accessions collected from different sources based on morphological traits using basic statistical parameters and multivariate analyses (principal components and cluster analysis). This is with a view to clarify the existing genetic resources and provide valuable insights into trait diversity, which is essential for developing tomato varieties with better adaptability, yield, and quality characteristics.

MATERIALS AND METHODS

Planting Materials

A total of forty tomato accessions were gathered from two states (Benue State and Oyo State), a seed company and the National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan. (Table 1).

Experimental Design and Morphological Characters

The study was conducted and assessed in field conditions, employing a completely randomized design with three replications. Eighteen (18) morphological characters, comprising of five qualitative characters and thirteen quantitative characters, were selected from the International Plant Genetic Resources Institute Descriptors for Tomato (IPGRI, 1996) and evaluated. (Table 2)

Experimental site and Planting Method

The field experiment took place at the nursery farm, Department of Botany, University of Ibadan, Ibadan, Nigeria. Fifteen seeds of each tomato accession were raised in perforated polythene bags filled with 5kg top loam soil. After four weeks, each accession was transplanted to a fresh polythene bag containing 5kg top loam soil. Plant spacing was set at 60 cm × 60 cm.

Statistical Analysis

The data collected from tomato accessions were analysed using the SAS ver.9.3 software program generate Analysis of Variance (ANOVA). Mean differences were analyzed and distinguished using Duncan's Multiple Range Test (DMRT) at a 95% confidence level ($p < 0.05$). Associations between traits were determined through Pearson's Correlation Coefficient and Principal Component Analysis (PCA).

Table 1: List of tomato accessions, their sources and genetic code used for this study

S/N	Accession Name	Source	Genotypic Code
1	NGB/00718b	NACGRAB	G1
2	NGB/00714	NACGRAB	G2
3	NGB/05081	NACGRAB	G3
4	NGB/00717	NACGRAB	G4
5	NGB/05075	NACGRAB	G5
6	NGB/00752	NACGRAB	G6
7	NGB/00740	NACGRAB	G7
8	NGB/00713	NACGRAB	G8
9	NGB/00697	NACGRAB	G9
10	NGB/05080	NACGRAB	G10
11	NGB/00724	NACGRAB	G11
12	NGB/00735b	NACGRAB	G12
13	NGB/00729	NACGRAB	G13
14	NGB/00696	NACGRAB	G14
15	NGB/00754	NACGRAB	G15
16	NGB/00727	NACGRAB	G16
17	NGB/00710	NACGRAB	G17
18	NGB/00711	NACGRAB	G18
19	NGB/00721	NACGRAB	G19
20	NGB/00743	NACGRAB	G20
21	NGB/00735a	NACGRAB	G21
22	NGB/00739	NACGRAB	G22
23	NGB/00737	NACGRAB	G23
24	NGB/00722	NACGRAB	G24
25	NGB/00746	NACGRAB	G25
26	NGB/00718a	NACGRAB	G26
27	NGB/02695	NACGRAB	G27
28	NGB/00725	NACGRAB	G28
29	NGB/00715	NACGRAB	G29
30	NGB/00759	NACGRAB	G30
31	Cashew	Local Variety, Ushongo LGA, Benue State	G31
32	Kerewa	Local Variety, Ibadan	G32
33	Hausa	Sango market, Ibadan	G33
34	Royal	Shasha Market, Ibadan	G34
35	Hausa	Challenge Market, Ibadan	G35
36	Hausa	Gbagi Market, Ibadan.	G36
37	Hausa	Dugbe Market, Ibadan	G37

38	Roli	Local Variety, Ushongo LGA, Benue State	G38
39	Roma	Commercial Variety	G39
40	UC82B	Commecial Variety	G40

Table 2: Quantitative and Qualitative Characters of Tomato Accessions

S/N	Quantitative Traits	Qualitative Traits
1	Primary leaf length	Hypocotyl colour
2	Primary leaf width	Corolla colour
3	Plant height	Foliage density
4	Number of branches	Stem pubescence
5	Number of days to flowering	Inflorescence Type
6	Number of leaves under first inflorescence	
7	Number of days to fruiting	
8	Number of inflorescences	
9	Number of flowers per inflorescence	
10	Number of fruits per inflorescence	
11	Internode length	
12	Fruit weight	
13	Number of leaves	

RESULTS

Quantitative Trait Analysis of Tomato Accessions

The accessions NGB/05080, NGB/00722, NGB/02695, and NGB/00718 exhibited low values for several traits, including the number of leaves, plant height, internode length, number of branches, and fruit set per inflorescence (Table 6). In contrast, high values for primary leaf length, plant height, and primary leaf width were observed in NGB/005081, NGB/005075, and NGB/00735a. NGB/00746 recorded the highest number of days to first fruit set (72.3), while NGB/00735b showed the lowest (59.5). The NGB/00696 accession recorded the highest mean values ($p < 0.05$) for several traits, including number of leaves (31), number of inflorescences (4), number of leaves under the first inflorescence (22.7), number of branches (3.2), and fruit set per inflorescence (4.6). In contrast, the NGB/00735b accession showed the highest fruit weight (76.1g), the shortest time to flowering (51 days), and the fewest days to first fruit set (59.5).

Quantitative Character Variance in Tomato Based on Mean Squares

Highly significant differences were noted for plant height, primary leaf length and width, and internode length (Table 5). Additionally, significant variations ($p < 0.01$) were observed in the number of inflorescences, number of leaves, and the number of leaves under the first inflorescence, as presented in Table 5.

Qualitative Traits Analysis of Tomato

Foliage density was categorized into three types: sparse, intermediate, and dense. Among the accessions, intermediate foliage density was the most common, occurring in 30 accessions (75%), followed by dense foliage density in 7 accessions (17.5%), and sparse foliage density in 3 accessions (7.5%). Two inflorescence types were identified: uniparous, found in thirty-one accessions, while the remaining accessions exhibited both uniparous and multiparous types (Table 3). For hypocotyl color, four types were observed among the forty tomato accessions:

green, purple, ¼ purple from the base, and ½ purple from the base. The purple color type was the most prevalent, occurring in 47.5% of the accessions, followed by seventeen accessions with green color, three accessions (7.5%) with ½ purple from the base, and one accession (2.5%) with ¼ purple from the base. Tomato descriptors (Lycopersicon spp.) by IPGRI (1996) outlined three corolla colors in tomatoes; white, yellow, or orange. As shown in Table 3, all the observed inflorescences in this study exhibited the yellow color type. Stem pubescence was observed in all the matured tomato stems.

Qualitative Character Variance in Tomato Based on Mean Squares

The number of days to flowering ranged from 51 days (NGB/00735b) to 72 days (NGB/00746), while the number of days to first fruit set varied between 59.5 days (NGB/00735b) and 82 days (NGB/00725. As shown in Table 4, significant variation ($p < 0.01$) was found in the number of days to first fruit set. Highly significant differences were also recorded for hypocotyl color, days to germination, and foliage density. However, no significant differences were observed in corolla color, inflorescence type, stem pubescence, and days to flowering (Table 4).

Descriptive Statistics for Traits

Descriptive statistics such as mean, standard deviation (SD), minimum and maximum values and coefficient of variation (CV%) are summarized in Table 7. Plant height (cm) ranged from 4.30 to 100.50 (mean: 43.71), primary leaf length (m) ranged from 8.00 to 42.00 (mean: 27.63), primary leaf width (m) ranged from 3.00 to 26.00 (Mean: 31.24), plant height (cm) ranged from 4.30 to 100.50 (mean: 43.71), number of leaves ranged from 2.00 to 43.00 (mean: 13.37), number of inflorescence ranged from 0.70 to 8.00 (Mean: 1.67). The mean values of yield traits such as the fruit set per inflorescence, number of days to first fruiting and fruit weight, respectively, were 1.77, 38.05 and 16.93. Maximum SD (21.00) corresponded to number of days to first fruiting and minimum SD (0.6) corresponded to number of days to germination and number of branches. The coefficient of variation (CV%) varied from 11.47% for number of days to germination to 86.96% for number of branches.

Correlation Analysis of Quantitative Traits

Days to germination exhibited negative correlations with most traits, except for the number of leaves, number of branches, number of inflorescences, flowers per inflorescence, and fruit set per inflorescence (Table 11). Plant height showed a significant positive relationship with internode length ($r = 0.8642$), while the number of leaves was significantly and positively correlated with both the number of inflorescences ($r = 0.8395$) and the number of leaves under the first inflorescence ($r = 0.8408$). Furthermore, a strong positive correlation ($r = 0.9206$) was found between the number of days to flowering and the number of flowers per inflorescence. A significant positive correlation was also observed between primary leaf length and primary leaf width ($r = 0.9619$) (Table 11). Significant positive correlations were found between days to first fruit set and fruit set per inflorescence, days to flowering and internode length, fruit weight and plant height, as well as between the number of leaves and the number of branches.

Principal Components and Cluster Analysis of Accessions

The PCA was conducted to determine traits that most strongly contribute to the total variation. PC1 accounted for 55.84 % of the total variation. As shown in Table 9, the first three principal components, with eigenvalues greater than 1, accounted for 74.80% of the total variation observed among the 40 genotypes. The morphological traits that loaded highly for PC1 were Number of leaves under first inflorescence, internode length and plant height. PC2 accounted for 12.13 % of the total variation and the traits with the greatest weight on this component were number of days to germination, primary leaf length and primary leaf width. PC3 contributed

6.83 % of the total variation and mainly related to number of days to flowering, hypocotyl colour, stem pubescence and number of branches (Table 8). Figure 1 signifies the biplot formation on basis of PC1 and PC2 values and it contains the relative contribution of both traits and genotypes. PC1 and PC2 loading were presented in the horizontal and vertical axes, respectively. In this study, all quantitative traits, but days to germination, were positively correlated. The days to germination negatively correlated with primary leaf length, primary leaf width, plant height, internode length, number of leaves under first inflorescence, fruit weight, days to flowering and days to first fruiting.

The dendrogram, which illustrates the relationships among the accessions, was produced by employing 18 morphological descriptors and utilizing the UPGMA clustering method, as depicted in Figure 2. The forty tomato accessions were grouped into two primary clusters, further divided into six sub-clusters. The first major cluster consisted of 10 accessions, which were further divided into two sub-clusters. The second major cluster, the largest, included 30 accessions and was split into four sub-clusters (Table 10). Among these sub-clusters, sub-cluster D had the highest number of accessions (11), followed by sub-cluster C with 10 accessions (Figure 2).

Table 3: Frequency distribution of 5 qualitative traits of tomato.

No	Plant Character	Character State	Percentage (%)
1	Hypocotyl Colour	Green	42.5
		1/4 purple from the base	2.5
		1/2 purple from the base	7.5
		Purple	47.5
2	Foliage Density	Sparse	7.5
		Intermediate	75
		Dense	17.5
3	Inflorescence Type	Generally uniparous	77.5
		Both	22.5
		Generally multiparous	0
4	Corolla Colour	White	0
		Yellow	100
		Orange	0
5	Stem Pubescence	Present	100
		Absent	0

Table 4: Summary of mean squares of qualitative traits of tomato

Qualitative traits	Mean Squares		
	Replicates (df=2)	Accessions (df=39)	Error (df=78)
Hypocotyl Colour	0.00	6.28^{***}	0.00
Inflorescence Type	1.01	1.09^{NS}	1.06
Corolla Colour	0.46	1.05^{NS}	0.79
Foliage Density	0.99	5.89^{**}	2.67
Stem Pubescence	0.03	0.17^{NS}	0.09

* = Significant at p<0.01, ** = highly significant at p<0.001, *** = highly significant at p<0.0001, ns = nonsignificant, df = Degree of freedom.

Table 5: Summary of mean squares of quantitative traits of tomato

Quantitative traits	Mean Squares		
	Replicates (df=2)	**Accessions (df=39)**	**Error (df=73)**
Days to Germination	0.00	2.84***	0.00
Primary leaf length	0.00	193.49***	0.00
Primary leaf width	0.00	73.21***	0.00
Plant Height	135.10	771.14**	338.56
Number of Leaves	7.18	76.73*	44.99
Number of Branches	0.00	0.01NS	0.01
Days to Flowering	502.96	1097.31NS	793.18
Number of leaves under 1st Inflorescence	1.45	7.57*	4.08
Number of Inflorescence	4.34	3.23*	2.27
Days to first fruit set	22.94	319.98*	224.30
Flowers per Inflorescence	4.52	5.37NS	4.31
Fruit set per inflorescence	0.03	0.27NS	0.25
Internode length	0.16	5.19***	1.86
Fruit Weight	1.10	3.40NS	3.55

* = Significant at p<0.01, ** = highly significant at p<0.001, *** = highly significant at p<0.0001, ns = nonsignificant, df = Degree of freedom.

Table 6: Quantitative Trait Analysis of Tomato Accessions
Means with the same letter in the same column are not significantly different at p≥0.05 according to Duncan Multiple Range Test (DMRT)

Accession Name	PLL(m)	PLW(m)	PH (cm)	NOL	NOB	DTF	LUFI	NOI	DTFF	FPI	FSPI	IL	FW (g)
NGB/00696	2.1^{t}	1.4^{l}	49.1^{ebdagcf}	31.0^{a}	3.2^{a}	56.3^{ba}	22.7^{a}	4.0^{a}	67.0^{a}	4.3^{ba}	4.6^{a}	5.3^{bac}	29.7^{ba}
NGB/00697	2.6^{o}	1.4^{l}	44.1^{ebdhagcf}	14.0^{bedc}	1.6^{ba}	70.5^{a}	14.5^{ba}	1.0^{bdac}	76.0^{a}	3.3^{ba}	1.6^{ba}	4.0^{ebdac}	22.3^{ba}
NGB/00710	2.5^{p}	1.5^{k}	43.5^{ebdhigcf}	12.0^{bedc}	1.9^{ba}	67.5^{ba}	12.0^{bac}	1.7^{bdac}	78.0^{a}	2.3^{ba}	1.6^{ba}	4.7^{bdac}	20.9^{ba}
NGB/00711	3.3^{h}	1.7^{i}	57.8^{ebdac}	17.0^{bc}	1.9^{ba}	61.3^{ba}	12.0^{bac}	2.0^{bdac}	69.7^{a}	4.3^{ba}	2.9^{ba}	5.7^{ba}	31.0^{ba}
NGB/00713	2.7^{n}	1.5^{k}	40.0^{ebdhigcf}	14.3^{bedc}	1.9^{ba}	68.0^{ba}	14.0^{ba}	1.3^{bdac}	77.0^{a}	3.0^{ba}	1.2^{ba}	5.3^{bac}	60.2^{ba}
NGB/00714	3.7^{e}	2.4^{c}	69.3^{bac}	22.0^{ba}	2.9^{a}	56.7^{ba}	14.7^{ba}	3.0^{bdac}	65.0^{a}	4.3^{ba}	4.6^{a}	5.0^{bac}	51.6^{ba}
NGB/00715	1.8^{v}	1.0^{o}	33.3^{edhigcf}	21.7^{ba}	2.4^{ba}	57.0^{ba}	12.5^{bac}	3.7^{ba}	66.0^{a}	3.7^{ba}	2.4^{ba}	3.7^{ebdacf}	11.5^{ba}
NGB/00717	3.8^{d}	2.3^{d}	65.6^{bdac}	16.7^{bdc}	1.9^{ba}	57.3^{ba}	13.3^{ba}	2.7^{bdac}	65.7^{a}	4.3^{ba}	2.9^{ba}	5.0^{bac}	46.2^{ba}
NGB/00718a	2.1^{t}	1.2^{m}	36.9^{ebdhigcf}	9.7^{bedc}	1.9^{ba}	63.0^{ba}	13.0^{ba}	0.7^{bdc}	71.0^{a}	2.3^{ba}	0.9^{ba}	2.0^{ebdacf}	14.2^{ba}
NGB/00718b	0.8^{y}	0.3^{q}	8.0^{hi}	2.0^{e}	1.0^{b}	0.0^{b}	0.0^{bc}	0.0^{d}	0.0^{b}	0.0^{b}	0.3^{b}	3.7^{edgf}	0.0^{b}
NGB/00721	2.5^{p}	1.6^{j}	46.5^{ebdhagcf}	15.7^{bedc}	1.6^{ba}	63.7^{ba}	14.3^{ba}	2.0^{bdac}	72.0^{a}	4.3^{ba}	0.7^{ba}	4.3^{bdac}	9.1^{ba}
NGB/00722	2.6^{o}	1.4^{l}	5.3^{i}	2.0^{e}	1.0^{b}	0.0^{b}	0.0^{bc}	0.0^{d}	0.0^{b}	0.0^{b}	0.3^{b}	0.0^{g}	0.0^{b}
NGB/00724	3.4^{g}	1.9^{h}	52.0^{ebdacf}	10.3^{bedc}	2.2^{ba}	57.0^{ba}	13.5^{ba}	1.3^{bdac}	65.5^{a}	2.3^{ba}	1.3^{ba}	5.3^{bac}	24.8^{ba}
NGB/00725	1.7^{w}	0.8^{p}	34.7^{edhigcf}	13.0^{bedc}	1.6^{ba}	71.3^{a}	11.0^{bac}	2.0^{bdac}	82.0^{a}	5.0^{a}	2.6^{ba}	5.0^{bac}	12.9^{ba}
NGB/00727	2.2^{s}	1.4^{l}	36.9^{ebdhigcf}	10.3^{bedc}	1.9^{ba}	65.0^{ba}	11.0^{bac}	1.0^{bdac}	74.5^{a}	3.0^{ba}	2.1^{ba}	4.3^{bdac}	19.1^{ba}
NGB/00729	3.1^{j}	2.0^{g}	34.6^{edhigcf}	9.3^{bedc}	1.9^{ba}	70.0^{a}	13.5^{ba}	1.3^{bdac}	76.5^{a}	2.0^{ba}	2.1^{ba}	4.0^{ebdac}	41.4^{ba}
NGB/00735a	4.1^{a}	2.6^{a}	65.8^{bdac}	12.3^{bedc}	1.9^{ba}	57.3^{ba}	11.7^{bac}	1.7^{bdac}	73.0^{a}	5.3^{a}	2.2^{ba}	5.0^{bac}	14.7^{ba}
NGB/00735b	2.8^{m}	1.7^{i}	66.0^{bdac}	19.3^{bac}	1.9^{ba}	51.0^{ba}	11.5^{bac}	3.7^{ba}	59.5^{a}	3.7^{ba}	2.6^{ba}	5.7^{ba}	76.1^{a}
NGB/00737	2.4^{q}	1.5^{k}	40.8^{ebdhigcf}	12.7^{bedc}	1.9^{ba}	65.5^{ba}	15.0^{ba}	3.0^{bdac}	74.0^{a}	3.7^{ba}	1.9^{ba}	3.7^{ebdacf}	22.6^{ba}
NGB/00739	1.6^{x}	1.1^{n}	31.9^{edhigcf}	15.0^{bedc}	1.6^{ba}	64.0^{ba}	14.0^{ba}	2.7^{bdac}	68.0^{a}	3.0^{ba}	2.4^{ba}	3.3^{ebdcf}	12.4^{ba}
NGB/00740	2.3^{r}	1.6^{j}	50.4^{ebdagcf}	14.0^{bedc}	1.9^{ba}	70.0^{a}	13.5^{ba}	1.0^{bdac}	77.0^{a}	2.7^{ba}	0.7^{ba}	4.7^{bdac}	10.2^{ba}
NGB/00743	2.7^{n}	1.5^{k}	44.3^{ebdhagcf}	14.3^{bedc}	1.9^{ba}	65.0^{ba}	17.0^{ba}	1.7^{bdac}	71.0^{a}	3.0^{ba}	0.9^{ba}	4.7^{bdac}	43.7^{ba}
NGB/00746	2.9^{l}	1.7^{i}	49.3^{ebdagcf}	14.3^{bedc}	1.6^{ba}	72.3^{a}	14.3^{ba}	1.0^{bdac}	76.5^{a}	4.7^{a}	2.1^{ba}	4.7^{bdac}	33.8^{ba}
NGB/00752	2.4^{q}	1.4^{l}	49.4^{ebdagcf}	16.7^{bdc}	1.9^{ba}	63.0^{ba}	12.0^{bac}	1.7^{bdac}	72.0^{a}	4.3^{ba}	2.5^{ba}	5.0^{bac}	11.3^{ba}
NGB/00754	1.9^{u}	1.2^{m}	27.8^{edhigf}	11.0^{bedc}	1.9^{ba}	63.0^{ba}	10.0^{bac}	1.0^{bdac}	72.0^{a}	1.3^{ba}	0.9^{ba}	2.7^{edcf}	36.0^{ba}
NGB/00759	1.9^{u}	1.0^{o}	24.8^{ehigf}	12.7^{bedc}	1.9^{ba}	55.0^{ba}	16.0^{ba}	0.7^{bdc}	68.0^{a}	1.3^{ba}	0.9^{ba}	2.0^{edgf}	25.9^{ba}
NGB/02695	1.9^{u}	1.2^{m}	12.7^{hig}	5.7^{edc}	1.0^{b}	0.0^{b}	0.0^{bc}	0.0^{d}	0.0^{b}	0.0^{b}	0.3^{b}	1.3^{egf}	0.0^{b}
NGB/05075	4.1^{a}	2.4^{c}	81.9^{a}	15.0^{bedc}	1.9^{ba}	60.0^{ba}	13.0^{ba}	2.3^{bdac}	66.3^{a}	4.0^{ba}	2.9^{ba}	6.3^{a}	33.3^{ba}
NGB/05080	3.4^{g}	2.1^{f}	15.2^{higf}	2.5^{ed}	1.0^{b}	0.0^{b}	0.0^{bc}	0.0^{d}	0.0^{b}	0.0^{b}	0.0^{b}	1.0^{gf}	0.0^{b}
NGB/05081	4.2^{a}	2.5^{b}	73.7^{ba}	18.0^{bc}	1.6^{ba}	58.0^{ba}	14.7^{ba}	3.3^{bac}	67.0^{a}	3.3^{ba}	2.9^{ba}	5.3^{bac}	30.1^{ba}

PLL = Primary Leaf Length, **PLW** = Primary Leaf Width, **PH** = Plant Height, **NOL** = Number of Leaves, **NOB** = Number of Branches, **DTF**= Number of days to flowering, **LUFI** = Number of leaves under first inflorescence, **NOI** = Number of Inflorescence, **DTFF**= Number of days to first fruit set, **FPI** = Flowers per Inflorescence, **FSPI** = Fruit set per Inflorescence, **IL** = Internode Length (3 = short, 5 = intermediate, 7 = long), and **FW** = Fruit Weight

Table 6 (Continued): Quantitative Trait Analysis of Tomato Accessions
Means with the same letter in the same column are not significantly different at p≥0.05 according to Duncan Multiple Range Test (DMRT)

Accession Name	PLL(m)	PLW(m)	PH (cm)	NOL	NOB	DTF	LUFI	NOI	DTFF	FPI	FSPI	IL	FW (g)
Cashew	4.1^{a}	2.5^{b}	63.5^{ebdac}	16.5^{bdc}	2.6^{ba}	57.5^{ba}	12.5^{bac}	3.5^{bac}	72.0^{a}	3.5^{ba}	1.0^{ba}	6.5^{a}	35.8^{ba}
Hausa (challenge)	3.2^{i}	1.7^{i}	51.7^{ebdagcf}	11.7^{bedc}	1.9^{ba}	68.0^{ba}	11.0^{bac}	2.0^{bdac}	75.0^{a}	4.3^{ba}	0.9^{ba}	5.0^{bac}	39.4^{ba}
Hausa (dugbe)	2.3^{r}	1.6^{j}	40.8^{ebdhigcf}	9.3^{bedc}	1.0^{b}	66.5^{ba}	11.0^{bac}	1.0^{bdac}	74.0^{a}	3.3^{ba}	1.2^{ba}	4.7^{bdac}	62.1^{ba}
Hausa (gbagi)	4.0^{c}	2.2^{e}	52.7^{ebdacf}	17.7^{bc}	2.2^{ba}	64.0^{ba}	12.5^{bac}	1.3^{bdac}	72.5^{a}	2.3^{ba}	2.6^{ba}	4.3^{bdac}	36.4^{ba}
Hausa (sango)	3.2^{i}	1.9^{h}	34.7^{edhigcf}	8.7^{bedc}	1.9^{ba}	63.0^{ba}	12.0^{bac}	0.7^{bdc}	71.0^{a}	1.7^{ba}	1.0^{ba}	4.0^{ebdac}	43.4^{ba}
Kerewa	3.0^{k}	1.7^{i}	29.8^{edhigf}	8.0^{bedc}	1.0^{b}	65.0^{ba}	14.0^{ba}	0.7^{dc}	74.0^{a}	1.0^{ba}	0.9^{ba}	2.0^{edgf}	19.0^{ba}
Roli	2.5^{p}	1.7^{i}	36.2^{ebdhigcf}	11.7^{bedc}	1.6^{ba}	68.0^{ba}	10.0^{bac}	1.7^{bdac}	73.0^{a}	4.0^{ba}	0.9^{ba}	4.0^{ebdac}	33.2^{ba}
Roma	2.8^{m}	1.6^{j}	41.8^{ebdhigcf}	11.3^{bedc}	1.9^{ba}	66.0^{ba}	9.7^{bac}	1.7^{bdac}	70.5^{a}	3.3^{ba}	2.6^{ba}	5.3^{bac}	31.4^{ba}
Royal (shasha)	3.6^{f}	2.0^{g}	37.8^{ebdhigcf}	12.3^{bedc}	2.2^{ba}	57.0^{ba}	11.5^{bac}	1.0^{bdac}	66.0^{a}	3.0^{ba}	0.9^{ba}	4.7^{bdac}	22.8^{ba}
UC82B	2.3^{r}	1.5^{k}	28.4^{edhigf}	9.0^{bedc}	1.6^{ba}	68.0^{ba}	17.0^{ba}	0.7^{bdc}	77.0^{a}	1.7^{ba}	0.9^{ba}	3.00^{ebdcf}	17.4^{ba}

PLL = Primary Leaf Length, **PLW** = Primary Leaf Width, **PH** = Plant Height, **NOL** = Number of Leaves, **NOB** = Number of Branches, **DTF**= Number of days to flowering, **LUFI** = Number of leaves under first inflorescence, **NOI** = Number of Inflorescence, **DTFF**= Number of days to first fruit set, **FPI** = Flowers per Inflorescence, **FSPI** = Fruit set per Inflorescence, **IL** = Internode Length (3 = short, 5 = intermediate, 7 = long), and **FW** = Fruit Weight

Table 7: Basic statistics of quantitative traits of tomato

Variable	Mean	SD	Minimum	Maximum	CV(%)
PLL	27.63	4.6	8.00	42.00	16.67
PLW	16.43	2.9	3.00	26.00	17.65
PH	43.71	13.0	4.30	100.50	29.74
NOL	13.37	4.4	2.00	43.00	32.91
NOB	0.69	0.6	1.00	4.00	86.96
NOI	1.67	1.0	0.70	8.00	59.89
IL	4.23	1.0	1.00	8.00	23.64
LUFI	9.17	3.9	9.70	31.00	42.53
FPI	3.02	1.3	1.00	7.00	43.05
FSPI	1.77	1.1	0.30	5.00	62.15
FW	16.93	12.8	9.10	128.90	75.61
DTF	44.11	17.6	51.00	76.00	39.90
DTFF	38.05	21.0	59.50	83.00	55.19
DTG	5.23	0.6	3.00	10.00	11.47

PLL = Primary Leaf Length, **PLW** = Primary Leaf Width, **PH** = Plant Height, **NOL** = Number of Leaves, **NOB** = Number of Branches, **DTF**= Number of days to flowering, **LUFI** = Number of leaves under first inflorescence, **NOI** = Number of Inflorescence, **DTFF**= Number of days to first fruit set, **FPI** = Flowers per Inflorescence, **FSPI** = Fruit set per Inflorescence, **IL** = Internode Length and **FW** = Fruit Weight

Table 8: Principal Component Axes of Quantitative and Qualitative Characters in Tomato Accessions

Characters	PC1	PC2	PC3
DTG	-0.0091	**0.4360**	-0.1192
HC	-0.0556	0.2193	**0.3624**
PLL	0.1549	**-0.4669**	-0.2312
PLW	0.1613	**-0.4656**	-0.2175
PH	0.2697	-0.1757	-0.0366
NOL	0.2567	0.2355	-0.1483
NOB	0.1961	0.2257	**-0.3230**
DTF	0.2514	0.0038	**0.3482**
LUFI	**0.2720**	0.0655	0.0950
NOI	0.2475	0.2101	-0.1970
IT	0.2007	-0.0569	0.0364
DTFF	0.2302	0.0356	-0.0851
CC	**0.2756**	0.0162	0.2278
FPI	0.2588	0.0745	**0.2711**
FSPI	0.2280	0.1752	-0.1915
SP	0.2113	-0.1696	**0.3279**
FD	0.2330	-0.0734	0.2222
IL	0.2621	-0.0441	0.1558
FW	0.2229	-0.0938	**-0.2883**

CC = Corolla Colour, **DTF** = Number of days to flowering, **DTG** = Days to Germination, **DTFF** = Number of days to first fruit set, **FD** = Foliage Density, **FPI** = Flowers per Inflorescence, **FSPI** = Fruit set per Inflorescence, **FW** = Fruit Weight, **HC** = Hypocotyl Colour, **IL** = Internode Length, **IT** = Inflorescence Type, **LUFI** = Number of leaves under first inflorescence, **NOB** = Number of Branches, **NOI** = Number of Inflorescence, **NOL** = Number of Leaves, **PH** = Plant Height, **PLL** = Primary Leaf Length, **PLW** = Primary Leaf Width and **SP** = Stem Pubescence

Table 9: Eigen vectors and Eigen values of 3 principal components for Quantitative and Qualitative characters of 40 Tomato genotypes

Statistics	PC1	PC2	PC3
Proportion of Variance	**0.5584**	**0.1213**	**0.0683**
Cumulative Proportion	**0.5584**	**0.6797**	**0.7480**
Eigen Values	**11.1680**	**2.4259**	**1.3668**

Table 10: Grouping of 40 tomato accessions based on morphological traits through cluster analysis

Cluster	Sub-clusters	Total Entries	Genotypes
I	E	7	NGB/05080, NGB/00754, NGB/00759, Kerewa, NGB/00718a, Hausa (Sango), UC82B
	F	3	NGB/00718b, NGB/00722, NGB/02695
II	A	2	NGB/00696, NGB/00715
	B	7	NGB/00735b, NGB/00711, NGB/00714, NGB/00717, NGB/05081, NGB/05075, NGB/00735a
	C	10	NGB/00729, NGB/00727, NGB/00697, NGB/00743, NGB/00737, NGB/00746, Hausa (Challenge), Cashew Royal, Hausa (Gbagi)
	D	11	NGB/00724, NGB/00710, NGB/00721, NGB/00740, Hausa (Dugbe), Roli, NGB/00713, Roma, NGB/00752 NGB/00739, NGB/00725

Table 11: Correlation Coefficients among Quantitative Characters in *Solanum lycopersicum*.

	PLL	PLW	PH	NOL	NOB	NOI	IL	LUFI	FPI	FSPI	FW	DTF	DTFF	DTG
PLL	-													
PLW	0.96**	-												
PH	0.68**	0.69**	-											
NOL	0.20	0.23	0.67**	-										
NOB	0.26	0.27	0.48	0.79**	-									
NOI	0.24	0.29	0.67**	0.84**	0.69**	-								
IL	0.46	0.45	0.86**	0.66**	0.52*	0.65**	-							
LUFI	0.35	0.38	0.76**	0.84**	0.62**	0.75**	0.78**	-						
FPI	0.30	0.31	0.75**	0.70**	0.46	0.69**	0.81**	0.85**	-					
FSPI	0.21	0.23	0.57*	0.74**	0.57*	0.72**	0.57*	0.63**	0.57*	-				
FW	0.51*	0.53*	0.75**	0.61**	0.46	0.62**	0.62**	0.57*	0.51*	0.71**	-			
DTF	0.35	0.36	0.72**	0.62**	0.41	0.59*	0.82**	0.86**	0.92**	0.51*	0.46	-		
DTFF	0.36	0.37	0.69**	0.62**	0.49	0.64**	0.61**	0.65**	0.63**	0.83**	0.57*	0.59*	-	
DTG	-0.32	-0.38	-0.16	0.16	0.21	0.26	-0.07	-0.07	0.07	0.09	-0.12	-0.02	-0.08	-

** = significant at $p < 0.01$; * = significant at $p < 0.05$

PLL= Primary Leaf Length, **PLW**= Primary Leaf Width, **PH**= Plant Height, **NOL**= Number of Leaves, **NOB**= Number of Branches, **NOI**= Number of Inflorescence, **IL**= Internode Length, **LUFI**= Leaves under First Inflorescence, **FPI**= Flowers per Inflorescence, **FSPI**= Fruit set per Inflorescence, **FW**= Fruit Weight, **DTF**= Days to Flowering, **DTFF**= Days to First Fruit Set, **DTG**= Days to Germination.

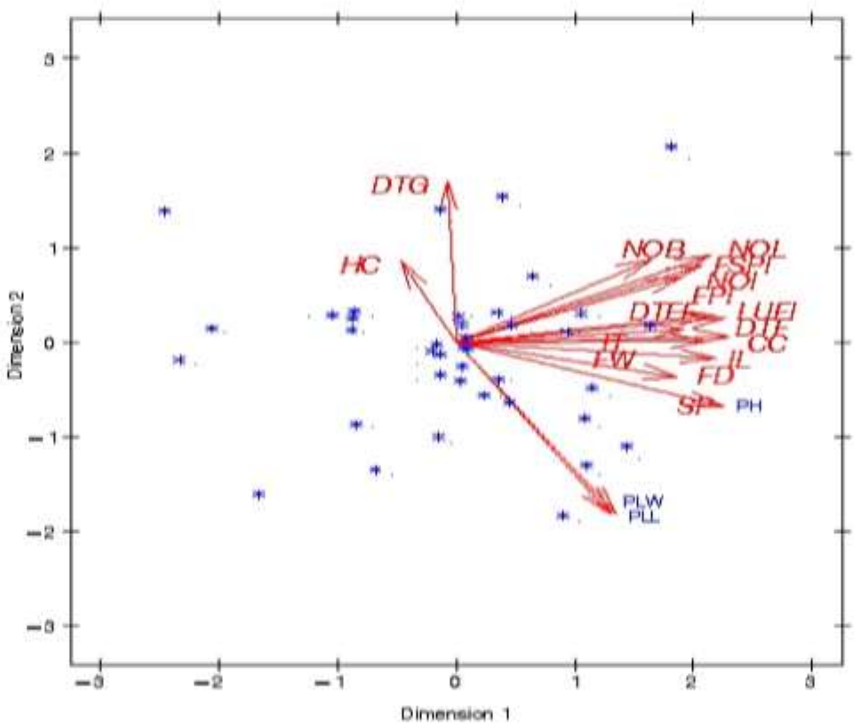

Figure 1: Scatter plot of the first (PC1) and second (PC2) principal components showing variation for quantitative and qualitative traits among 40 Tomato accessions.

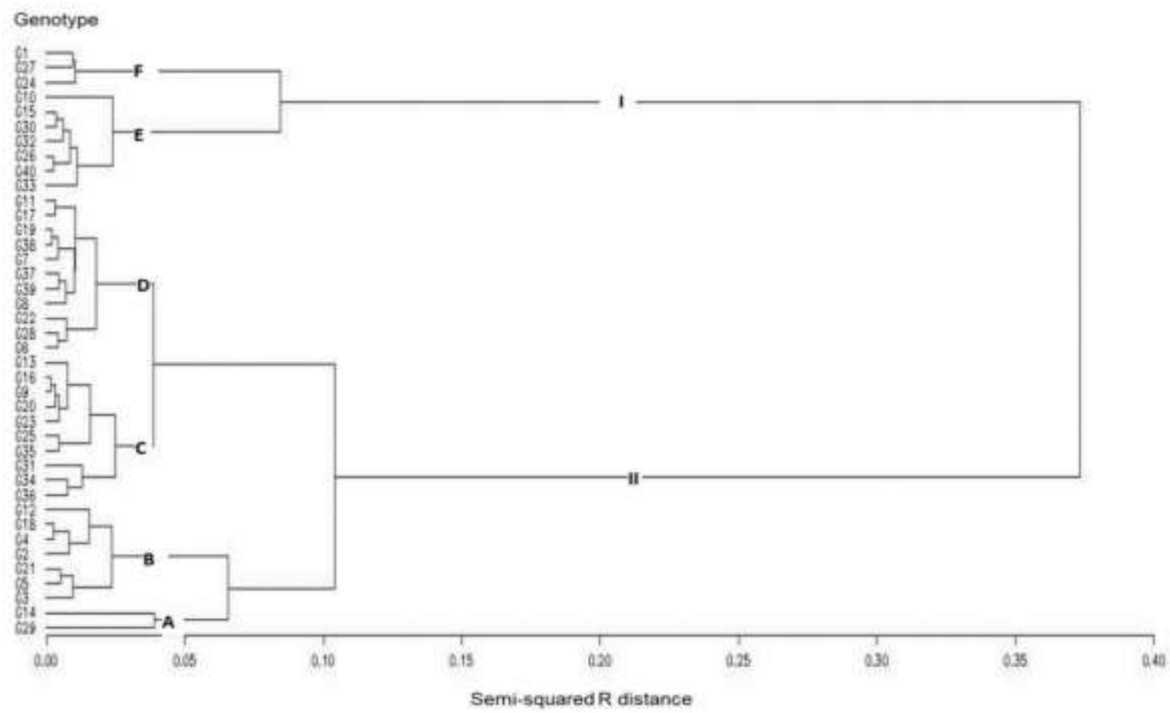

Figure 2: Dendrogram Generated Based on Quantitative and Qualitative Characters of *Solanum lycopersicum* Using UPGMA

DISCUSSION

Tomato genotypes could be differentiated based on their morphological traits. Kaya et al. (2022) identified leaf variation as a key factor for distinguishing tomato genotypes, a finding consistent with the present study, which observed significant variation in plant leaf length, leaf width, number of leaves, and leaves under the first inflorescence. Selecting for these traits could improve photosynthetic capacity, promote better nutrient uptake, and enhance overall plant health, leading to increased growth and higher yields. The tomato genotypes grown exhibited no significant differences in days to flowering, but there was variation in the days to fruit set. Earliness in flowering and fruiting is desirable in plant selection because it leads to faster crop turnover, allows for earlier harvesting, and can increase the overall yield potential, especially in regions where market demand for early produce is high. The results of this study differ from those of Gbadamosi et al. (2020), who observed significant variations in days to flowering, days to first fruit, and fruit weight. The variation in the duration between flowering and fruiting might be attributed to genetic factors, environmental conditions, and differences in plant developmental processes (Mujica and Jacobsen, 2003). The non-significant variation in some yield-related traits in the study may be due to genetic homogeneity, environmental consistency, or the limited range of traits assessed within the genotypes.

Among qualitative traits, significant variation was found for hypocotyl colour and foliage density but a narrow diversity was recorded corolla colour, stem pubescence and inflorescence type. The variation observed among the tomato phenotypes can be attributed to genetic diversity, environmental factors, and the influence of specific traits on growth and development. Foliage density is an important vegetative character as it influences photosynthesis, water retention, and protection against environmental stressors, contributing to overall plant health and productivity. The intermediate foliage type was the most frequent, occurring in 75% of the genotypes, followed by dense (17.5%) and sparse (7.5%) types, respectively. A similar dominance of intermediate foliage density was noted by Williams and Yesudhas (2023), who reported a frequency of 76%. The preponderance of intermediate foliage density in tomato plants may be due to its optimal balance for photosynthesis, water retention, and overall growth, offering better adaptability to various environmental conditions (Bhattarai *et al*., 2018).

The study identified two inflorescence types: the uniparous type, found in thirty-one accessions, and both uniparous and multiparous types in the remaining accessions. This was in agreement with Farinon *et al*., (2022), where two inflorescence types were found. Variations in flower complexity may be related to domestication and selection processes. Corolla color is used in plants as an important characteristic for identification, classification, and attracting pollinators. Variation in corolla color was absent as all accessions showed the yellow corolla color. The lack of variation in corolla color among the tomato phenotypes may be due to genetic uniformity or the predominance of a single-color trait within the studied genotypes. Similar findings were reported by Kathimba et al. (2021) in their study of ten tomato genotypes.

Hypocotyl color serves as a distinctive marker for differentiating tomato cultivars during the seedling stage. Nineteen accessions exhibited purple hypocotyls, seventeen were green, three had ½ purple from the base, and one showed ¼ purple from the base. The finding in the present study is similar to that of Williams and Yesudhas (2023) where one hundred and four genotypes of tomato were investigated for the genetic diversity of seedling traits. This pattern of hypocotyl color variation suggests that genetic factors influencing this trait are likely governed by distinct alleles that express in a limited range of phenotypic combinations. This trend is also in agreement with IPGRI descriptors for tomato that gives similar variations of the seedling stem color being of the four types for tomato varieties (IPGRI, 1996). In this study, all tomato genotypes displayed stem pubescence. Similar observations were reported by Salma et al. (2019) in their research on twenty-five tomato genotypes. Stem pubescence in plants serves various functions, including protection against herbivores, reduction of water loss, and enhanced tolerance to environmental stress by reflecting sunlight.

4.1 Correlation Analysis

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for yield improvement (Basfore *et al*., 2020). An understanding of the magnitude and interrelationship of traits, both among themselves and with target yield and quality, is crucial for improving selection efficiency through the combination of characters (Ahmad et al., 2013). The correlation analysis indicates that most traits were positively related, which aligns with the findings of Ajayi et al. (2022). The number of branches and plant height had positive correlations with all the yield related characters. This strong positive correlation suggests that traits such as the number of branches and plant height play a significant role in enhancing yield-related characters, likely because both contribute to greater photosynthetic capacity and resource allocation in the plant. An increase in the number of branches can provide more sites for flower and fruit development, while taller plants may better access light and promote vigorous growth. This is similar to findings of Sharma *et al*. (2021) and Panchbhai (2023). Furthermore, earliness traits were positively correlated with each other, a finding consistent with Gbadamosi et al. (2020). These traits also exhibited a positive correlation with yield-related traits, suggesting that selecting for earliness could ultimately enhance fruit yield. Significant correlation between the number of leaves under the first inflorescence and yield traits suggests that genotypes with a higher number of leaves at the first inflorescence are likely to produce better fruit yields.

4.2 Principal Component Analysis

The Principal Component Analysis (PCA) enables the transformation of a group of mutually associated traits (variables) into a new set of characteristics known as principle components, which are not correlated (Sinha *et al*., 2021). All traits, except for days to germination, positively contributed to PC1, while in PC2, all traits except fruit weight, internode length, and primary leaf length were positive contributors. Traits with high positive and negative loadings in PCA are crucial for tomato improvement because they significantly influence key characteristics, allowing breeders to select genotypes with optimal combinations of desirable and manageable traits for better yield and quality (Mellidou *et al*., 2020; Kayak *et al*., 2022). It has been stated that PCA can be used effectively when the first two components explain more than 25% of the variation in the studies (Seymen *et al*., 2019). In this study, the first principal component (PC1) accounted for 51.84% of the total variation among the ten traits, consistent with Azeez et al. (2020). The second and third components (PC2 and PC3) contributed 12.13% and 6.83%, respectively, with the first three components together explaining over 70% of the total variation, similar to the findings of Olawuyi (2017).

4.3 Cluster Analysis

Cluster analysis is an efficient tool for defining clustering patterns and helps establish relationships between genetic divergence (Shoba *et al*., 2019). Accessions that are genetically distinct could be valuable for breeding purposes, while those within the same cluster may belong to a single genetic pool. The cluster analysis resulted in the classification of the accessions into two primary clusters. The clustering of accessions from different origins into different clusters suggests genetic diversity and adaptation to specific environments may be influencing the grouping, which could provide valuable insights for breeding programs targeting diverse traits such as yield, or environmental adaptability. The lack of a significant relationship between the clustering arrangement and the spatial origin of the materials aligns with the findings of Hussain et al. (2018), who observed similar results in their study of 40 tomato accessions in Pakistan. As indicated by the findings, clustering emerges as a valuable tool facilitating the categorization of germplasm, thereby providing a dependable foundation for the selection of material in forthcoming breeding initiatives.

This study demonstrated significant genetic diversity among the evaluated tomato accessions, with notable variation observed across most morphological traits. The results highlight the utility of morphological markers as effective tools for assessing genetic diversity in tomatoes. Four accessions emerged as outstanding due to their superior performance in key yield traits. These accessions show strong potential for incorporation into future tomato breeding programs in Nigeria, offering opportunities to enhance yield and fruit quality. However, to further refine these findings and identify even more promising genotypes, additional research involving a broader set of accessions from diverse geographical regions is recommended. This could lead to the discovery of new genetic resources with enhanced traits suitable for optimizing tomato production in varied environmental conditions.

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