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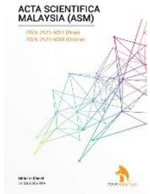

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RESEARCH ARTICLE

EVALUATION OF TOMATO GERMPLASMS (*SOLANUM LYCOPERSICUM* L.) FOR GENETIC DIVERSITY USING MORPHO-AGRONOMIC TRAITS AND FRUIT LYCOPENE CONTENT

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ABSTRACT

Tomato germplasm consisting of eighteen accessions and eight landraces were evaluated for morpho-agronomic traits and fruit-lycopene content to assess genetic diversity for fruit yield and quality improvement. Results obtained showed significant variability for the characters studied ($p<0.05$). The range of number of fruits per plant was 1.90-33.30 with the highest in L00169, while lycopene content was 2.562-13.312 µg with the highest in ABE. Positive and significant ($p<0.01$) correlations were recorded for number of fruits at 75 days (NOF) versus number of fruits per plant (FPP) ($r = 0.916$) while negative correlation was obtained for weight of fruit (WGH) versus number of fruits per plant (FPP) (-0.499). High heritability with high genetic gain was estimated for leaf area (LEA) and lycopene content (LCP). The first three principal components accounted for 63.63% of the observed variation. The 24 accession/landraces were grouped into three (Clusters I, II, and III) based on the dendrogram's clustering structure. Cluster III had the greatest intra-cluster distance while Clusters III and I had the most inter-cluster distance. In conclusion, these results can be utilized to choose accessions that will serve as the starting point for breeding to improve tomato lycopene content and fruit yield.

KEYWORDS

Clusters; Dendrogram; Heritability; Variability; Genotype

1. Introduction

Tomato (*Solanum lycopersicum L.*) is a member of the Solanaceae family, class Dicotyledonae, division Spermatophyta and subdivision Angiospermae. Although technically a vegetable in the eyes of the trade, tomatoes are a luscious berry fruit of the nightshade family (Alam et al., 2007; Laskar et al., 2016). Tomato is a significant vegetable crop that can be cultivated in greenhouses or open fields and due to its health advantages, it is valued in human nutrition. Solanaceous vegetables include more than 3000 different species comprising of various cultivated and wild cousins believed to have originated in Peru (South America) and first domesticated in Mexico (Sharma, et al., 2019). Tomato crop is widely cultivated throughout the world's tropical and subtropical regions (Fentik, 2017).

Due to strong market demand and its position as industry leader, tomato breeding firms are growing rapidly, necessitating the need for on-going creation of superior cultivars with added value through creative commercial tomato breeding programs (Bai and Lindhout, 2007). Being a self-pollinating crop, hybridization within the species or in crosses with wild relatives for gene introgression can be accomplished with ease under the right circumstances (Passam et al., 2007). Approximately 186.8 million metric tonnes of tomatoes were produced worldwide in 2020 on 5.05 million hectares of land, yielding 37.1 metric tonnes per hectare on average (EC, 2021). According to this report, China produced more than any other country, followed by India and Turkey. Nigeria with a total production of roughly 3.69 million metric tonnes on 844.4 thousand hectares and an average yield of 4.4 metric tonnes per hectare is seen to be relatively low and came far behind at position eleven. Lack of improved tomato varieties that are resistant to pests, illnesses, and physiological problems have been identified as the main obstacles to tomato production in Nigeria (Abdul et al., 2020).

Because of the health advantages associated with its nutritional components, mostly consisting of lycopene and beta-carotene as well as other nutrients like fibre, vitamin C, and phenolics, tomatoes are regarded as protective foods. Various studies (Bhowmik et al., 2012; Kearney et al., 2005; Collins et al., 2022), have reported lycopene and some phenolics to have anti-inflammatory, anti-cancer, and anti-angiogenic properties in addition to antioxidant activity. They have also been implicated as neuro-protective agents. Abiotic stress tolerance, high sugar content, and pest and disease resistance are among the desirable features that have been the focus of breeding efforts to increase fruit yield and quality (Prins, 2013; Lucatti et al., 2013). Pedigree methods, hybridization, mass selection and backcrossing are just a few of the traditional techniques used in tomato breeding. However, the development of molecular biology and bioinformatics has revolutionized breeding strategy by increasing the efficacy of traditional breeding programs (Caliman et al., 2008; Iqbal et al., 2019).

The demand for tomatoes is rising globally, thus it is clear that improving this crop is a crucial task to perform to lessen or eliminate production constraints (Fentik, 2017; Sharma, et al., 2019). In comparison with other major crops, tomato breeding sector has not received the necessary attention in Nigeria, and it appears there are significant genetic variations of key qualities that could be investigated for use in improvement programs. The need to discover and choose parent plant materials to be utilized as baseline parents for improving fruit yield and quality, prompted

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this study aimed to examine genetic diversity in 24 tomato germplasm using morpho-agronomic traits and fruit's lycopene contents.

2. Materials and Methods

In this study, *Solanum Lycopersicum* (tomato) seeds from 24 different germplasms were employed. They included seeds of five landraces gathered from local farmers in Ogbomoso, and one from Oke Ogun, while the seeds of other eighteen (18) accessions were collected from the National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Oyo State, Nigeria. The study was carried out on the research plots at the Botanical Gardens of Ladoke Akintola University of Technology, Ogbomoso, Nigeria (Table 1).

Seed viability test and germination were first performed, followed by raising of the seedlings of the twenty-four accessions on nursery beds. The seedlings after twenty-one days were transplanted (one plant per bag) into two hundred and forty (240) planting bags (punctured at the base) already filled with loamy soil. The bags were arranged in a 50 by 60 cm within and between row distances, respectively. Each of the accessions was represented in Ten bags arranged using a Complete Randomized Design (CRD) and the plants received two regimes of watering every other day. The plants were assessed for morpho-agronomic and biochemical features. They were scored for morphological characteristics such as; flower colour (COC), type of fruit (TOP), fruit shape (SOF) and fruit colour (COF) and evaluated for vegetative parameters and fruits lycopene content (Table 2)

Table 1: Identity of accessions and landraces of twenty-four tomatoes germplasm used in the study and place collection

S/N	ACCESSIONS	SOURCE
1	NGB01254	NACGRAB
2	NHGB/09/113	NACGRAB
3	L00169	NACGRAB
4	NG/AA/SEP/09/042	NACGRAB
5	NGB01410	NACGRAB
6	NG/MR/JAN/10/001	NACGRAB
7	NG/AA/SEP/09/045	NACGRAB
8	NG/SA/01/10/002	NACGRAB
9	NG/AA/SEP/09/037	NACGRAB
10	NGB01357	NACGRAB
11	NG/MR/MAY/09/006	NACGRAB
12	NG/AA/SEP/09/040	NACGRAB
13	NG/AA/SEP/09/050	NACGRAB
14	NHGB/09/120	NACGRAB
15	NG/AA/SEP/09/043	NACGRAB
16	NG/AA/SEP/09/053	NACGRAB
17	NG/MR/MAY/09/005	NACGRAB
18	L00170	NACGRAB
19	ROMA	Ogbomoso
20	KEREWA	Ogbomoso
21	OGBOMOSO NATIVE	Ogbomoso
22	ALAWUSA TYPE	Ogbomoso
23	ALARA (ALA)	Ogbomoso
24	ABEOKUTA NATIVE (ABE)	Oke Ogun

NACGRAB: National Centre for Genetic Resources and Biotechnology Moor Plantation, Ibadan, Oyo State Nigeria.

Table 2: Vegetative parameters and lycopene content of twenty – four accessions/landraces of tomato plants studied

S/N	Variable	Symbol	Method of scoring
1	Plant height	PHT	Measured
2	Leaf area at 75 days	LEA	Calculated
3	Number of leaves per plant	NLP	Counted
4	Number of branches per plant	BPP	Counted
5	Number of flowers per truss	FPT	Counted
6	Number of fruits per truss	NFT	Counted
7	Number of fruit at 75 days per plant	NOF	Counted
8	Number of fruits per plant	FPP	Counted
9	Weight of fruits	WGH	Measured
10	Diameter of fruits	DMF	Measured
11	Number of seeds per fruit	NSF	Counted
12	Lycopene content of the fruit	LCP	Calculated

2.1 Extraction of Fruits Lycopene

Tomato fruits lycopene was extracted using acetone, n-hexane, and 100% ethanol as solvents. The solution used for lycopene extraction was prepared in a 2:1:1 ratio (two parts hexane, one part acetone, and one part ethanol) and kept in a bottle with a tight stopper. In a 125 ml Erienmeyer conical flask was measured one gram (1 g) of perfectly ripe tomato fruit, followed by addition of 100 ml of extractant. The flask was covered immediately with a rubber stopper and wrapped with aluminium foil to prevent photooxidation. After an hour of extraction, 15 ml of distilled water was used to separate the phases (Barrett et al., 2005). The samples were again left for 10 minutes to allow the phases to further separate and the air bubbles to completely dissipate. The lycopene top layer was identified, and the absorbance of the extract was taken at 503 nm on spectrophotometer with the concentration of lycopene determined using the expression according to (Barretts and Antony, 2001; Fish et al., 2002; Barrett et al., 2005).

Lycopene (mg/kg fresh wt.) = $A_{503} \times 171.7 / w$

where 'w' is the exact weight of tomato added in grams; and mg/kg is equivalent to μg/g

2.2 Statistical Analyses

Data collected on morpho-agronomic and biochemical traits were subjected to Analysis of Variance (ANOVA) and significant means were separated using Duncan Multiple Range Test (DMRT) at $p < 0.05$ probability level. The central tendency and dispersion of the observed morpho-agronomic and biochemical parameters were determined. A genetic diversity estimate was carried out using SPSS for Windows 7.0, version 20 (Norusis, Munich, Germany). Using Pearson's correlation, the degree of relationships among the various morpho-agronomic and biochemical variables was determined. The contribution of each trait to genetic diversity was assessed using principal component analysis, and the total variation was determined by adding the extracted eigenvalues. Hierarchical cluster analysis and dendrogram of relationships based on Ward's method using estimates for Euclidean dissimilarity coefficients for characteristics measured at maturity classified the accessions and landraces studied into heterogeneous groups (Azeez et al., 2016).

2.2.1 Estimates of Variance Components

The variance components such as phenotypic, genotypic and environmental variances were estimated using formula according to (Alake, 2012; Bello et al., 2012; Rosmaina et al., 2016; Meena et al., 2017).

Genotypic variance ($\delta^2 g$) = (Mean sum of squares due to genotypes – Error mean sum of squares) ÷ Replication

Phenotypic variance ($\delta^2 p$) = $\delta^2 g + \delta^2 e$

Environmental variance ($\delta^2 e$) = (Error mean sum of squares) ÷ Replication

2.2.2 Estimate of Genotypic And Phenotypic Coefficients of Variation

The following formulas were used to calculate the genotypic and phenotypic coefficients of variation in accordance with method by (Meena et al., 2017):

Genotypic Coefficient of Variation in percentage (GCV%) $= \frac{\sqrt{\delta^2 g}}{\pi} \times 100$

Phenotypic Coefficient of Variation in percentage (PCV%) $= \frac{\sqrt{\delta^2 p}}{\pi} \times 100$

Where 'π' is the grand mean of a character

The PVC and GCV were classified as suggested by (Meena et al., 2017).

Less than 10% = Low

10 - 20% = Moderate

More than 20% = High

2.2.3 Estimation of Heritability in Broad Sense

The broad sense heritability (h^2(bs) was determined for all the traits studied using the formula provided as follows (Rosmaina et al., 2016; Meena et al., 2017):

$$h^2\,(bs) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

The heritability estimate (h^2 bs) was classified as;

0 - 30% = Low
31 - 60% = Medium
61 % and above = High

2.2.4 Estimation of Genetic Advance

Genetic advance (GA) was estimated by employing the procedure used by (Rosmaina et al., 2016) as:

GA = K × δp x h^2 (bs)

Where:

K = the selection differential (K = 2.06 at 5% selection intensity)

δP = the phenotypic standard deviation of the character or square root of the phenotypic variance of a particular trait

h^2 (bs) = broad sense heritability.

2.2.5 Estimation of Genetic Advance Over Mean

Genetic advance over mean was calculated and expressed in percentage using the following formula;

GAM (%) = $\frac{GA}{\pi}$ x 100

Genetic advance over mean (GAM) was categorised as suggested by (Meena et al., 2017)

Less than 10% = Low

10 - 20% = Moderate

More than 20% = High

3. Results

The twenty-four accessions and landraces of tomato studied were characterized based on flower colour, fruit colour, shape and type as well as their maturity, these characters varied among the accessions and landraces, and with the exception of L00 169, NG/AA/SEP/042, and NGB01410 which produced bright yellow blooms, all others produced yellow flowers. Most of the accessions produced fruits that were red, except for L00169, an Ogbomoso native, and Ala fruits that were bright red and NG/AA/SEP/09/042 fruits that were light red (Table 3). Some fruits were round, oblong, or oval; some were also pointed, long, or even ridged. NHGB/09/113, L00 169 and NG/AA/SEP/09/043 were smooth-bodied and precisely round, but NGB01254, Kerewa and Hausa types were long and pointed. Seventy percent of the collections examined had fruits that were non-cracking (Table 3).

Table 3: List of twenty-four tomato accessions and landraces studied with description of their blossoms and fruits

Accessions No	Code	Source/ Origin	Flowers' colour	Fruits' Colour	Fruits' shape	Type of fruit
Accessions						
1	NGB01254	NACGRAB	Yellow	Red	Oblong	Non- cracking
2	NHGB/09/113	NACGRAB	Yellow	Red	Perfectly round	Cracking
3	L00169	NACGRAB	Bright yellow	Bright Red	Round	Non- cracking
4	NG/AA/SEP/09/042	NACGRAB	Bright yellow	Light Red	Oblong / Oval	Non- cracking
5	NGB01410	NACGRAB	Bright yellow	Red	Ridge and round	Non- cracking
6	NG/MR/JAN/10/001	NACGRAB	Yellow	Red	Oblong/oval	Cracking
7	NG/AA/SEP/09/045	NACGRAB	Yellow	Red	Oval	Cracking
8	NG/SA/01/10/002	NACGRAB	Yellow	Red	Oval	Non- cracking
9	NG/AA/SEP/09/037	NACGRAB	Yellow	Red	Round	Non- cracking
10	NGB01357	NACGRAB	Yellow	Red	Round	Non- cracking
11	NG/MR/MAY/09/006	NACGRAB	Yellow	Red	Round	Non- cracking
12	NG/AA/SEP/09/040	NACGRAB	Yellow	Red	Round	Cracking
13	NG/AA/SEP/09/050	NACGRAB	Yellow	Red	Round	Non- cracking
14	NHGB/09/120	NACGRAB	Yellow	Red	Ridge	Non- cracking
15	NG/AA/SEP/09/043	NACGRAB	Yellow	Red	Round	Cracking
16	NG/AA/SEP/09/053	NACGRAB	Yellow	Red	Round	Non- cracking
17	NG/MR/MAY/09/005	NACGRAB	Yellow	Red	Three ridge on fruit	Non- cracking
18	L00170	NACGRAB	Yellow	Red	Round	Cracking
landraces						
19	Roma	Ogbomoso	Yellow	Red	Round	Non- cracking
20	KEREWA	Ogbomoso	Yellow	Red	Pointed and Long	Non- cracking
21	OGBOMOSO NATIVE	Ogbomoso	Yellow	Bright Red	Ridge and partly round	Non- cracking
22	HAUSA TYPE	Ogbomoso	Yellow	Red	Pointed and Long	Non- cracking
23	ALAARA (ALA)	Ogbomoso	Yellow	Bright Red	Ridge in nature	Cracking
24	ABEOKUTA NATIVE (ABE)	Oke Ogun	Yellow	Red	Oblong	Non- cracking

Evaluated vegetative and yield traits also differed greatly amongst accessions. The accession determined to have the maximum height was NG/MR/MAY/09/005 (113.90 cm), and the one with the lowest height was ROMA (48.60 cm) (Table 4a). The leafiest plants were found in NHGB/09/120 (65.30), while ROMA had the fewest (18.60). The leaf area ranged from 34.50 to 202.80 with accession L00170 showing the largest leaf area and NG/MR/JAN/10/001 the smallest. Hausa type had the highest number of branches (5.70), while NG/AA/SEP/09/045 had the lowest (1.80). Accession L00169 had the largest average number of fruits per plant at 75 days and maturity (9.40; 33.30), whereas ROMA had the lowest values (0.00; 1.90).

In the same vein, NG/AA/SEP/09/050 and Ogbomoso Native had the lowest average number of fruits per truss (NFT) (1.00), while accession L00169 had the highest average (5.90). The heaviest fruits with 51.11g on average were produced by accession NGB01410, while the lightest fruits (1.92g on average) were produced by accession L00169. The average number of seeds per fruit ranged from 23.80 in NGB01254 to 93.20 in NG/AA/SEP/09/042. According to Table 4b, tomato fruits with the highest lycopene concentration were recorded for ABE (13.312μg), followed by NG/MR/MAY/09/006 (12.464 μg), ALARA (11.675 μg), and L00169 (2.562 μg).

Table 4a: Duncan Multiple Range Test (DMRT) of growth and vegetative parameters of agronomic importance of tomato

S/N	Varieties	PHT (cm)	LEA	NLP	BPP	FPT	NFT
1	**NGB01254**	58.40_{fgh}	95.30_{ij}	23.40_{jk}	2.60_{cdef}	6.30_{ab}	1.30_{hi}
2	**NHGB/09/113**	49.80_{h}	134.70_{defg}	59.50_{b}	4.90_{ab}	3.50_{g}	1.60_{efghi}
3	**L00169**	57.20_{fgh}	66.80_{k}	51.20_{cd}	3.90_{abcde}	5.90_{abcd}	5.90_{a}
4	**NG/AA/SEP/09/042**	97.00_{bc}	41.30_{l}	39.20_{ef}	3.20_{bcdef}	6.30_{ab}	2.60_{bcd}
5	**NGB01410**	65.50_{efg}	38.40_{l}	39.10_{ef}	2.30_{cdef}	5.80_{abcde}	1.50_{fghi}
6	**NG/MR/JAN/10/001**	55.90_{gh}	34.50_{l}	28.20_{hi}	2.70_{cdef}	$4,10_{fg}$	2.20_{cdefgh}
7	**NG/AA/SEP/09/045**	66.90_{ef}	82.50_{jk}	24.40_{ij}	1.80_{f}	5.30_{abcdef}	2.50_{bcde}
8	**NG/SA/01/10/002**	73.10_{e}	115.0_{fghi}	22.00_{jk}	2.00_{def}	4.80_{cdefg}	1.70_{defghi}
9	**NG/AA/SEP/09/037**	90.90_{b}	174.10_{bc}	43.20_{e}	3.90_{abcde}	4.60_{defg}	1.80_{defghi}
10	**NGB01357**	63.90_{efg}	174.10_{bc}	35.80_{fg}	3.90_{abcde}	4.40_{efg}	1.50_{fghi}
11	**NG/MR/MAY/09/006**	88.20_{d}	137.00_{defg}	54.80_{c}	4.00_{abcde}	6.20_{abc}	2.50_{bcde}
12	**NG/AA/SEP/09/040**	104.60_{b}	145.00_{de}	51.50_{cd}	2.80_{cdef}	5.10_{abcdef}	1.20_{i}
13	**NG/AA/SEP/09/050**	89.70_{d}	99.40_{hij}	21.10_{jk}	3.00_{bcdef}	5.40_{abcdef}	1.00_{i}
14	**NHGB/09/120**	83.80_{d}	175.00_{abc}	65.30_{a}	3.70_{abcdef}	5.90_{abcd}	1.50_{fghi}
15	**NG/AA/SEP/09/043**	87.50_{d}	114.90_{fghi}	42.90_{e}	2.90_{bcdef}	6.50_{a}	2.40_{cdef}
16	**NG/AA/SEP/09/053**	92.50_{bc}	151.00_{cd}	55.70_{bc}	5.50_{a}	6.00_{abcd}	2.50_{bcde}
17	**NG/MR/MAY/09/005**	113.90_{a}	186.50_{ab}	39.30_{ef}	4.00_{abcde}	6.10_{abc}	2.30_{cdefg}
18	**L00170**	72.00_{e}	202.80_{a}	32.20_{gh}	2.80_{cdef}	5.20_{abcdef}	3.30_{b}
19	**ROMA**	48.60_{h}	99.75_{hij}	18.60_{k}	1.90_{ef}	5.70_{abcde}	1.70_{defghi}
20	**KEREWA**	58.00_{fgh}	127.50_{defgh}	28.40_{hi}	4.20_{abc}	5.50_{abcdef}	2.90_{bc}
21	**OGB. NATIVE**	70.30_{e}	108.20_{ghij}	47.60_{d}	4.10_{abcd}	4.60_{defg}	1.00_{i}
22	**HAUSA TYPE**	82.30_{d}	121.80_{efghi}	20.00_{jk}	5.70_{a}	5.30_{abcdef}	1.50_{fghi}
23	**ALA**	84.30_{d}	130.00_{defg}	19.60_{jk}	3.90_{abcde}	5.00_{bcdef}	1.80_{defghi}
24	**ABE**	88.10_{d}	142.80_{def}	30.70_{h}	5.60_{a}	5.20_{abcdef}	1.40_{ghi}

Note: *Mean in a column with any group followed by the same letters are significant difference using DMRT (Duncan Multiple Range Test)*
PHT *=Plant height in (cm);* ***LEA*** *75 = Leaf area (cm);* ***NLP*** *= Number of leaf per plant;* ***BPP*** *= Number of branch per plant;* ***FPT*** *= Number of flower per truss;* ***NFT*** *= Number of fruits per truss.*

Table 4b: Duncan Multiple Range Test (DMRT) of yield parameter and biochemical content of tomato studied

S/N	Varieties	NOF'75	FPP	WGH	DMF	NSF	LCP
1	**NGB01254**	1.60_{bcde}	4.70_{de}	20.21_{cd}	5.57_{klm}	23.80_{k}	6.791_{j}
2	**NHGB/09/113**	2.20_{bcde}	7.30_{de}	19.56_{cdef}	3.15_{ghi}	89.10_{b}	10.601_{de}
3	**L00169**	9.40_{a}	33.30_{a}	1.92_{j}	1.53_{o}	38.40_{ij}	2.562_{l}
4	**NG/AA/SEP/09/042**	2.80_{bcd}	15.00_{b}	16.04_{defgh}	2.66_{jkl}	93.20_{a}	6.459_{j}
5	**NGB01410**	0.30_{e}	2.50_{e}	51.11_{a}	4.13_{c}	44.80_{hi}	7.822_{hi}
6	**NG/MR/JAN/10/001**	1.80_{bcde}	8.00_{cd}	7.80_{j}	2.91_{hijk}	43.80_{hij}	6.594_{j}
7	**NG/AA/SEP/09/045**	1.90_{bcde}	3.40_{de}	19.78_{cde}	3.25_{fjh}	54.50_{f}	10.120_{e}
8	**NG/SA/01/10/002**	1.60_{bcde}	4.40_{de}	16.44_{defgh}	3.63_{d}	65.80_{cde}	7.188_{ij}
9	**NG/AA/SEP/09/037**	1.40_{bcde}	4.90_{de}	21.02_{cd}	3.00_{hij}	58.90_{ef}	8.168_{gh}
10	**NGB01357**	1.70_{bcde}	8.30_{cd}	15.58_{defgh}	2.63_{klm}	42.70_{hij}	9.024_{fg}
11	**NG/MR/MAY/09/006**	3.50_{b}	12.50_{bc}	11.16_{hi}	3.56_{d}	69.30_{cd}	12.464_{b}
12	**NG/AA/SEP/09/040**	1.60_{bcde}	7.30_{de}	12.90_{gh}	2.30_{mn}	68.00_{cd}	5.391_{k}
13	**NG/AA/SEP/09/050**	0.60_{de}	6.60_{de}	23.54_{c}	2.09_{n}	64.10_{de}	8.748_{fg}
14	**NHGB/09/120**	1.90_{bcde}	8.50_{cd}	18.72_{cdefg}	3.46_{efg}	47.30_{gh}	11.139_{cd}
15	**NG/AA/SEP/09/043**	3.30_{bc}	4.10_{de}	18.20_{cdefg}	3.19_{9hi}	77.90_{ab}	8.838_{fg}
16	**NG/AA/SEP/09/053**	1.80_{bcde}	6.00_{de}	20.78_{cd}	3.01_{hij}	45.20_{hi}	3.302_{l}
17	**NG/MR/MAY/09/005**	1.30_{bcde}	5.70_{de}	13.67_{efgh}	3.77_{d}	37.50_{ij}	2.868_{l}
18	**L00170**	1.90_{bcde}	4.20_{de}	5.77_{jh}	2.06_{n}	36.40_{j}	7.146_{ij}
19	**roma**	0.00_{e}	1.90_{e}	31.13_{b}	4.95_{b}	44.60_{hi}	5.522_{k}
20	**KEREWA**	1.70_{bcde}	4.70_{de}	12.84_{gh}	2.40_{lmn}	52.80_{f}	10.804_{de}
21	**OGB. NATIVE**	0.80_{de}	2.20_{e}	30.68_{b}	3.84_{cd}	67.60_{cd}	9.235_{f}
22	**HAUSA TYPE**	1.00_{cde}	3.90_{de}	13.55_{gh}	2.82_{ijk}	47.40_{gh}	10.302_{de}
23	**ALA**	1.90_{bcde}	3.40_{de}	47.72_{a}	5.88_{a}	65.80_{cde}	11.675_{c}
24	**ABE**	1.00_{bcde}	8.50_{de}	22.82_{c}	3.15_{ghi}	56.10_{f}	13.312_{a}

Note: *Mean in a column with any group followed by the same letter are significant difference using DMRT (Duncan Multiple Range Test).*
NOF75 *=Number of fruits at 75 days per plant;* ***FPP*** *= number of fruit per plant;* ***WGH*** *= Weight of fruits in (g);* ***DMF*** *= Diameter of fruits in (cm);* ***NSF*** *= Number of seeds per fruit;* ***LCP*** *= Lycopene.*

In Table 5, there were five positive and significant correlation coefficients, of which four (4) were highly significant ($p < 0.01$). The highest positive correlation was found between the number of fruits at 75 days (NOF) versus the number of fruits per plant (FPP) (r = 0.916), followed by the number of fruits at 75 days (NOF) versus the number of fruits per truss (NFT) (r = 0.861), and the weight of fruit (WGH) versus the diameter of the fruit (DMF) (r = 0.765). Additionally, five correlation coefficients (Table 5) were negative and significant at ($p < 0.05$). These include weight of fruit (WGH) versus number of fruits per plant (FPP) (r = -0.499), weight of fruit (WGH) versus number of fruits at 75 days (NOF) (r = -0.488), number of fruits per truss (NFT) versus weight of fruit (WGH) (r = -0.501), and number of fruits at 75 days (NOF) versus diameter of fruit (DMF) (r = -0.408).

Phenotypic Coefficients of Variation (PCV) and Genotypic Coefficients of Variation (GCV) of the investigated plant features were measured using variance components analysis, which revealed high to low values. Tables 6 provide estimates for phenotypic variances ($\delta^2 p$), genotypic variances ($\delta^2 g$), phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV). All the characters studied had strong heritability in the broadest sense. The range was 95.79% for the number of flowers per truss (FPT) to 99.91% for the fruits lycopene content (LCP) in µg/g. High heritability implied that the characters are less influenced by the environmental effect. Additionally, the number of fruits per plant (FPP) had the maximum genetic advance over mean (GAM) (185.00%), while the number of flowers per truss (FPT) had the lowest value (25.14%).

Table 5: Correlation coefficients of growth and yield parameters of agronomic important traits of 24 accessions of *Solanum lycopersicum*

Variable measured	PHT	LEA	NLP	BPP	FPT	NFT	NOF75	FPP	WGH (g)	DMF (cm)	NSF	LCP
PHT	1											
LEA	.376	1										
NLP	.216	.263	1									
BPP	.245	.386	.333	1								
FPT	.363	-.106	.051	-.128	1							
NFT	-.164	-.136	.181	.015	.288	1						
NOF75	-.110	-.175	.373	.094	.227	.861**	1					
FPP	-.062	-.248	.388	0.103	.198	.765**	.916**	1				
WGH (g)	-.041	-.200	-.201	-.117	-.012	-.501*	-.488*	-.499*	1			
DMF (cm)	.005	-.015	-.188	-.107	-.031	-.379	-.408*	-.477*	.751**	1		
NSF	.208	-.060	.263	.104	-.275	-.234	-.019	-.071	.145	.173	1	
LCP	-.085	.137	-.088	.250	-.248	-.404	-.276	-.360	.259	.251	.415*	1

Note: * Correlation is significant at the 0.05 level.
** Correlation is significant at the 0.01 level.

Table 6: Mean, genetic variance and heritability in broad sense at evaluation stage

Traits	Range			$\delta^2 g$	$\delta^2 e$	$\delta^2 p$	GCV (%)	PCV (%)	$h^2 b$ (%)	GA	GAM (%)
	Min	Mean (π)	Max.								
PHT	34.00	76.78	140.00	302.03	1.082	303.11	22.64	22.68	99.64	35.87	46.71
LEA	28.00	121.02	300.00	2074.93	7.994	2082.92	37.64	37.71	99.62	94.02	77.69
NLP	12.00	37.24	76.00	189.71	0.819	190.53	36.99	37.07	99.57	28.43	76.36
BPP	1.00	3.55	11.00	0.91	0.038	0.95	26.87	27.43	95.99	2.01	56.50
FPT	2.00	5.36	10.00	0.41	0.018	0.43	11.95	12.21	95.79	1.35	25.14
NFT	1.00	2.07	7.00	0.97	0.008	0.98	47.58	47.78	99.18	2.04	98.42
NOF75	0.00	1.95	21.00	2.72	0.047	2.77	84.58	85.30	98.30	3.43	175.73
FPP	1.00	6.94	56.00	38.59	0.254	38.84	89.51	89.81	99.35	12.84	185.00
WGH	1.60	19.68	63.80	127.08	0.356	127.44	57.28	57.36	99.72	23.26	118.17
DMF	1.30	3.16	7.00	0.87	0.001	0.87	29.52	29.53	99.89	1.92	60.84
NSF	17.00	54.79	99.00	232.54	0.618	233.15	27.83	27.87	99.74	31.46	57.42
LCP	2.060	8.170	14.595	849.66	0.801	850.46	35.68	35.70	99.91	60.08	73.53

As presented in Table 7 for principal component analysis, three main components accounted for 63.632% of the total variation among the accessions and landraces investigated. The first component (32.370%), followed by the second (17.427%) and third (12.567%), explained most of the variations observed. The first component had high positive loadings for the number of fruits per plant (FPP), the number of fruits at 75 days (NOF), and the number of fruits per truss (NFT), but high negative loadings for the weight of fruits in grams (WGH), the diameter of fruits in centimetres (DMF), and the amount of lycopene in microgram per gram (LCP) (-0.510). Branches per plant (BPP) (0.725), leaf area (LEA) (0.689), and number of leaves per plant (NLP) (0.609) had positive loadings in the second component. In the third component, the height of the plant at 75 days (PHT) and the number of seeds per fruit (NSF) both had strong positive loadings, but the number of flowers per truss (FPT) had a negative loading of -0.653. None of the characters were found to be redundant. Furthermore, some of the accessions were clearly distinct from one another while others were closely related as suggested by the spatial representations of the accessions on components 1, 2, and 3 (Figure 1). For instance, W, D, S M, U, G, and H are distantly related but not close to N, Q, L, and P.

Table 7: Eigenvectors and percentage explained variation by the first four principal components of the characters in twenty-four accessions of tomatoes studied

Characters	Eigenvectors			
	PC1	PC2	PC3	PC4
Height of plant at (75 days)	-.037	0.556	0.608	0.320
Leaf area at 75days	-0.109	0.689	-0.347	-0.361
Number of leaves per plant	0.380	0.609	0.092	0.303
Number of Branches per plant	0.079	0.725	0.082	-0.081
Number of flowers per truss	0.298	-0.155	-0.653	0.474
Number of fruits per truss	0.869	-0.155	0.062	0.092
Fruits number at 75 days	0.894	0.009	0.241	0.244
Number of fruits per plant	0.901	-0.004	0.203	0.213
Weight of fruits in gram	-0.712	-0.227	0.017	0.474
Diameter of fruits in cm	-0.664	-0.139	-0.011	0.465
Number of seeds per fruit	-0.239	0.429	0.517	0.458
Lycopene microgram per gram (µg/g)	-0.510	0.329	0.453	0.023
Eigenvalue	3.884	2.091	1.508	1.320
Individual percentage (%)	32.370	17.427	12.567	11.004
Cumulative percentage (%)	32.370	49.797	63.632	73.368

***Note**: PC, Principal component*

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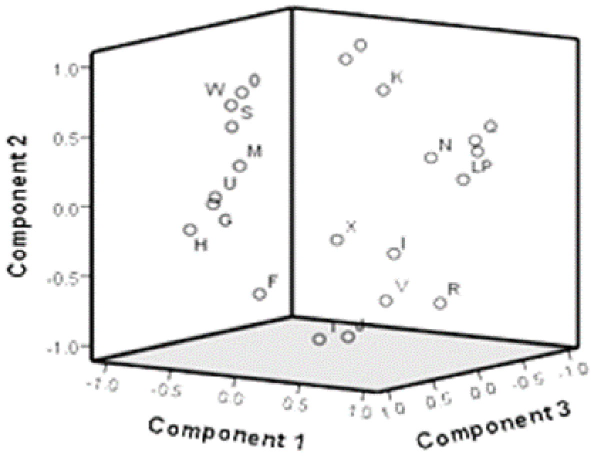

Figure 1: Principal component of relationship among the accessions and landraces of tomatoes studied

Note: *A*= NGB 01254; B=NHGB/09/113; C= L00 169; D= NG/AA/SEP/09/042; E= NGB 01419; F= NG/MR/JAN/10/001; G = NG/AA/SEP/09/045; H = NG/SA/01/10/002; I =NG/AA/SEP/09/037; J = NGB 01357; K = NG/MR/MAY/09/006; L= NG/AA/SEP/09/040; M = NG/AA/SEP/09/050; O = NHGB/09/120; P = NG/AA/SEP/09/043; Q = NG/AA/SEP/09/053; R =NG/MR/MAY/09/005; S = L00 170; T =ROMA; U = KEREWA; V = OGBOMOSO NATIVE; 22= HAUSATPYE;23 = ALARA and 24= ABEOKUTA NATIVE

On the basis of the characters evaluated at maturity, the dendrogram of linkages drawn using Ward's approach (Figure 2) and Table 8 divided the twenty-four (24) accessions and landraces into three (3) major heterotic groups (Cluster I, Cluster II, and Cluster III). Cluster I, which included eleven (11) individuals was further separated into two sub-clusters, I_1 and I_2, each of which had five (5) and six (6) members, respectively. Cluster II, which contained a total of seven (7) members was further divided into two sub-clusters; II_1 and II_2, each of which had four (4) and three (3) members, respectively. Furthermore, Cluster III was separated into two (2) sub-clusters, III_1 and III_2, each of which contained three accessions (Table 8). The dendrogram of relationships and the spatial distribution of the twenty-four (24) accessions and landraces utilised in this study indicate the existence of genetic diversity among the tomato germplasm studied. The intra-cluster distances ranged from 32.803 to 44.091, with cluster III having the highest value and cluster II having the lowest (Table 9). Cluster III and I had the greatest inter-cluster distance (111.907), followed by cluster III and II (72.893), while cluster II and I had the smallest inter-cluster distance (66.709).

Table 8: Cluster composition of twenty-four tomatoes accessions and landraces evaluated

Cluster	Sub-Cluster	Number of accessions	Percent %	Accession code number
I	I_1	5	20.83	NG/AA/SEP/09/043, OGBOMOSO NATIVE, NG/SA/01/10/002, NG/AA/ SEP / 09 / 050, NG/AA/SEP/045
	I_2	6	25.00	KEREWA, HAUSA TYPE, NG/MR/MAY/09/006, ABEOKUTA NATIVE, ALARA, NHGB/09/113
II	II_1	4	16.67	NG/AA/SEP/09/037, NGB 01357, NHGB/09/120, L00 170
	II_2	3	12.50	NG/AA/SEP/09/040, NG/AA/SEP/09053, NG/MR/MAY/09/005.
III	III_1	3	12.50	ngb 01419, ng/mr/jan/10/001, ng/aa/sep/09/042
	III_2	3	12.50	ngb 01254, roma, l00 169

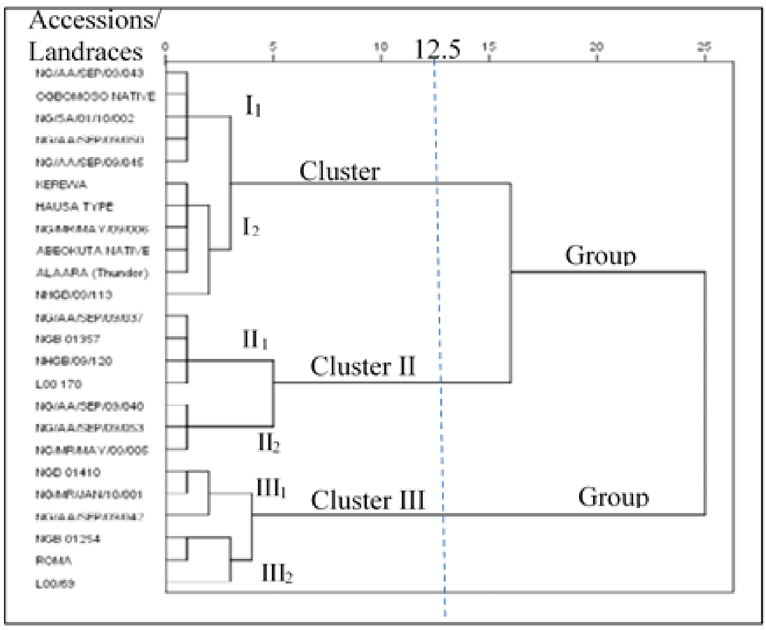

Figure 2: Dendrogram of relationship of the twenty-four accessions and landraces of tomato studied using Ward's method

Table 9: Estimates of inter and intra-cluster distances for *Solanum lycopersicum* accessions and landraces studied			
Clusters	1	2	3
1	**39.489**	66.709	111.907
2		**32.803**	72.893
3			**44.091**

4. Discussion

Evaluation of morpho-agronomic and yield parameters, as well as the calculation of genetic components, are thought to be essential to the identification and selection of genotypes that will serve as the foundational parents for future improvement activities in breeding programmes. The differences in the genetic backgrounds of germplasm studied might have greatly influenced the morpho-agronomic, yield, and lycopene content expressed by the twenty-four accessions studied (Getachew and Tewodros, 2017). These subsequently affect how well they perform, how adaptable they are, what features they have morphologically, and how they react to physiological stimuli as they grow. A large range of variation in tomato yield and features associated with yield has been documented in several reports (Ghosh et al., 2010; Meseret et al., 2012; Benti et al., 2017; Zakari et al., 2017). For example, the present study revealed that plant heights varied from 48.60 (Roma) to 113.90 (NG/MR/MAY/09/005), which is similar to the findings of who reported plant heights of 39.34 to 107cm (Meseret et al., 2012; Benti et al., 2017). The fruits of ABE Native had the highest lycopene content (13.312 µg/g), while NGB01410 had the highest average weight of fruits (51.11g), with accession L00169 recording the highest number of fruits per plant (33.30). The highest number of fruits per plant (115.33) and average fruit weight (80 g) have been reported for 24 tomato genotypes in a related study, also reported some hybrid tomatoes with the highest number of fruits per plant (40.49) and average fruit weight of 126.9 g (Kaushik et al., 2011; while Binalfew et al., 2016; Bai and Lindhout, 2007).

The most significant qualities can be determined by analysing the associations between different plant characters (Sarwar et al., 2005; Azeez and Morakinyo, 2011a). The selection for high fruit yield and lycopene content in tomato can directly take advantage of the positive correlations between number of fruits per plant (FPP) and number of fruits per truss (NFT) and lycopene content (LCP) versus number of seeds per fruit (NSF), which can subsequently lead to yield and quality improvement. High broad sense heritability were estimated for all the traits studied, suggesting that environment has little influence on these features and their suitability for selection was based on phenotypic performance (Haydar et al., 2007; Kaushik et al., 2011). A group researcher also found high heritability for average fruit weight, number of fruits per plant, yield per plant, and plant height, which agrees with the present findings (Meena et al., 2017). Some researchers also found significant heritability for average fruit weight and fruit production (Kaushik et al., 2011). The use of heritability and genetic advance as opposed to heritability alone, has been found to be more fruitful in the prediction of the subsequent effect of selection of the best genotype (Kaushik et al., 2011; Meena et al., 2017). High heritability and high genetic advance for leaf area (LEA) and lycopene in the current study are suggestive of the two traits being under additive control of genes. As a result, the required improvement may be achieved by using these qualities for directional selection from the available plant materials.

The twenty-four tomato germplasms were divided into three (3) primary groups at a cut-off of 50% on the dendrogram of cluster analysis using Ward's technique and PCA. Gizachew and Gebeyaw observed six primary clusters in a related investigation that was carried out on 49 tomato genotypes (Gizachew and Gebeyaw, 2021). The perceived differences in level of variability between the two studies might not be unconnected with the large number of tomato germplasms employed by the authors compared to the number used in the present investigation. Furthermore, this may also depend on differences in the genetic background of the germplasms employed for the study. Clustering pattern observed revealed that accessions with the highest fruit yield (L00169) and average fruit weight (NGB01419) were together in cluster III, whereas accessions with the highest lycopene content (ABE and NG/MR/MAY/09/006) were in cluster I.

Maximum variability for selection of desirable genotypes may be achieved in a segregating population when baseline parents for crosses are chosen from various clusters (Tsige et al., 2005; Azeez and Morakinyo, 2011b; Henareh, 2015). This is because accessions in the same cluster more likely to represent distinct heterotic groups. Additionally, most of the landrace collections and NACGRAB accessions were discovered together in cluster I, demonstrating that genetic diversity is not always represented by distinctions in origin (Meena et al., 2021; Gizachew and Gebeyaw, 2021). The maximum intra-cluster distances (44.091) recorded for cluster III indicate the possibility of choosing advantageous parents for within-cluster hybridization. According to a study, cluster III and cluster I had the maximum inter-cluster distance (111.907), a pointer to greater genetic variation between the groups that can aid selection of appropriate baseline parents for the development of transgressive hybrids (Kaushik et al., 2011).

5. Conclusion

The findings of the current study showed that the twenty-four (24) accessions and landraces of tomatoes exhibited genetic diversity for the traits assessed. The accessions NGB01410 and ALA (with the greatest fruit weight), ABEOKUTA NATIVE (ABE) and NG/MR/MAY/09/006 (with the highest lycopene) demonstrated superior performance and might be used for commercial production quality tomato fruits. Estimated broad sense heritability was high for all the traits evaluated, indicating that they were less influenced by environment. Lycopene and leaf area per plant had high heritability and genetic gains, indicating additive gene control of genes for these traits, which can be used as guide in the selection of suitable parents for breeding purposes. The twenty-four collections of tomatoes used in this study manifested considerable genetic diversity further supported by the estimated intra- and inter-cluster distances, and dendrogram of association. Therefore, the accessions L00169, NGB01410, and ABE Native that are members of various clusters and possess desirable traits can be chosen as ideal baseline parents to initiate crosses in improvement programme for enhancement of tomato fruit yield and quality. In addition, the three accessions can equally be adopted for production by farmers for high yield and lycopene content.

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