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GENETIC VARIABILITY IN NUTRITIONAL QUALITY, YIELD AND YIELD ATTRIBUTES OF TOMATO (*SOLANUM LYCOPERSICUM* L.)

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Abstract

The experiment was conducted to evaluate variability estimates for yield contributing and nutritional traits in 60 tomato (*Solanum lycopersicum* L.) hybrids and their parents. The trial was laid out in alpha lattice design and data pertaining to 13 quantitative, six nutritional and four qualitative characters have been presented. The estimates of mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) revealed significant phenotypic and nutritional variations among the genotypes for most of the characters under study. The principal component analysis showed that number of marketable fruits, number of non-marketable fruits, marketable yield, total yield, total number of fruits, number of fruits per cluster, fruit length and width, beta carotene, vitamin C, lycopene and acidity content contributed most to observed variations in the population. Five clusters were identified among the tomato population and they significantly associated with high nutritional content, high yield, yield contributing traits and fruit size related traits. For association among traits, moderate to very strong significant ($P < 0.05$) positive correlation was recorded for yield with number of branches (0.40), number of marketable fruit (0.84), number of non-marketable fruits (0.71), marketable yield (.98) and non-marketable yield (0.71). On the contrary, brix recorded weak negative significant correlation (-0.32) with non-marketable yield-while no significant association was observed between the agronomic and nutritional variables. Estimates of moderate to high heritability in the broad sense coupled with high genetic advance as a percentage of mean showed the feasibility of improving fruit nutritional quality, yield and yield contributing traits in this population through selection.

Keywords: heritability, yield, clusters, hybrids, association

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is an important vegetable widely grown in the tropics and sub-tropics for economic and nutritional purposes. As a major ingredient in most dishes, it has risen in status to 'one of the most consumed vegetable' across sub-Saharan Africa (Grandillo *et al.*, 1999; Ceylan and Alidou, 2021). By volume of its consumption on a daily basis, it contributes significantly to the dietary intake of essential minerals, vitamins A and C (Fufa *et al.*, 2009). They are considered as an important source of lycopene and other similar bioactive components such as beta-carotene, flavonoids and phenolic (Rao and Ali, 2007). Lycopene which is the main constituent of the red pigmentation in ripe tomato fruits is the principle carotenoid in tomato (Shi and Le-Maguer, 2000). Current research has highlighted the relationship between lycopene content of tomatoes with reduced risk of various maladies such as cancer insurgence (prostate cancer), cardiovascular diseases, obesity and diabetes (Perveen *et al.*, 2015).

Nigeria has approximately 836,320 ha of agricultural land under tomato cultivation and produced about 3.8 million metric tons of tomato in 2019. This accounts for about 73.4% of West Africa, 17.6% of Africa and 2.1% of world tomato output (FAO, 2019). Comparable to most sub-Saharan African countries, tomato production in Nigeria is plagued with different constraints such as biotic (pest and diseases) and abiotic (heat, drought and high incidence of rainfall) factors, market monopoly and low breeding activities targeting specific traits, regions and production systems (Dube *et al*., 2020). In the west Africa sub regions, predominance of open field rainfed tomato production leads to low productivity due to high incidence of rainfall and humidity that promotes pest and disease proliferation (Agele *et al*., 2002; Oladitan and Akinseye, 2014). Furthermore, the establishment of commercial seed companies and more organized seed system for vegetable crops across sub-Sahara Africa of recent has led to the introduction of new commercial tomato varieties (OP and hybrid varieties) with varying agronomic (yield and plant architecture) and fruit attributes such as colour, size and shape. This has led to most tomato farmers in the region relying heavily on importation of improved seeds not bred for the varying tropical environments. Majority of these exotic tomato varieties exhibit poor adaptation and productivity under west Africa local climatic conditions due to high susceptibility to prevalent pest and diseases. Some are deficient in desired fruit quality (morphological and nutritional), sufficient fruit firmness and long shelf life to withstand long-distance transport and rough handling usually encountered along the tomato value chain across the region (Fufa *et al.*, 2009). Furthermore, in most countries of sub-Saharan Africa like Nigeria, tomato production is carried out by resource-poor farmers who favour traditional cultivars (despite their poor fruit quality) because of their unique adaptation to local environment where most commercial varieties do not excel.

Production of high value fruits and vegetables like tomato offers smallholder farmers the opportunity of transiting from subsistence to commercial farming and subsequently increase their standard of living (Fan *et al.*, 2013). Considering the importance of tomato as a vegetable crop for domestic consumption with its potential as an export earner across the west Africa states, it becomes very vital to increase its productivity, resistance to pest and diseases along with improved fruit attributes through genetic improvement. Development of hybrid tomato varieties having desirable characters has proven to be an effective strategy to increase production on the short term compared to creation of inbred varieties (Islam *et al*., 2012). It is reported that heterosis in tomato resulted in increased yield of 20 to 50% (Chowdhury *et al*., 1965). To achieve this, plant breeders rely on genetically diverse parents as sources of elite alleles controlling desired traits in most tomato genetic improvement programmes (Kouam *et al*., 2018). Initially in the tropics, breeding efforts on tomato genetic improvement focused on yield, and resistance to major pest and diseases with minimal effort directed towards creation of varieties adapted to open field rainfed conditions with enhanced nutritional fruit quality (Goff and Klee, 2006). Desirable traits such as taste, colour, total soluble solids, firmness and storability are important traits that largely determine the acceptability of a new variety along the tomato value chain. Efforts towards improving the quality of fresh market tomatoes can be achieved through creation of new adapted varieties from hybridizing popular improved varieties and widely adapted popular local cultivars in the region. Understanding the diversity, association, heritability and genetic advance of desired traits in a new breeding population is essential for effective selection, efficient utilization and advancement of promising genotypes in genetic improvement programmes. This study was conducted to characterize newly developed tomato hybrids for improved nutritional quality, yield and yield contributing traits under open field rainfed conditions.

MATERIALS AND METHODS

Study Area

The trial was carried out at the National Horticultural Research Institute (NIHORT), Ibadan, Nigeria, located in the humid forest Agro-ecological zone (210 masl, 7°30′N, 3°54′E). The location is characterized by bimodal annual rainfall of about 120–128 rainy days amounting to 1,200–1,400 mm. Pan evaporation is between 1,550 and 1,600 mm. The wet season is from March through October and the dry season from November through February. Annual maximum temperature ranges between 27 °C and 34 °C while annual minimum temperature is between 20–23 °C (Ogungbenro and Morakinyo, 2014).

Plant Material and Field Establishment

Experimental materials comprised of two commercial checks (Roma VF and Roma VF^{+}), sixty hybrids (F_1) developed by crossing selected parents comprising of popular tomato landraces/cultivars in Nigeria and exotic advanced breeding lines from AVRDC. These landraces were collections from farmers' field across different tomato growing regions in Nigeria. They have undergone over 4 generations of selfing with selections and are maintained in the Institute's tomato genetic improvement programme and Genebank.

For the field experiment, seeds were sown in perforated plastic trays containing sterilized top soil in a screen house (soil was sterilized by steaming). Emerging plants were watered 3 times a week until

30 days after sowing using 75 cl of water for each tray. The field was arranged in an alpha lattice design (10 stands per plot) with plant spacing of 0.5 m within row and 0.6 m between rows with 2 replications. Fertilizer was applied 3 weeks after transplanting at 140 kg·ha^{-1} of N and 25 kg·ha^{-1} of P. The N was from urea and the P from single superphosphate. Manual weeding was carried out at 3 and 8 weeks after transplanting, while staking of plants was done at one week prior to the onset of flowering.

Data Collection

Data were obtained on plant height measured using a graduated metallic tape from the apical meristem of the plant to the soil level, number of branches (ratio between total branches counted and number of plants in each plot), days to 50% flowering was estimated as the days from nursery establishment to flowering of 50% of established plants per plot. Fruit length and fruit width were estimated as the longitudinal length from one fruit tip to the bottom and fruit cross section diameter respectively. Average number of fruits per plot, marketable and non-marketable yield, total fruit yield per plot were determined by the ratio between the total number of fruits harvested per plot, marketable and non-marketable yield per plot (determined as the average number of healthy and non-healthy fruits harvested per plot), and total fruit weight per plot over the total number of plants per plot respectively. Number of fruits per cluster was estimated as the ration of average number of fruit counted per cluster divided by the number of clusters counted per plot while number of fruit lobes was determined by the ratio of number of lobes counted on a fruit over the total number of fruit counted. The number of locus per fruit was estimated as ratio of the number of locus per fruit over the total number of fruits counted after cutting each fruit through the cross-section. Qualitative traits recorded were depression at peduncle, fruit shape at maturity, fruit end shape and mature fruit colour; while nutritional traits comprised of Vitamin C, lycopene, soluble solids, acidity and β-carotene. Characterization for most characters was on 5 randomly selected plants from each genotype as per descriptors for tomato (IPGRI, 2015).

Standard analytical procedures were followed in determining the nutritional parameters. The amount of vitamin C were estimated by titrating tomato extracts obtained by soaking tomatoes samples in metaphosphoric acid-acetic acid against 0.5 g/l of dichlorophenol-indophenol (DCPIP). (Pongracz *et al*., 1971). For Beta carotene, 0.5 g of homogenous samples of fresh tomato were extracted with 5 ml cold acetone and 5 ml ethanol, until the total loss of pigmentation. A 3 ml portion of distilled water was added which was later partitioned with 10 ml petroleum ether. The ether phase was passed through Neutral Alumina (activity III) packed column. The column was eluted with petroleum ether and the first band was collected into 25 ml volumetric flask. The extract was read at 450 mm, and beta-carotene content calculated as follows:

$$C\ (\mu g/g) = \frac{A \times \text{Volume (ml)} \times 10^4}{A1\% \times 1\ \text{cm} \times \text{sample weight (g)}}, \quad (1)$$

where A = Absorbance, A1 % = absorption coefficient of beta –carotene in PE (2592) (Rodriguez-Amaya, 2001). Total carotenoids content was subsequently estimated using a calibration curve of β-carotene as standard.

For Lycopene, the same extract from the above procedure was read at 510 nm, and lycopene content was calculated using the same formula (Rodriguez-Amaya, 2001).

Acidity was determined following the method of Association of Official Analytical Chemists. Ten milliliter aliquot of tomato sample was thoroughly mixed with two drops of phenolphthalein indicator. The mixture was titrated against 0.1 M NAOH until there was a change in color to persistent pink, the end point and acidity was calculated (James, 1999). Total soluble solid content was determined using a refractometer (ERMA, TOKYO. One drop of tomato juice extracted from a homogenous mixture of tomato fruits was dropped on the refractometer and the value was read and recorded in degrees (AOAC, 2005).

Data Analysis

Analysis of variance and heritability estimates (broad sense) were obtained with PB Tools (ver. 1.1.0, http://bbi.irri.org/products); while phenotypic correlation, multivariate PCA and clustering (Un-weighted pair group method with arithmetic mean) were developed with STAR statistical software and used to determine relationships and diversity among breeding lines. The estimates of phenotypic and genotypic coefficient of variation were calculated as described by Singh and Chaudhary, 1979 as follows:

$$\text{PCV (\%)} = \frac{\sqrt{Vp}}{\bar{x}} \times 100, \quad (2)$$

$$\text{GCV \%} = \frac{\sqrt{Vg}}{\bar{x}} \times 100, \quad (3)$$

where PCV is Phenotypic Coefficient of Variation, GCV is Genotypic Coefficient of Variation. GCV and PCV values were categorized as low (0–10%), moderate (10–20%), and high (20% and above) as indicated by Subramanian and Menon, 1973.

Heritability was estimated as the ratio of total genotypic variance to the phenotypic variance

according to Falconer, 1981: Heritability (Broad sense): = H_b^2 = v_g/v_p, where h_B^2 = Broad Sense heritability of the trait; V_g = Genotypic variance, *Vp* = Phenotypic variance. The heritability percentage was categorized as low (0–30%), moderate (30–60%), and high ≥ 60% as given by Johnson *et al.* (1955).

Expected genetic advances (GA) for characters were estimated according to the formulae of Johnson *et al.* (1955) and Allard (1960). Genetic advance, as percent of mean (GAM), was estimated using formulae of Comstock and Robinson (1952). Genetic Advance (GA) = $H \times P \times K$, where *H* is heritability, *P* is phenotypic standard deviation, and *K* is selection deferential (1.755 at 10%). Genetic advance expressed as percentage of mean was estimated by using the formulae as described by Comstock and Robinson, 1952. Genetic Gain (%) = GA × 100; it is categorized as: 0–10% = low, 10–20% = moderate, 20% and above = high (Johnson *et al.*, 1955). Correlation coefficients "r" were considered very weak (0–0.19), weak (0.20–0.39), moderate (0.40–0.59), strong (0.60–0.79), very strong (0.80–1.00) according to Evans (1996).

RESULTS

Data on qualitative traits for the tomato genotypes are presented in Tab. I. Majority of the genotypes had red fruits at maturity (67.14 %) while only 5.71 % exhibited orange-red (Tab. I). There was predominance of slightly flattened fruit shape (31.14 %) followed by cylindrical fruit shape (21.43 %) while round, circular and heart fruit shapes were the least and equally represented in the population at 7.14 % respectively. For the fruit base, a large proportion of the tomato genotypes exhibited flat fruit base (38.57 %), indented base (18.57 %), pointed base (10 %), indented to flat (18.57 %), flat to indented (12.86 %), with only 1.43 % having medium fruit base. Depress at peduncle end recorded weak (55.75 %), absent (21 %), strong (3 %) and medium (12 %).

The descriptive statistics for all traits considered in this study are presented in Tab. II. Genotypic differences among the tested genotypes were significant ($p < 0.05$) for all nutritional and most phenotypic traits except for plant height, average number of fruits per clusters, average number of non-marketable fruits, and non-marketable weight. High differences were recorded between the minimum and maximum mean values for most of the characters in this study. A wide range was observed for marketable yield (343–6059.5 g), non-marketable yield (74–1066 g), and total yield (453–7057.5 g) while vitamin C (0.01–0.36 mg/100 g), lycopene (0.7–2.02 mg/100 g) and number of locus (2–5) had the least range (Tab. II).

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) can be categorized as low (< 10%), moderate (10–20%) and high (> 20%) according to Deshmukh *et al.* (1986). High PCV and GCV were observed for all traits considered in this study except for days to flowering and fruit acidity level that recorded low and moderate PCV and GCV respectively (Tab. II). In general, the PCV were higher than the GCV for most of the agronomic traits except for non-marketable yield and fruit width. However, estimates of the difference between values of PCV and corresponding GCV were small for all the nutritional variables but higher for the agronomic traits (Tab. II).

From the results of this study, moderate to high broad sense heritability was recorded for most agronomic traits except plant height at maturity, number of non-marketable fruits and non-marketable fruit weight that recorded low heritability at 19%, 14% and 4% respectively. However, estimates of heritability were high (> 95%) for all the nutritional traits (Tab. II). Wide range of Genetic Advance as a percentage of Mean (GAM) was recorded for among the traits and ranged from 0.03% for number of marketable yield to 111.49% for vitamin C content. At 5% selection intensity, GAM is considered to be high (> 20%) and vice versa. High GAM was recorded for most traits

I: *Qualitative variation in fruit characteristics among the 70 tomato genotypes*

Traits	Observation	Frequency	Percentage
Ripe fruit colour	red	47	67.14
	orange	19	27.14
	orange red	4	5.71
Fruit shape	slightly flattened	22	31.43
	obovate	6	8.57
	round	5	7.14
	cylindrical	15	21.43
	circular	5	7.14
	flat	1	1.43
	rectangular	11	15.71
	heart	5	7.14
Fruit base	indented to flat	13	18.57
	pointed	7	10
	flat	27	38.57
	indented	13	18.57
	flat to pointed	9	12.86
	medium	1	1.43
Depress at peduncle end	weak	39	55.71
	absent	15	21.43
	strong	3	4.29
	medium	12	17.14

II: *Estimates of range, heritability, GA, GCV and PCV of traits among tomato genotypes evaluation under field condition*

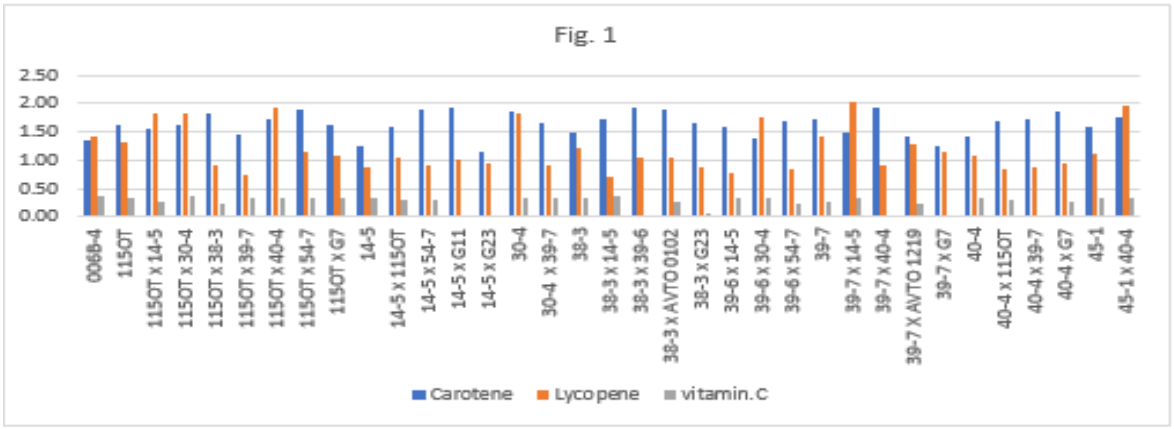
Variable	Min	Max	Mean	StdDev	Vg	Vp	GCV (%)	PCV (%)	RD	GA (%)	H^2 (%)
DTF	45.50	59.00	50.11*	2.41	4.73	10.83	4.34	6.57	2.23	5.65	43.00
PH	42.50	334.25	79.85	35.36	490.70	2500.57	27.74	62.62	34.88	23.80	19.00
NB	3.25	8.00	5.32*	1.15	0.23	1.26	8.96	21.10	12.14	17.30	41.00
NoClus	2.00	7.00	4.2	1.02	0.81	2.12	21.45	34.69	13.23	25.67	37.00
M.No.	20.00	389.00	116.16**	72.28	5607.08	10367.99	64.46	87.66	23.19	94.67	54.00
Nm.No	4.50	59.50	29.75	13.40	49.25	359.27	23.59	63.71	40.12	17.84	14.00
M.Wt	343.00	6059.50	2128.95*	1214.95	1379126.24	2945306.00	55.16	80.61	25.45	74.16	46.00
Nm.Wt	74.00	1066.00	498.76	255.50	116064.22	341.18	68.31	3.70	-64.60	0.30	4.00
Fr.L	15.95	83.40	40.93**	11.28	203.32	254.39	34.84	38.97	4.13	62.35	80.00
Fr.W	17.25	69.43	41.17**	8.89	42.59	7.08	15.85	6.46	-9.39	8.79	68.00
Total.YLD	453.00	7057.50	2627.71*	1382.79	1656765.06	3802374.00	48.98	74.21	25.22	63.82	43.00
Total.NoF	34.50	438.50	145.91*	81.24	6725.41	13114.41	56.20	78.49	22.28	80.06	51.00
Nolocus	2.00	5.00	2.54**	0.61	0.42	0.71	25.59	33.16	7.57	39.12	59.00
Beta.Carotene	0.49	1.76	1.07**	0.32	0.21	0.21	42.62	42.66	0.05	85.33	98.00
Lycopene	0.70	2.02	1.1**	0.33	0.21	0.21	41.32	41.97	0.64	81.41	97.00
Carotene	1.13	2.45	1.63**	0.25	0.12	0.13	21.17	21.78	0.61	41.38	95.00
vitamin.C	0.01	0.36	0.25**	0.10	0.02	0.02	56.80	56.85	0.05	111.43	98.00
Acid	3.10	4.80	4.16**	0.30	0.18	0.18	10.22	10.26	0.04	19.70	96.00
Brix	2.30	7.55	4.32**	1.08	2.29	2.32	35.06	35.28	0.23	69.15	98.00

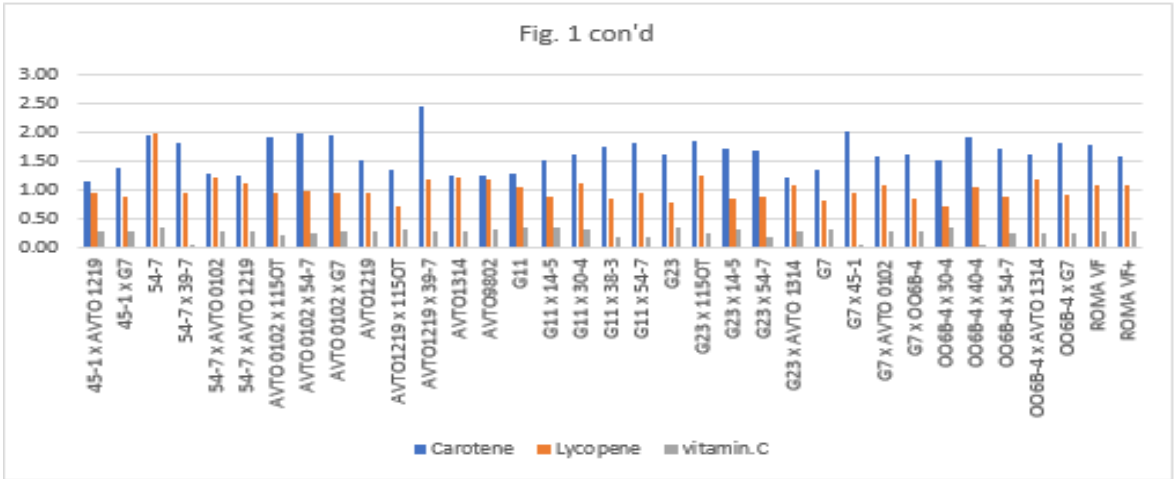
DTF = Days to 50% flowering; PH = Plant height at maturity; NB = Number of branches; No. C=Number of clusters; No. MF = Number of marketable fruits; No. NMF = Number of non-marketable fruits; MY = Marketable Yield; NMY = Non-marketable yield; FL = Fruit Length; FWD = Fruit width at maturity; TYLD = Total yield; T. NoF = Total number of fruits; NoL = average number of locus per fruit; Beta. C = β-carotene; Lyco = Lycopene content; T. caro = Total carotene; Vit. C = Vitamin C; PhL = Acid base level; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; RD = Relative difference between GCV and PCV; GA = Genetic advance; H^2 = Broad sense Heritability. ** = statistically highly significant at 1%; * = statistically significant at 5% Probability

except days to 50% flowering (5.65%), number of branches (17.3%), number of non-marketable fruits (17.84%), non-marketable yield (0.30%), fruit width (8.79%) and pH level (19.70%). High heritability coupled with high GAM was recorded for fruit length at maturity, beta carotene content, total carotene, vitamin C and brix.

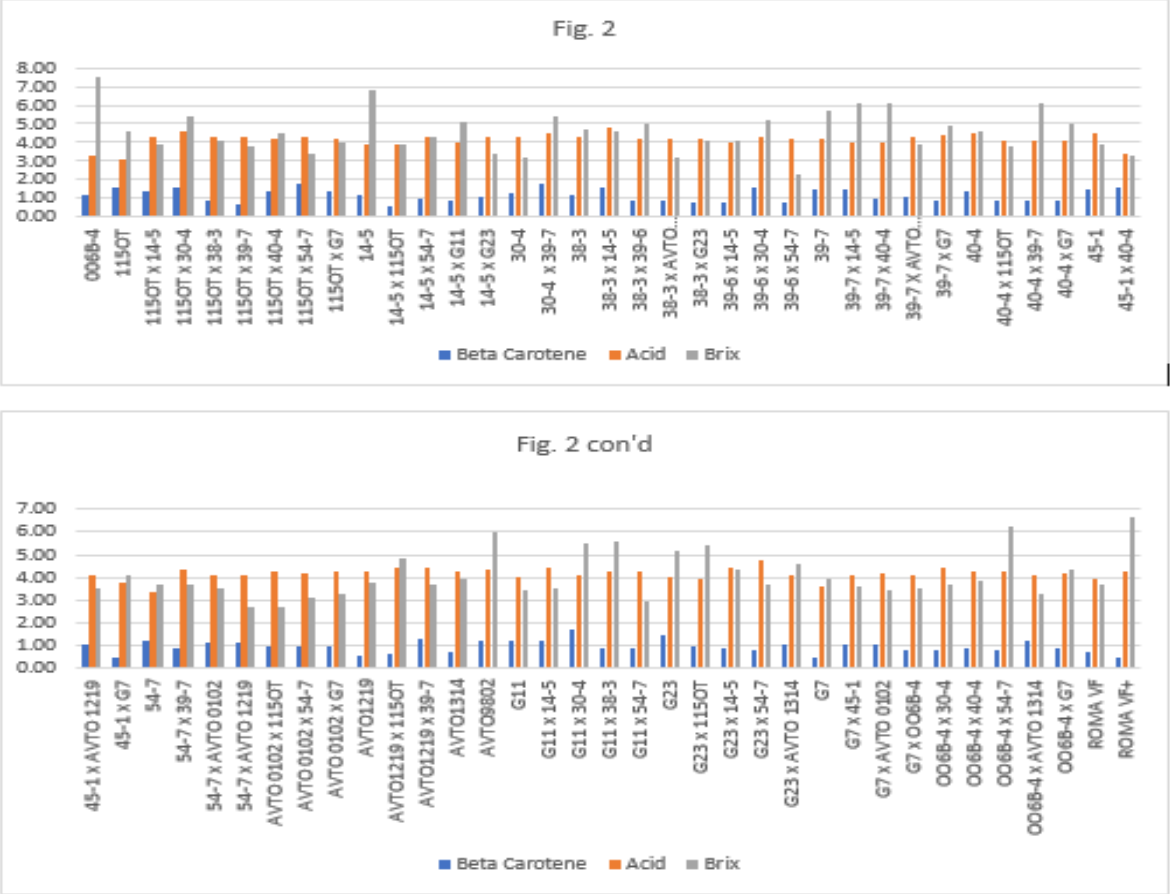
For the parental lines, genotype 30-4 exhibited outstanding performance for days to flowering (47.5 days) while G7 had the highest plant height (91 cm) and number of branches (8 branches). Tomato accession 54-7 was the top performer for marketable yield (3006.5 g) and average number of marketable fruits (228.5 fruits) while 39-7 exhibited highest number of fruits per cluster (7 fruits). Genotypes 30-4, 39-7, G11 and AVTO1219 were highest for non-marketable yield (908 g), number of non-marketable fruits (54 fruits), highest fruit length (83 mm) and fruit width (61.45 mm) respectively. The accessions with highest nutritional content were 39-7, 54-7, 006B-4 and 45-1 for Beta carotene (1.5 mg/100 g), lycopene (1.98 mg/100 g), vitamin C (0.36 mg/g), brix (7.55 mg/100 g) and acidity (4.51) respectively. Hybrids 115OT × 14-5, 38-3 × 14-5, 38-3 × 14-5, 115OT × 14-5 and 14-5 × 54-7 were top performers for marketable yield (6059.50 g), non-marketable yield (1066.00 g), total yield (7057.50 g), number of marketable fruits (389 fruits) and number of non-marketable fruits (59.50 fruits) respectively. Best performers for days to flowering (45 days), plant height at maturity (334.25 cm), number of branches (8), number of fruits per cluster (6.5), fruit length (64.88 mm), fruit width (69.43 mm) were recorded for 54-7 × AVTO 1219, G11 × 14-5, 38-3 × 14-5, 45-1 × G7, 38-3 × 14-5, 45-1 × G7 and G7 × OO6B-4 (for fruit length and width) respectively. Based on results from nutritional analysis, the means of beta carotene, lycopene and vitamin C are presented in Fig 1. Hybrid combinations 115OT × 54-7, 39-7 × 14-5, OO6B-4 × 54-7 exhibited the highest nutritional content for beta carotene (1.76 mg/100 g), lycopene (2.02 mg/100 g) and brix (6.2 mg/100 g) respectively while 38-3 × 14-5 was top performer for both pH level (4.8) and vitamin C content (0.35 mg/g) (Fig. 1 and 2).

The first five (5) components of PCA accounted for 65.1 % of the total observed variations among the genotypes with PCs I, II and III contributing 51 % (Tab. III). Number of marketable fruits, number of non-marketable fruits, marketable yield, total yield and total number of fruits were the main





1: *Comparison of carotene (mg/100g), Lycopene (mg/100 g) and vitamin C (mg/100 g) among 70 tomato genotypes (hybrids, parents and checks)*



2: *Comparison of Beta carotene (mg/100 g), Acidity and Brix among 70 tomato genotypes (hybrids, parents and checks)*

contributors to the genetic divergence observed in PCI. Average number of fruits per cluster, fruit length, fruit width at maturity and total carotene content had the highest loading in PCII while beta-carotene content, lycopene, vitamin C and PH level contributed more to the formation of PC3. Except for number of fruits per cluster, total carotene content and PH (Acid/Base), all the main contributors in PCs I to III contributed negatively to the loadings. The remaining three contributors are loaded in PCs IV and V.

The clustering pattern of each tomato genotype as revealed by Ward's Minimum Variance showed five clusters with 4 to 22 genotypes/hybrids in each cluster (Tab. IV). Cluster I comprised of eleven (11) genotypes with five parental lines and six hybrids, while cluster two had the least number of members comprising of 4 hybrid lines. Cluster III comprised of 21 genotypes dominated by new hybrid combinations with only one parental genotype while cluster IV had the highest number of members comprising of 22 genotypes with eight parental lines and 14 hybrids. Cluster V had 12 tomato genotypes comprising of two commercial checks (ROMA VF and ROMA VF^{+}) and ten hybrid combinations. The descriptive statistics for the cluster groups are presented in Tab. V. The cluster results showed that Cluster I comprised mainly of genotypes with high beta carotene content (1.14–1.74 mg/100 g), vitamin C and high lycopene content (0.79–2.02 mg/100 g). Cluster II are characterized by high number of fruits per cluster with range from 5–7 fruits, high number of marketable fruits (230–389 fruits), marketable yield (3791–6059.5 g), total number of fruits (378–438.5 fruits) and total yield (4389.5–7057.5 g). Clusters IV comprised of genotypes with increased fruit width (28–69 mm) and fruit length (35–83 mm). Genotypes in clusters V had high total carotene (1.5–1.93 mg/100 g) content while the remaining genotypes are grouped in Cluster III based on combination of different characteristics.

Significant phenotypic correlation ($P < 0.05$) was observed among some of the traits (Tab. VI). Moderate to very strong significant positive correlation was recorded for total yield with number of branches (0.40), number of marketable fruit (0.84), number of non-marketable fruits (0.71), marketable yield (0.98) and non-marketable yield (0.71). Fruit length exhibited negative significant association (-0.34) with number of fruits per clusters but showed moderate positive significant association with fruit width (0.55) while fruit width exhibited negative significant association with number of marketable fruits (0.30). Plant height

III: *Contribution of each quantitative trait to the five principal components (PC) among 70 tomato genotypes*

Variables	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	0.1681	-0.1273	0.1253	-0.0933	0.4998
Plant height at maturity	-0.1657	-0.159	-0.1004	-0.1253	-0.2051
Number of branches	-0.2104	-0.0401	-0.0866	-0.3883	-0.2562
Number of clusters	-0.1983	0.3186	0.1886	0.1114	-0.1745
Number of marketable fruits	-0.3829	0.0444	-0.0107	-0.1343	0.0339
Number of non-marketable fruits	-0.331	0.0411	0.1482	0.1174	0.1287
Marketable Yield	-0.3955	-0.0984	0.0032	-0.0228	0.1037
Non-marketable yield	-0.2774	-0.2171	0.1694	0.2723	0.1986
Fruit Length	0.0367	-0.5223	-0.0501	-0.122	-0.1573
Fruit width at maturity	0.0974	-0.4593	-0.0129	0.154	-0.3568
Total yield	-0.3988	-0.1266	0.0341	0.0302	0.1278
Total number of fruits	-0.3953	0.0463	0.0149	-0.1001	0.0514
Average number of locus per fruit	0.0635	-0.1206	-0.0662	0.5666	0.2674
Beta-carotene (mg/100g)	-0.1345	0.141	-0.4515	0.2988	-0.1299
Lycopene (mg/100g)	-0.0619	0.2032	-0.5016	0.1959	0.0276
Carotene (mg/100g)	0.0346	0.3326	0.1572	0.2267	-0.4041
Vitamin. C (mg/100g)	-0.0842	-0.2611	-0.4741	0.0959	-0.0278
PH (Acid/Base)	-0.0327	-0.1296	0.318	0.3116	-0.1116
Brix (^{0})	0.0985	0.1473	-0.2566	-0.2239	0.3278
Standard deviation	**2.3666**	**1.4835**	**1.3899**	**1.1992**	**1.0941**
Proportion of Variance	**0.2948**	**0.1158**	**0.1017**	**0.0757**	**0.063**
Cumulative Proportion	**0.2948**	**0.4106**	**0.5123**	**0.588**	**0.651**
Eigen values	**5.6008**	**2.2007**	**1.9319**	**1.4381**	**1.197**

IV: *Cluster analysis showing the relationships among tomato hybrids and their parents*

Cluster	No. of genotypes	Genotypes
I	11	006B-4, 115OT, 115OT x 30-4, 115OT x 40-4, 30-4, 30-4 x 39-7, 39-6 x 30-4, 39-7 x 14-5, 45-1 x 40-4, 54-7, G23,
II	4	115OT x 14-5,14-5 x 54-7, 38-3 x 14-5, 45-1 x G7.
III	21	115OT x 38-3, 115OT x 54-7, 115OT x G7, 14-5 x 115OT, 14-5 x G11, 14-5 x G23, 38-3 x AVTO 0102, 39-7,39-7 X AVTO 1219, 39-7 x G7, 54-7 x 39-7, 54-7 x AVTO 0102, AVTO 0102 x 54-7, AVTO 0102 x G7, G11 x 14-5, G11 x 30-4, G11 x 38-3, G11 x 54-7, G7 x 45-1, OO6B-4 x 40-4, OO6B-4 x AVTO, 1314.
IV	22	115OT x 39-7, 14-5, 38-3, 39-6 x 14-5, 40-4, 45-1, 45-1 x AVTO 1219, 54-7 x AVTO 1219, AVTO1219, AVTO1219 x 115OT, AVTO1219 x 39-7, AVTO1314, AVTO9802, G11, G23 x 14-5, G23 x 54-7, G23 x AVTO 1314, G7, G7 x AVTO 0102, G7 x OO6B-4, OO6B-4 x 30-4, OO6B-4 x G7.
V	12	38-3 x 39-6, 38-3 x G23, 39-6 x 54-7, 39-7 x 40-4, 40-4 x 115OT, 40-4 x 39-7, 40-4 x G7, AVTO 0102 x 115OT, G23 x 115OT, OO6B-4 x 54-7, ROMA VF, ROMA VF+.

at maturity correlated positively with number of marketable fruit (0.33), marketable yield (0.40) and total number of fruits (0.31) while number of branches negatively associated with number of fruit locus (-0.30) but showed moderate, positive significant association with number of marketable fruits (0.43), marketable yield (0.41), and total number of fruits (0.44). Beta carotene content had moderate significant positive correlation (0.52) with lycopene and vitamin C content (0.38). Except for brix that recorded weak negative significant correlation (-0.32) with non-marketable yield, no significant association was observed between the agronomic and nutritional variables (Tab. VI).

V: *Descriptive statistics for cluster groups among tomato genotypes*

Variable	Cluster	Min	Max	Mean	StdDev
No.C	1	2.5	5	4.09	0.86
No.C	2	5	6.5	5.62	0.63
No.C	3	3.5	7	4.79	0.85
No.C	4	2	5.5	3.61	0.96
No.C	5	2.5	5	3.88	0.71
No.Mf	1	43.5	228.5	105.59	53.09
No.Mf	2	230	389	318.62	65.9
No.Mf	3	66	231	145.74	44.86
No.Mf	4	26.5	155	91.68	34.75
No.Mf	5	20	90.5	51.5	24.67
No.NMF	1	8.5	40.5	24.95	11.6
No.NMF	2	46	59.5	53.25	6.54
No.NMF	3	21.5	59.5	38.05	12.2
No.NMF	4	4.5	43.5	25.99	9.12
No.NMF	5	10.5	32	18.67	6.78
MY	1	940	3006.5	1845.27	689.52
MY	2	3791	6059.5	5093.88	1117.98
MY	3	970.5	4944.5	2659.67	970.47
MY	4	853	3382	1894.53	720.45
MY	5	343	1761.5	901.71	463.7
FL	1	28.24	51.96	36.24	7.32
FL	2	31.15	41.04	37.38	4.44
FL	3	28.09	53.35	38.57	6.57
FL	4	35.03	83.4	49.7	13.8
FL	5	15.95	50.55	34.45	8.06
FW	1	32.4	55.74	39.86	7.28
FW	2	30.77	41.04	36.84	4.45
FW	3	29.29	46.55	37.97	5.69
FW	4	28.4	69.43	48.5	9.22
FW	5	17.25	45.91	35.98	7.5
T.YLD	1	1078.5	3625.5	2222.91	879.85
T.YLD	2	4389.5	7057.5	5927.88	1249.06
T.YLD	3	1806	5896	3282.52	1021.67
T.YLD	4	1165	3858	2404.95	807.14
T.YLD	5	453	2115	1161.21	578.87
T.NoF	1	54	269	130.55	61.49
T.NoF	2	276	438.5	371.88	68.55
T.NoF	3	121	252.5	183.79	42.54
T.NoF	4	42.5	198.5	117.67	40.3
T.NoF	5	34.5	122.5	70.17	29.92
Beta.C	1	1.14	1.74	1.47	0.19
Beta.C	2	0.5	1.6	1.1	0.48
Beta.C	3	0.56	1.76	1.09	0.3
Beta.C	4	0.51	1.44	0.97	0.26
Beta.C	5	0.49	1.01	0.84	0.14
Lycopene	1	0.79	2.02	1.61	0.44
Lycopene	2	0.72	1.82	1.08	0.5
Lycopene	3	0.85	1.41	1.05	0.14
Lycopene	4	0.7	1.22	0.96	0.17
Lycopene	5	0.83	1.24	0.96	0.12
T.Caro	1	1.36	1.94	1.63	0.18
T.Caro	2	1.38	1.88	1.64	0.22
T.Caro	3	1.14	1.99	1.69	0.25
T.Caro	4	1.13	2.45	1.48	0.29
T.Caro	5	1.56	1.93	1.77	0.12
Vit.C	1	0.32	0.36	0.34	0.01
Vit.C	2	0.27	0.35	0.3	0.04
Vit.C	3	0.01	0.34	0.2	0.12
Vit.C	4	0.17	0.34	0.3	0.04
Vit.C	5	0.02	0.29	0.18	0.11
PHL	1	3.1	4.61	3.91	0.53
PHL	2	3.8	4.8	4.28	0.41
PHL	3	3.85	4.41	4.21	0.14
PHL	4	3.57	4.77	4.25	0.25
PHL	5	3.9	4.3	4.13	0.14

No. C = Number of clusters; No. MF = Number of marketable fruits; No. NMF = Number of non-marketable fruits; MY = Marketable Yield; NMY = Non-marketable yield; FL = Fruit Length; FWD = Fruit width at maturity; TYLD = Total yield; T. NoF = Total number of fruits; NoL = average number of locus per fruit; Beta. C = β-carotene; Lyco = Lycopene content; T. caro = Total carotene; Vit. C = Vitamin C; PhL = Acid base level

VI: *Phenotypic correlation for quantitative traits among 70 tomato genotypes*

Traits	DTF	PH	NB	No.C	No.Mf	No.NMF.	MY	NMY	FL	FW	T.YLD	T.NoF	NoL	Beta.C	Lycopene	T.Caro	vit.C	PHL
PH	-0.1707																	
NB	-0.2245	0.2395																
No.C	-0.264*	0.0352	0.1445															
No.Mf	-0.3081	0.3317*	0.4346**	0.3556*														
No.NMF.	-0.2447	0.0621	0.2974	0.3977**	0.6176													
MY	-0.2994	0.3945**	0.4108**	0.3517*	0.8766**	0.6174**												
NMY	-0.0872	0.142	0.2362*	0.2587*	0.3802*	0.7573**	0.5971**											
FL	0.1772	0.0561	0.086	-0.3422*	-0.0775	-0.0751	0.0031	0.0717										
FW	-0.0336	-0.0539	0.0098	-0.2061	-0.3002*	-0.2199	-0.1571	0.1027	0.553**									
T.YLD	-0.2792	0.3729	0.4046**	0.3568*	0.8405**	0.6824**	0.989**	0.7094**	0.016	-0.119								
T.NoF	-0.3145	0.3054*	0.4357**	0.382*	0.9915**	0.7145**	0.8818**	0.4632*	-0.0813	-0.3033*	0.8603**							
NoL	0.0661	-0.0441	-0.3001*	-0.2033	-0.1769	-0.1117	-0.0613	0.1307	-0.0168	0.1453	-0.0297	-0.1758						
Beta.C	-0.2811	0.1	0.0779	0.2082	0.2232	0.2133	0.2291	0.0534	-0.0802	-0.0908	0.2111	0.2338	0.0339					
Lycopene	-0.1463	-0.0134	0.1069	0.0461	0.0946	0.0415	0.0651	0.0223	-0.2026	-0.1346	0.0613	0.091	0.0708	0.5173**				
T.Caro	-0.0777	-0.1223	-0.0317	0.2368	-0.0167	0.0265	-0.2003	-0.1857	-0.2138	-0.1483	-0.2103	-0.0105	0.0606	0.0412	0.0197			
vit.C	-0.0712	0.2484	0.0748	-0.2109	0.1748	-0.0004	0.2135	0.0931	0.2488	0.1547	0.2048	0.1555	0.0923	0.3765*	0.2605*	-0.204		
PHL	0.0472	0.0686	-0.1423	0.126	0.0247	0.0302	0.1245	0.1726	0.0222	0.1525	0.1412	0.027	0.056	0.0164	-0.289	0.0548	-0.1004	
Brix	0.1206	-0.1812	-0.0085	-0.0532	-0.1431	-0.2232	-0.1657	-0.3148*	-0.079	-0.0956	-0.2038	-0.1641	-0.0098	0.1339	0.0925	-0.1463	0.0014	-0.1371

DTF = Days to 50% flowering; PH = Plant height at maturity; NB = Number of branches; No. C = Number of clusters; No. MF = Number of marketable fruits; No. NMF = Number of non-marketable fruits; MY = Marketable Yield; NMY = Non-marketable yield; FL = Fruit Length; FWD = Fruit width at maturity; TYLD = Total yield; T. NoF = Total number of fruits; NoL = average number of locus per fruit; Beta. C = β-carotene; Lyco = Lycopene content; T. caro = Total carotene; Vit. C = Vitamin C; PhL = Acid bae level; ** Significant at $P \leq 0.01$; * Significant at $P < 0.05$

DISCUSSION

The wide range recorded for percentage occurrence of observations for most qualitative traits considered in this study showed clear distinction among the tomato genotypes thereby indicating availability of sufficient phenotypic variation for possible selection and advancement. This agrees with Tembe *et al.* (2018) on the wide phenotypic variability of tomato crop. Fruit colour at maturity and depression at peduncle end might be promising qualitative traits for identifying genotypes in this population. Fruit quality traits, yield and yield contributing traits are important parameters in tomato genetic improvement programmes. Moreover, nutritional traits such as lycopene, vitamin C and beta carotene are imperative in daily healthy lives of millions of children and adults while high yield tomato varieties with desired fruit attributes corresponds to higher market returns to farmers in the sub-Sahara region. Wide range of significant variability was recorded for days to flowering, average number of branches, number of marketable fruits, marketable yield, fruit length, fruit width, total yield and all the nutritional parameters considered in this study. This agrees with EL-Mansy, 2021 who reported a wide range of diversity for most vegetative, fruit, yield and yield components related traits among six tomato genotypes evaluated in Egypt. Furthermore, the reports of Tembe *et al.* (2019) on observed significant variation in days to maturity, number of fruits per plant and average fruit weight among tomato accessions are consistent with the results of this report.

The results of our study revealed a wide range of diversity for vegetative, fruit, yield and yield contributing traits in this population. Significant variations observed for most characters shows the feasibility of identifying cross combinations with diverse traits suitable for selection and advancement of promising segregants. The wide range of variation may be attributed to divergent genotypes and different cross combinations deployed in this study. This agrees with the reports of Dar RA *et al.* (2012) and Patil *et al.* (2013) on the high variability of agronomic traits in tomato.

Even though this report is not for combining ability of the parents, the hybrids outperformed the parents for most considered traits in this study except for number of fruits per cluster, fruit length, average number of fruit lobes, vitamin C content and brix establishing the feasibility of hybrid variety development using parents from this study. To develop tomato inbreds with increased beta carotene, vitamin C and high lycopene content, advancing materials from cluster I should be considered while progenies originating from cluster II would probably produce promising segregants with increased yield and associated high yield contributing traits. However, advancing families from clusters IV and V will create genotypes with bigger fruit shapes and size.

Association among traits is an important attribute in most breeding programmes since selection of traits depends on their association with yield and other yield related traits of interest. Yield is a complex trait and is related to other traits. The positive, moderate to strong significant association between yield and yield related traits observed in this study is in agreement with the reports of Hassan *et al.* (2021) who observed strong relationship between fruit yield and yield related traits. Thus, selection in favour of genotypes and hybrid combinations with increased number of branches, number of marketable fruits and number of marketable yield might lead to indirect selection of genotypes with increased total yield per plot. For the nutritional traits, selecting genotypes with high beta carotene content might simultaneously lead to increase in the frequency of genotypes with high lycopene and vitamin C content in this population. Increasing the frequency of alleles for fruit size might favour selection of tomato genotypes with reduced fruit yield while selecting tall plants might favour tomato genotypes with high yield potential in this population. This result is not in agreement with the findings of Tembe *et al.* (2018) who reported that tomato genotypes with increased fruit size tend to have higher yields compared to those with smaller fruits. However, this contradicts the submissions of Shafiul Islam *et al.* (2022) on the poor yield performance of tomato plants with tall plant architecture. The non-significant association between yield and nutritional values indicates that selection in favour of yield and yield related traits might reduce the frequency of genes associated with improved nutritional content in this population.

Adequate knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is important towards predicting the amount and nature of variation available in a given population in a breeding programme. High PCV and GCV recorded for most traits in the present study is an indication of high variability among the traits and possibility of improvement through selection. This supports the reports of Meena *et al.* (2015) and Shafiul Islam *et al.* (2022) on high PCV and GCV in tomato as reported for most of the considered traits in this study. The low PCV and GCV recorded for days to flowering is an indication of low variability among the genotypes for this trait while moderate PCV and GCV for pH level implies that the expression of this trait is equally influenced by additive and non-additive gene action. This is in agreement with Bhuiyan *et al.* (2016) who reported low PCV and GCV for days to flowering in tomato but contradicts their submission on moderate PCV and GCV for plant height and fruit diameter. The narrow difference between PCV and GCV for all the nutritional parameters shows that they are not easily influenced by the environment which is an indication of their high heritable nature. However, the wider PCV and GCV values obtained for most

of the agronomic traits suggests the dominant role of non-additive genes in expression of these traits. Similar reports have been made by Narolia (2012) and Bhuiyan *et al.* (2016) in tomato while the findings of this study are in contrast with earlier submission by Farzaneh *et al.* (2013) on the narrow GCV and PCV values observed for agronomic traits in tomato.

Heritability determines the extent to which variability of a character is transmitted to the next generation whereas genotypic coefficient of variation estimates total genetic variation according to Falconer (1960). Understanding the estimates of heritability along with GCV is a reliable indicator of expected genetic gain through selection in a breeding programme. The high estimates of heritability in the broad sense (> 0.90) observed for most traits in this study implies that expression of these traits are under genetic control thereby indicating the feasibility of selections based on observable traits. The results are in line with Kumar (2010) who reported high heritability in the broad sense for days to flowering, average fruit weight, average number of fruits and nutritional parameters but contradicts the work of Meena *et al.* (2015) who reported high heritability estimates for plant height in tomato. The high heritability values in combination with wide range of phenotypic variability observed for yield, yield contributing traits and nutritional traits indicates the feasibility of genetic gain by deploying these genotypes in breeding programmes targeting improvement of these traits. The high genetic advance as a percentage of mean (GAM) recorded for most traits except for days to 50 % flowering, number of branches, number of non-marketable fruits, non-marketable yield, fruit width and pH level shows that these traits are under additive gene control indicating the feasibility of improving these traits through selection. This agrees with earlier reports by Meena *et al*., (2015) and Kumar *et al.* (2013) on high GAM for yield, yield contributing traits and nutritional variables in tomato. Traits with strong correlation, high heritability and GAM are likely to spring higher genetic gain in subsequent generation in a genetic improvement programme (Sharmin *et al*., 2019; Hassan *et al*., 2021).

CONCLUSION

High heritability and genetic advance as a percentage of mean (GAM) for yield and most nutritional traits was observed in this study suggesting the possibility of selecting promising genotypes with desired trait combinations. Selecting top performing hybrid combinations and genotypes for traits with high heritability and genetic advance as a percentage of mean coupled with strong correlation might lead to higher genetic gain for improvement of desired traits in later generation in this population. Furthermore, we recommend hybridization of tomato hybrids from clusters I and II to create elite promising progenies combining high yield potentials and enhanced nutritional fruit qualities.

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APPENDIX

Appendix I: *Status and source of 70 evaluated tomato genotypes*

S/N	Genotypes	Parent/Hybrids	Status	
1	006B-4	Parent	Purified landrace	Nigeria
2	115OT	Parent	Purified landrace	Nigeria
3	115OT x 14-5	Hybrid	F1	Nigeria
4	115OT x 30-4	Hybrid	F1	Nigeria
5	115OT x 38-3	Hybrid	F1	Nigeria
6	115OT x 39-7	Hybrid	F1	Nigeria
7	115OT x 40-4	Hybrid	F1	Nigeria
8	115OT x 54-7	Hybrid	F1	Nigeria
9	115OT x G7	Hybrid	F1	Nigeria
10	14–5	Parent	Purified landrace	Nigeria
11	14-5 x 115OT	Hybrid	F1	Nigeria
12	14-5 x 54-7	Hybrid	F1	Nigeria
13	14-5 x G11	Hybrid	F1	Nigeria
14	14-5 x G23	Hybrid	F1	Nigeria
15	30–4	Parent	Purified landrace	Nigeria
16	30-4 x 39-7	Hybrid	F1	Nigeria
17	38-3	Parent	Purified landrace	Nigeria
18	38-3 x 14-5	Hybrid	F1	Nigeria
19	38-3 x 39-6	Hybrid	F1	Nigeria
20	38-3 x AVTO 0102	Hybrid	F1	Nigeria
21	39-6 x 14-5	Hybrid	F1	Nigeria
22	39-6 x 30-4	Hybrid	F1	Nigeria
23	39-6 x 54-7	Hybrid	F1	Nigeria
24	39-7	Parent	Purified landrace	Nigeria
25	39-7 x 14-5	Hybrid	F1	Nigeria
26	39-7 X AVTO 1219	Hybrid	F1	Nigeria
27	39-7 x G7	Hybrid	F1	Nigeria
28	40-4	Parent	Purified landrace	Nigeria
29	40-4 x 115OT	Hybrid	F1	Nigeria
30	40-4 x 39-7	Hybrid	F1	Nigeria
31	40-4 x G7	Hybrid	F1	Nigeria
32	45-1	Hybrid	Purified landrace	Nigeria
33	45-1 x 40-4	Hybrid	F1	Nigeria
34	45-1 x AVTO 1219	Hybrid	F1	Nigeria
35	45-1 x G7	Hybrid	F1	Nigeria
36	54-7	Parent	Purified landrace	Nigeria
37	54-7 x 39-7	Hybrid	F1	Nigeria
38	54-7 x AVTO 0102	Hybrid	F1	Nigeria
39	54-7 x AVTO 1219	Hybrid	F1	Nigeria
40	AVTO 0102 x 115OT	Hybrid	F1	Nigeria

S/N	Genotypes	Parent/Hybrids	Status	
41	AVTO 0102 x 54-7	Hybrid	Hybrid variety	Nigeria
42	AVTO 0102 x G7	Hybrid	F1	Nigeria
43	AVTO1219	Parent	Purified landrace	AVRDC
44	AVTO1219 x 115OT	Hybrid	F1	Nigeria
45	AVTO1219 x 39-7	Hybrid	F1	Nigeria
46	AVTO1314	Parent	Elite breeding line	AVRDC
47	AVTO9802	Parent	Elite breeding line	AVRDC
48	CHIBILI	Commercial Check	Hybrid variety	Seed store
49	COBRA26	Commercial Check	Hybrid variety	Seed store
50	G11	Parent	Purified landrace	Nigeria
51	G11 x 14-5	Hybrid	F1	Nigeria
52	G11 x 30-4	Hybrid	F1	Nigeria
53	G11 x 38-3	Hybrid	F1	Nigeria
54	G11 x 54-7	Hybrid	F1	Nigeria
55	G23	Hybrid	Purified landrace	Nigeria
56	G23 x 115OT	Hybrid	F1	Nigeria
57	G23 x 14-5	Hybrid	F1	Nigeria
58	G23 x 54-7	Hybrid	F1	Nigeria
59	G23 x AVTO 1314	Hybrid	F1	Nigeria
60	G7	Parent	Purified landrace	Nigeria
61	G7 x 45-1	Hybrid	F1	Nigeria
62	G7 x AVTO 0102	Hybrid	F1	Nigeria
63	G7 x OO6B-4	Hybrid	F1	Nigeria
64	OO6B-4 x 30-4	Hybrid	F1	Nigeria
65	OO6B-4 x 40-4	Hybrid	F1	Nigeria
66	OO6B-4 x 54-7	Hybrid	F1	Nigeria
67	OO6B-4 x AVTO 1314	Hybrid	F1	Nigeria
68	OO6B-4 x G7	Hybrid	F1	Nigeria
69	ROMA VF	Commercial Check	OPV	Seed store
70	ROMAVF+	Commercial Check	OPV	Seed store

AVRDC = World vegetable Center; OPV = Open pollinated variety