DE GRUYTER OPEN
DOI: 10.2478/ats-2018-0008 AGRICULTURA TROPICA ET SUBTROPICA, 51/2, 71–82, 2018

Original Research Article

Exploring morphological variation in tomato (*Solanum lycopersicum)*: A combined study of disease resistance, genetic divergence and association of characters

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Abstract

Genetic variation of quantitative traits is a prevalent characteristic among cultivated tomato varieties. Twenty tomato genotypes comprising indigenous varieties and commercial cultivars, cultured in the Western Region of Cameroon were evaluated using fourteen quantitative traits for disease resistance, phenotypic divergence and heritability estimates. The experiment was carried out using a randomized completed blocks design with three replications. Data collections were disease characteristics, plant development features and yield attributes. The analysis of variance revealed significant variation among genotypes for all the experimental quantitative traits. Hybrid varieties had significantly more fruit yield (1066.00 g/plant), single fruit weight (57.28 g), fruit diameter (4.47 cm) and pericarp thickness (0.54 cm) compared to standard and indigenous varieties. These indigenous varieties were significantly more resistant to late blight, alternaria leaf spot and viral diseases. They also had significantly higher collar diameter (16.30 mm), number of primary branches per plant (8.45), number of fruit per plant (31.58) and plant height (88.33 cm) compared to standard and hybrid plants. The genotype local 2 was the third most productive (1576.39 g/plant) after Rio Semagri (1984.80 g/plant) and Sakato F1 (1691.69 g/plant). Heritability and genetic advance estimates were high for twelve of the fourteen studied quantitative traits. Fruit yield showed significant positive correlations with single fruit weight and number of fruit per plant. However, significant negative correlation was found between fruit yield and time to 50% flowering, 50% fruiting, 50% maturity and viral disease. The first three and the first four components in the principal component analysis explained, respectively, 77.85% and 88.38% of the total variation observed among genotypes. The first component determined 41.42% of the total variation, dominated by the collar diameter, the number of primary branches per plant and plant height. This study clearly indicated that indigenous varieties are the most disease resistant genotypes and are having substantial fruit yield (945.30 g/plant) similar to standard varieties and at a touching distance to hybrid cultivars.

Keywords: Disease resistance; genetic divergence; indigenous genotypes; quantitative traits; germplasm; *Solanum lycopersicum.*

INTRODUCTION

Tomato (*Solanum lycopersicum*) is a diploid plant species (2n = 24) native of South America (Tasisa et al., 2012). This plant is among the most important vegetable crop species in the world. It is cultivated worldwide over on around 4.8 million hectares area with an annual production of around 162 million tons in 2012 (FAOSTAT, 2014). Tomato fruit contains abundant and well balanced nutritional values consisting of minerals, vitamins, fibres, citric acid, beta-carotene and ascorbic acid (Thapa et al., 2014). These important nutritional values coupled withthe rapid degradation of fruits have made tomato a significant crop in the postharvest industry (Kumar et al., 2010). Because of the commercial importance of tomato, there is greatest need to develop new varieties with higher yield and disease resistance characteristics. For achieving this, plant breeders should rely on genetically diverse parents as broad genetic diversity plays an important role in breeding vegetables. Diseases in tomato are the source of significant yield loss. Three main diseases of

the tomato plant include late blight, alternaria and viral diseases (Culbreath et al., 2003; Bost, 2013). Late blight, transmitted by *Phytophthora infestans* is characterized by water-soaked lesions appearing on leaves that enlarge and form irregular and greenish-black marks (Bost, 2013). Alternaria disease is caused by *Alternaria solani* with the main symptoms being leaves turning yellow with concentric rings drying up (Bost, 2013). Plants infected with tomato virus show foliar symptoms of ringspots, leaf necrosis and chlorosis (Culbreath et al., 2003).

Estimating the genetic variability available in a crop collection is central for the genetic improvement of the crop. Moreover, analyzing interrelation among characters helps in selecting important yield contributing traits. Genetic evaluation of germplasm assists in interpreting the genetic background of a crop. As a plant breeder is interested in specific traits for the improvement program, he will use a much less diverse gene pool than the overall available, with local germplasm known to contribute significantly to the genetic variation (Zeven, 1998; Joshi et al., 2012). Genetic improvement of cultivated tomato for yield and quality can normally be achieved through selection of genotypes with desirable character combinations that may exist in nature or by hybridization. Therefore, the information in a collection of tomato genotypes can help formulating a sound breeding plan for its improvement (Narolia and Reddy, 2010).

Tanksley and McCouch (1997) stated that breeding efforts would remain unsuccessful and crops may lack important traits such as resistance if there is lack of genetic variation. Zamir (2001) added that wild germplasm constitutes potential valuable source of genes for crop improvement. Commercial and exotic varieties elaborated through breeding programs have greatly benefited from the use of indigenous and wild plant. For example, disease resistance that appears in some modern tomato varieties originated from wild plant according to Rick and Chetelat (1995). Despite the large cultivation of commercial varieties mostly because of trade, some farmers continue to cultivate indigenous tomato varieties for their local consumption. This important cultivation of commercial varieties contributes significantly to the vanishing of many landrace, narrowing therefore the gene pool of the crop. Indigenous genotypes are known to exhibit considerable amount of genetic variation and are highly used in plant breeding programs (Terzopoulos and Bebeli, 2008).

The use of morphological markers and agronomic traits has been extensively applied in studying genetic variation in plants. Compared to molecular markers and biochemical methods, morphological markers are very easy, more direct and less costly (Bernousi, 2011). Estimation of genetic diversity in tomato has been carried out by many researchers in the world using morphological approaches (Hu et al., 2012; Chernet et al., 2014; Osekita and Ademiluyi, 2014; Sacco et al., 2015). The objectives of this study were to: (1) assess the genetic variation of quantitative traits in commercial and indigenous

Table 1. List of genotypes of cultivated tomato (*Solanum lycopersicum*) used for the study

No	Genotype	Type	Origin/area of collection
1	Lindo F1	Hybrid	Commercial shop, west region, Cameroon
2	Cobra F1	Hybrid	Commercial shop, west region, Cameroon
3	Nadira F1	Hybrid	Commercial shop, west region, Cameroon
4	Rio de GrenierF1	Hybrid	Commercial shop, west region, Cameroon
5	Topspin F1	Hybrid	Commercial shop, west region, Cameroon
6	Sakato F1	Hybrid	Commercial shop, west region, Cameroon
7	Griffaton	Standard	Commercial shop, west region, Cameroon
8	Maxi Rio	Standard	Commercial shop, west region, Cameroon
9	Rio Semagri	Standard	Commercial shop, west region, Cameroon
10	Rio Master	Standard	Commercial shop, west region, Cameroon
11	Tomateronde	Standard	Commercial shop, west region, Cameroon
12	Vikima	Standard	Commercial shop, west region, Cameroon
13	Raishakti	Standard	Commercial shop, west region, Cameroon
14	Top Seed	Standard	Commercial shop, west region, Cameroon
15	Roma Savanna	Standard	Commercial shop, west region, Cameroon
16	Roma Rossol	Standard	Commercial shop, west region, Cameroon
17	Local 1	Indigenous	Bafou, west region, Cameroon
18	Local 2	Indigenous	Bafou, west region, Cameroon
19	Local 3	Indigenous	Dschang, west region, Cameroon
20	Local 4	Indigenous	Baham, west region, Cameroon

tomato genotypes, (2) highlight the characteristics of indigenous tomato genotypes compared to standard and hybrid commercial genotypes and (3) determine the significance of characters associations, especially for traits related to fruit yield.

MATERIAL AND METHODS

Plant material and study site

A total of 20 cultivated tomato genotypes comprising commercial and indigenous seeds, cultivated in the western region of Cameroon were used for the study. The details of the tomato planting material are shown in Table 1. The study was carried out at the Research and Teaching Farm of the Faculty of Agronomy and Agricultural Sciences of the University of Dschang, located in the West Region of Cameroon at latitude of 5°20′ North and longitude of 10°05′ East, and 1407 m above the sea level. The annual rainfall of the study site ranges from 1800 to 2000 mm with the average annual temperature around 20.50 °C and a relative humidity of about 76.8 %.

Experimental methodology

The tomato seeds were first raised in the nursery and were transplanted to the field after four weeks. The treatments were arranged in a randomized complete block design with three replicates. Each block consisted of twenty experimental units of 200 cm × 250 cm area each. Each experimental unit contained 20 individuals arranged in four rows of five plants each. The distance between adjacent plants within and between rows was 50 cm, giving a density of 40,000 plant/ha. Each experimental unit was separated from the next by 100 cm. The genotypes were randomized within the replicates using table of random numbers. Agronomic practices consisting of weeding were carried out to provide plants with adequate growth conditions. Ten plants were sampled for each experimental unit for quantitative traits analysis. A total of thirty plants for each genotype were subjected to data collection.

Phenotypic data collection

Phenotypic data collection consisted of disease characteristics, plant development features and yield attributes. A total of fourteen quantitative traits were recorded. Traits relative to plant development and yield are consigned in the descriptor list for tomato (IPGRI, 1996). For disease resistance, each plant was assessed for typical symptoms of late blight, alternaria leaf spot and viral diseases. Late blight is characterized by leaves with large, dark brown blotches with a green grey

Table 2. List of quantitative traits and their descriptions

N°	Quantitative trait	Description
1	Collar diameter (mm)	Mean collar diameter of ten selected plant at six weeks from transplanting
2	Primary branches / plant (No)	Mean number of primary branches per plant of ten selected plants in each replicates
3	Plant height (cm)	Mean height of ten selected plant at six weeks from transplanting
4	Single fruit weight (g)	Mean weight of one fruit per plant in ten selected plants in each replicates at harvest
5	Fruit diameter (cm)	Mean fruit diameter of one fruit per plant in ten selected plants in each replicates at harvest
6	Pericarp thickness (cm)	Mean pericarp thickness of one fruit per plant in ten selected plants in each replicates at harvest
7	50% Flowering (days)	Number of days from transplanting to flower appearance in 50% of plant in each replicates
8	50% Fruiting (days)	Number of days from transplanting to appearance of fruit in 50% of plants in each replicates
9	50% Maturity (days)	Number of days from transplanting to physiological maturity of fruits in 50% of plants in each replicates
10	Late blight (%)	Ratio of the surface area of infected leaves by *Phytophthora infestans* over the total area of leaf considered
11	Viral diseases (%)	Ratio of the surface area of infected leaves by tomato virus over the total area of leaves considered
12	Alternaria leaf spot (%)	Ratio of the surface area of infected leaves by *Alternaria solani* over the total area of leaves considered
13	Fruit/plant (No)	Total number of fruit per plant counted at the time of harvest
14	Fruit yield (g/plant)	Total weight of all the fruits per plant of ten selected plants in each replicates at harvest

edge; disease usually start at the top part of the plant; infections progress through leaflets and petioles, resulting in large sections of dry brown foliage. Under humid conditions, lesions become brown and pathogen sporulation can be seen. It is the most destructive disease of tomato. Alternaria develops in form of leaf spots with concentric rings with leaf spots and the lower leaves turning yellow. These two fungal diseases cause damage to the leaves, stems and fruit of the plant. The most frequent viral diseases of tomato were: Tomato Mosaic Virus (attack leaves show mottling, with alternating yellowish and darker green areas, the latter often appearing thicker and raised giving a blister-like appearance), Yellow Leaf Curl Virus (characterized by thickening of the shoots and reduced size of leaflets) and Cucumber Mosaic Virus (characterized by the shoestring symptoms on the leaves). The severity of each of these diseases was consecutively recorded by visual observation every two days for one month. It was defined as the percentage of foliage with symptoms on a scale ranging from 0% to 100%. The measurement of the severity follows the severity characteristics used by Bock et al. (2010). Details of the different traits used in this study are presented in Table 2.

Statistical analysis

Statistical analysis was performed using XLSTAT version 2014 and GraphPad Prism 6.0 computer software programs. The analysis of variance (ANOVA) was performed for each trait using the generalized linear model of GraphPad Prism computer program to test the variations among blocks and among genotypes. Genetic parameters were calculated to assess the genetic variability among genotypes and determine the genetic and environmental effects on the studied traits. Hence, the following parameters were measured for each trait: (1) mean of the trait: $\bar{X} = \Sigma x_i / n$, where x_i = value of an observation and n = number of observations, (2) genotypic variance: $\sigma^2_G = (MS_G - MS_E) / r$, with MS_G = mean square of genotypes, MG_E = mean square of error, r = number of replicates, (3) environmental variance: $\sigma^2_E = MS_E$, (4) phenotypic variance: $\sigma^2_P = \sigma^2_G + \sigma^2_E$ (5) broad sense heritability: $h^2_B = \sigma^2_G / \sigma^2_P$ (6) genotypic coefficient of variation: $GCV = 100 \times \sqrt{\sigma^2_G} / \bar{X}$ (7) phenotypic coefficient of variation: $PCV = 100 \times \sqrt{\sigma^2_P} / \bar{X}$ and (8) genetic advance as percentage of mean: $GA = k \times h^2_B \times 100 \times \sqrt{\sigma^2_P} / \bar{X}$ where k is a constant = 2.06 at 5% selection pressure. These formulations above are from Singh and Chaudhary (1977) and Fehr (1987). Pearson correlation coefficients were used to assess the relationship among the different phenotypic traits. These coefficients were computed using XLSTAT computer program. Quantitative data were exposed to principal component analysis (PCA) in order to determinate the patterns of quantitative variation with the eigenvectors and eigenvalues that were determined using the same XLSTAT program.

RESULTS

Genetic variation of quantitative traits

The most productive genotypes were Rio Semagri, Sakato F1 and Local 2 with fruit yield of 1984.80, 1691.69 and 1576.39 g/plant, respectively (Table 3). The least productive genotypes were Top seed and local 1 with seed yield of 426.48 and 492.44 g/plant, respectively (Table 3). Mean values of plant groups for the studied traits are shown in Table 4. Significant differences were found between plant groups in twelve of the fourteen studied traits. Indigenous genotypes showed significantly larger collar diameter (16.30 mm), primary branches per plant (8.45), plant height (88.33 cm) and fruit number per plant (31.58). These indigenous plants, however, had significantly lower single fruit weight (31.41 g), fruit diameter (4.05 cm), lower pericarp thickness (0.29 cm) and were in overall the most disease resistant. Hybrid genotypes however produced significantly higher fruit yield (1066.00 g/plant) compared to indigenous (945.30 g/plant) and standard (917.30 g/plant) varieties (Table 4). For the twenty considered tomato genotypes, the mean squares of the fourteen studied quantitative traits are presented in Table 5. The ANOVA results showed significant variation among tomato genotypes for all the studied traits. Significant differences were also found among blocks for eight of the fourteen studied traits. The coefficients of variation for the measured traits are presented in Table 3. High value of coefficient of variation indicates wide range of the measured trait. The highest coefficient of variation was observed in disease characteristics: Late blight (85.65%), viral disease (79.06%), Alternaria leaf spot (81.97%). The lowest coefficients of variation were found with time to 50% maturity (5.67%), fruit diameter (9.02%) and time to 50% fruiting (10.32%). Phenotypic and genotypic coefficients of variation for the studied quantitative traits are presented in Table 6. The highest values of these coefficients were recorded for disease characteristics, yield attributes and the number of primary branches per plant while the lowest values were noted for time to 50% maturity and time to 50% fruiting.

Genetic divergence and environmental influence

The phenotypic variance of a trait under study is composed of heritable (genotypic variance) and non-heritable (environmental variance) values related as follows: Phenotypic variance = Genotypic variance + Environmental variance. Phenotypic and genotypic variances of the 14 studied traits are presented in Table 6. The environmental variance was the main contributor to the phenotypic variance (total variance) for two

Table 3. Quantitative traits estimates for twenty (20) cultivated tomato genotypes

Genotype	Collar diameter (mm)	Primary branches/ plant (No)	Plant height (cm)	Single fruit weight (g)	Fruit diameter (cm)	Pericarp thickness (cm)	50% Flowering (days)	50% Fruiting (days)	50% Maturity (days)	Late blight (%)	Viral diseases (%)	Alternaria leaf spot (%)	Fruit/ plant (No)	Fruit yield (g/plant)
Lindo F1	10.40^{fgh}	3.67^{bc}	50.79^{def}	50.63^{defg}	4.27^{def}	0.55^{abcde}	22.00^{defg}	31.67^{abcd}	65.33^{def}	3.33^{c}	20.00^{a}	56.67a	11.40^{def}	573.10^{de}
Cobra F1	12.47^{cde}	4.17^{bc}	59.79^{bcd}	58.39^{cd}	4.53^{bc}	0.52^{bcde}	25.67^{cd}	30.67^{abcd}	70.33^{bcd}	5.67^{c}	3.33^{c}	13.33^{b}	20.40^{bcde}	1204.66^{bc}
Nadira F1	9.73^{h}	4.13^{bc}	45.06^{f}	43.09^{ghi}	4.19^{def}	0.50^{def}	21.67^{defg}	28.67^{d}	65.00^{def}	8.33^{bc}	0.00^{c}	18.33^{b}	22.20^{bcd}	979.83^{cd}
Rio de Grenier F1	10.23^{gh}	3.27^{c}	53.27^{def}	86.42^{a}	5.16^{a}	0.52^{bcde}	23.33^{cdef}	34.33^{abcd}	67.33^{bcdfe}	5.33^{c}	1.67^{c}	5.00^{c}	10.97^{ef}	946.09^{cde}
Topspin F1	11.63^{cdefg}	4.07^{bc}	51.36^{def}	49.02^{efgh}	4.39^{bcd}	0.54^{abcde}	22.67^{defg}	29.33^{cd}	66.67^{cdef}	5.00^{c}	8.33^{b}	18.33^{b}	20.33^{bcde}	998.81^{cd}
Sakato F1	12.60^{cd}	4.57^{bc}	65.73^{bc}	56.14^{cde}	4.29^{cdef}	0.58^{a}	21.67^{defg}	30.33^{bcd}	67.33^{bcdef}	6.67^{bc}	1.67^{c}	9.00^{bc}	29.77^{b}	1691.69^{ab}
Griffaton	11.37^{cdefg}	3.93^{bc}	55.09^{cdef}	42.00^{hi}	4.07^{fg}	0.58^{a}	21.00^{defg}	32.00^{abcd}	69.00^{bcde}	10.00^{b}	13.33^{b}	21.67^{b}	21.73^{bcde}	923.94^{cde}
Maxi Rio	12.87^{c}	5.03^{b}	58.37^{bcde}	71.23^{b}	5.32^{a}	0.45^{f}	19.67^{efg}	27.33^{d}	62.33^{f}	6.00^{c}	5.00^{c}	8.33^{bc}	17.73^{cdef}	1236.89^{bc}
Rio Semagri	10.90^{efgh}	4.13^{bc}	57.15^{bcde}	62.62^{c}	4.58^{b}	0.53^{abcde}	17.67^{g}	29.67^{cd}	63.67^{ef}	10.00^{b}	3.33^{c}	5.00^{c}	31.27^{b}	1984.80^{a}
Rio Master	10.30^{gh}	3.10^{c}	47.93^{ef}	44.46^{fghi}	4.06^{fg}	0.56^{abc}	34.67^{a}	39.33^{ab}	73.00^{abc}	7.00^{bc}	8.33^{b}	6.67^{c}	13.10^{def}	565.68^{de}
Tomateronde	10.07^{gh}	3.70^{bc}	45.80^{f}	38.44^{ijk}	4.10^{efg}	0.50^{cdef}	21.00^{defg}	31.33^{abcd}	65.67^{def}	2.67^{c}	10.33^{b}	16.67^{b}	22.40^{bcd}	855.80^{cde}
Vikima	11.23^{defgh}	3.90^{bc}	50.95^{def}	39.71^{ij}	3.90^{gh}	0.50^{ef}	28.33^{bc}	34.33^{abcd}	73.00^{abc}	15.67^{ab}	11.67^{b}	15.00^{b}	14.97^{cdef}	593.90^{de}
Raishakti	11.97^{cdef}	5.00^{b}	67.36^{b}	52.16^{def}	4.25^{def}	0.55^{abcd}	28.67^{bc}	32.33^{abcd}	69.33^{bcde}	16.67^{ab}	5.00^{c}	15.00^{b}	14.90^{cdef}	736.47^{cde}
Top Seed	10.37^{fgh}	3.23^{c}	47.25^{ef}	46.36^{fghi}	4.13^{efg}	0.51^{cde}	34.33^{a}	39.67^{a}	77.33^{a}	23.33^{a}	16.67^{ab}	10.00^{b}	9.17^{f}	426.48^{e}
Roma Savana	12.07^{cde}	4.93^{b}	48.20^{ef}	29.83^{l}	4.04^{fg}	0.50^{def}	31.67^{ab}	38.33^{abc}	73.33^{ab}	4.00^{c}	6.67^{cd}	10.00^{b}	22.43^{bcd}	641.31^{de}
Roma Rossol	11.00^{defgh}	5.00^{b}	57.17^{bcde}	49.62^{efgh}	4.08^{fg}	0.52^{cde}	25.33^{cd}	32.33^{abcd}	68.33^{bcdef}	10.00^{b}	10.00^{b}	11.67^{b}	24.40^{bc}	1207.50^{bc}
Local 1	17.57^{a}	8.97^{a}	89.13^{a}	32.49^{jkl}	4.35^{bcde}	0.22^{i}	23.67^{cde}	30.67^{abcd}	63.67^{ef}	0.33^{c}	1.67^{c}	5.67^{c}	15.07^{cdef}	492.44^{de}
Local 2	14.60^{b}	8.13^{a}	88.32^{a}	30.88kl	3.74^{h}	0.37^{g}	18.00^{fg}	34.00^{abcd}	68.67^{bcdef}	0.33^{c}	5.00^{c}	11.00^{b}	51.53^{a}	1576.39^{ab}
Local 3	16.01^{ab}	8.58^{a}	88.69^{a}	31.71^{jkl}	4.01^{fg}	0.29^{h}	20.59^{defg}	32.03^{abcd}	64.26^{def}	0.30^{c}	3.27^{c}	8.35^{bc}	33.27^{b}	1017.00^{cd}
Local 4	17.03^{a}	8.12^{a}	87.16^{a}	30.55^{kl}	4.08^{fg}	0.28^{h}	18.00^{fg}	32.67^{abcd}	67.17^{bcdef}	0.35^{c}	2.02^{c}	7.67^{c}	26.45^{bc}	695.28^{cde}
Minimum	9.73	3.10	45.06	29.83	3.74	0.22	17.67	27.33	62.33	0.30	0.00	5.00	9.17	426.50
Maximum	17.57	8.97	89.13	86.42	5.32	0.58	34.67	39.67	77.33	23.33	20.00	56.67	51.53	1984.80
Mean	12.22	4.98	60.73	47.29	4.28	0.48	23.98	32.55	68.04	7.05	6.87	13.67	21.67	967.40
Standard Error	0.52	0.42	3.44	3.28	0.09	0.02	1.15	0.75	0.86	1.35	1.21	2.51	2.19	93.81
Coefficient of Variation (%)	19.05	37.67	25.31	31.03	9.02	21.77	21.44	10.32	5.67	85.68	79.06	81.97	45.14	43.36

Means followed by the same letter in the same column are not significantly different at $P = 0.050$ probability level.

Table 4. Analysis of variance between cultivated tomato groups for 14 quantitative traits

Type	Collar diameter (mm)	Primary branches/ plant (No)	Plant height (cm)	Single fruit weight (g)	Fruit diameter (cm)	Pericarp thickness (cm)	50% Flowering (days)	50% Fruiting (days)	50% Maturity (days)	Late blight (%)	Viral diseases (%)	Alternaria leaf spot (%)	Fruit/plant (No)	Fruit yield (g/plant)
Indigenous	16.30±0.21^{a}	8.45±0.18^{a}	88.33±1.53^{a}	31.41±0.66^{c}	4.05±0.04^{c}	0.29±0.01^{b}	20.07±1.02^{b}	32.34±1.01^{a}	65.94±1.07^{a}	0.33±0.14^{b}	2.99±1.12^{b}	8.17±1.23^{b}	31.58±2.61^{a}	945.30±41.23^{b}
Standard	11.22±0.11^{b}	4.19±0.10^{b}	53.53±0.76^{b}	47.64±0.91^{b}	4.25±0.03^{b}	0.52±0.01^{a}	26.23±1.13^{a}	33.67±0.85^{a}	69.50±0.89^{a}	10.53±2.12^{a}	9.03±1.50^{a}	12.00±1.08^{b}	19.21±0.69^{b}	917.30±39.40^{b}
F1-Hybrid	11.18±0.15^{b}	3.98±0.16^{b}	54.33±1.03^{b}	57.28±1.21^{a}	4.47±0.03^{a}	0.54±0.01^{a}	22.84±0.42^{ab}	30.83±0.76^{a}	67.00±0.56^{a}	5.72±0.93^{a}	5.83±2.77^{ab}	20.11±4.62^{a}	19.18±0.91^{b}	1066.00±50.73^{a}
F-value	149.97	134.83	169.19	67.31	23.45	288.65	4.54	2.64	2.87	3.86	2.921	3.24	23.19	2.97
P-value	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.091	0.078	0.027	0.042	0.038	0.000	0.043
Significance	**	**	**	**	**	**	*	NS	NS	*	*	*	**	*

Mean of each genotype group represents the average of the different observations of the 3 replications. Means followed by the same letter in the same Column are not significantly different at $P = 0.050$ probability level. **: Significant at $P = 0.010$ probability level; *: Significant at $P = 0.050$ probability level; ^{NS}: Not significant

Table 5. Means squares of analysis of variance for 14 quantitative traits in cultivated tomato

		Mean square						
Source of variation	**df**	**Collar diameter (mm)**	**Primary branches / plant (No)**	**Plant height (cm)**	**Single fruit weight (g)**	**Fruit diameter (cm)**	**Pericarp thickness (cm)**	**50% Flowering (days)**
Block	2	11.45*	131.33**	222.03^{NS}	2441.72**	0.528**	0.037**	2.749^{NS}
Genotype	19	108.24***	73.39***	5019.36***	6195.35***	4.79***	0.213***	408.27***
Error	520	3.243	3.162	158.44	84.13	0.079	0.004	3.09

		Mean square						
Source of variation	**df**	**50% Fruiting (days)**	**50% Maturity (days)**	**Late blight (%)**	**Viral diseases (%)**	**Alternaria leaf spot (%)**	**Fruit/plant (No)**	**Fruit yield (g/ plant)**
Block	2	0.918*	2.978^{NS}	141.46*	153.39*	256.354^{NS}	245.01^{NS}	106695.90^{NS}
Genotype	19	37.79***	47.05***	104.55*	91.64*	408.27***	2905.86***	5760904.34***
Error	520	9.02	4.59	84.98	85.39	49.02	152.7	334222.5

df: Degree of freedom, ***: Significant at $P = 0.001$ probability level, **: Significant at $P = 0.010$ probability level; *: Significant at $P = 0.050$ probability level; ^{NS}: Not significant

Table 6. Estimates of genotypic and phenotypic variance, broad sense heritability and genetic advance for 14 quantitative traits in cultivated tomato

Quantitative trait	Mean	σ^2_G	σ^2_P	σ^2_E	GCV (%)	PCV (%)	h^2_B (%)	GA (%)
Collar diameter (mm)	12.22	35	38.24	3.24	48.41	50.61	91.52	95.41
Primary branches / plant (No)	4.98	23.41	26.57	3.16	97.12	103.47	88.1	187.78
Plant height (cm)	60.73	1620.31	1778.75	158.44	66.28	69.45	91.09	130.32
Single fruit weight (g)	47.29	2037.07	2121.2	84.13	95.44	97.39	96.03	192.67
Fruit diameter (cm)	4.28	1.57	1.65	0.08	29.3	30.03	95.21	58.89
Pericarp thickness (cm)	0.48	0.07	0.08	0.00	55.16	56.72	94.57	110.5
50% Flowering (days)	23.98	135.06	138.15	3.09	48.46	49.01	97.76	98.71
50% Fruiting (days)	32.55	9.59	18.61	9.02	9.51	13.25	51.53	14.07
50% Maturity (days)	68.04	14.15	18.74	4.59	5.53	6.36	75.51	9.9
Late blight (%)	7.05	6.52	91.5	84.98	36.23	135.7	7.13	19.93
Viral diseases (%)	6.87	2.08	87.47	85.39	21.03	136.24	2.38	6.68
Alternaria leaf spot (%)	13.67	119.75	168.77	49.02	80.05	95.03	70.95	138.91
Fruit/plant (No)	21.67	917.72	1070.42	152.7	139.8	150.98	85.73	266.65
Fruit yield (g/plant)	967.4	1808894	2143116	334222.5	139.03	151.33	84.4	263.12

σ^2_G: Genotypic variance, σ^2_P: Phenotypic variance, σ^2_E: Environmental variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2_B: Broad sense heritability, GA: Genetic advance as percentage of mean

of the fourteen studied traits. Late blight and viral disease were the two characters mostly influenced by the environment (92.87% and 97.62%, respectively) and the twelve other traits were affected by the environment by less than 50%. Broad sense heritability values in the cultivated tomato genotypes ranged from 2.38% (viral disease) to 97.76% (time to 50% flowering). Broad sense heritability was higher in general and exceeded 70% in 11 of the 14 studied traits. Single fruit weight (96.03%), time to 50% flowering (97.76%), fruit diameter (95.21%), pericarp thickness (94.57%) and plant height (91.09%) exhibited the highest broad sense heritability values. The lowest heritability values were found in late blight (7.13%) and viral disease (2.38%). Genetic advance as percentage of mean (GA) ranged from 6.68% (viral disease) to 266.65% (number of fruit par plant) (Table 6).

Characters associations and principal component analysis

Ninety one associations with their correlation coefficients were generated from the fourteen quantitative traits (Table 7). At 5% probability level, fifty six associations were found to be not correlated, seventeen associations were positively correlated and eighteen associations negatively correlated. Fruit yield was positively correlated with single fruit weight (r = 0.447) and number of fruit per plant (r = 0.689). Fruit yield was, however, negatively correlated with time to 50% fruiting (r = –0.505), time to 50% flowering (r = –0.598), time to 50% maturity (r = –0.454) and viral disease (r = –0.476). The number of fruit per plant correlated negatively with late blight (r = –0.444) and viral disease (r = –0.475). Considering all the 14 quantitative traits, the principal component analysis (PCA) was carried out. The first three and the first four component of the PCA explained, respectively, 77.85 and 88.38 % of the total variation (Table 8). The first component accounted for 41.42% of the total variation attributed to collar diameter, number of primary branches per plant, plant height, pericarp thickness, time to 50% flowering and late blight. The second component accounted for 24.03% of the total variation credited mostly to time to 50% fruiting, time to 50% maturity, fruit diameter and single fruit weight. The third component accounted for 12.41% of the total variation dominated alternaria and viral diseases. The fourth component mostly credited by yield attributes (Number of fruit per plant and fruit yield) accounted for 10.53% of the total variation.

DISCUSSION

As the magnitude of diversity and availability of plant resources are vital for crop improvement (Govindaraj et al., 2015), estimation of genetic diversity and relationships between crop germplasms is the key step (Rafalski, 2011) and the loss of genetic diversity is

Table 7. Pearson's correlation coefficients between 14 quantitative traits in cultivated *Solanum lycopersicum*

Variables	Collar diameter	Primary branches/ plant	Plant height	Single fruit weight	Fruit diameter	Pericarp thickness	50% Flowering	50% Fruiting	50% Maturity	Late blight	Viral diseases	Alternaria leaf spot	Fruit/ plant	Fruit yield
Collar diameter	1													
Primary branches / plant	0.943***	1												
Plant height	0.932***	0.943***	1											
Single fruit weight	–0.453*	–0.536*	–0.368^{NS}	1										
Fruit diameter	–0.131^{NS}	–0.250^{NS}	–0.177^{NS}	0.861***	1									
Pericarp thickness	–0.890***	–0.918***	–0.823***	0.498*	0.143^{NS}	1								
50% Flowering	–0.352^{NS}	–0.413^{NS}	–0.441^{NS}	–0.076^{NS}	–0.206^{NS}	0.332^{NS}	1							
50% Fruiting	–0.166^{NS}	–0.173^{NS}	–0.180^{NS}	–0.267^{NS}	–0.415^{NS}	0.094^{NS}	0.767***	1						
50% Maturity	–0.306^{NS}	–0.367^{NS}	–0.342^{NS}	–0.198^{NS}	–0.427^{NS}	0.334^{NS}	0.823***	0.850***	1					
Late blight	–0.538*	–0.561**	–0.490*	0.231^{NS}	–0.037^{NS}	0.535*	0.565**	0.317^{NS}	0.590**	1				
Viral diseases	–0.450*	–0.449*	–0.466*	–0.119^{NS}	–0.283^{NS}	0.393^{NS}	0.347^{NS}	0.365^{NS}	0.416^{NS}	0.498*	1			
Alternaria leaf spot	–0.321^{NS}	–0.282^{NS}	–0.296^{NS}	–0.050^{NS}	–0.145^{NS}	0.312^{NS}	–0.092^{NS}	–0.154^{NS}	–0.099^{NS}	–0.029^{NS}	0.658**	1		
Fruit/plant	0.399^{NS}	0.546*	0.545*	–0.352^{NS}	–0.364^{NS}	–0.323^{NS}	–0.582**	–0.216^{NS}	–0.266^{NS}	–0.444*	–0.475*	–0.234^{NS}	1	
Fruit yield	–0.005^{NS}	0.056^{NS}	0.163^{NS}	0.447*	0.225^{NS}	0.152^{NS}	–0.598**	–0.503*	–0.454*	–0.166^{NS}	–0.476*	–0.254^{NS}	0.689**	1

***: Significant at $P = 0.001$ probability level, **: Significant at $P = 0.010$ probability level; *: Significant at $P = 0.050$ probability level; ^{NS}: Not significant

Table 8. Eigenvectors and eigenvalues of the first four principle components for 14 quantitative traits of 20 tomato genotypes

Quantitative variables	Eigenvectors			
	PC1	PC2	PC3	PC4
Collar diameter (mm)	0.354	–0.195	–0.090	–0.198
Primary branches / plant (No)	0.374	–0.205	–0.019	–0.093
Plant height (cm)	0.364	–0.155	–0.072	–0.055
Single fruit weight (g)	–0.130	0.442	–0.252	–0.131
Fruit diameter (cm)	–0.015	0.420	–0.271	–0.379
Pericarp thickness (cm)	–0.333	0.221	0.065	0.276
50 % Flowering (days)	–0.294	–0.280	–0.272	–0.081
50 % Fruiting (days)	–0.196	–0.385	–0.218	0.088
50 % Maturity (days)	–0.265	–0.333	–0.211	0.200
Late blight (%)	–0.297	–0.036	–0.192	0.126
Viral disease (%)	–0.264	–0.142	0.428	–0.044
Alternaria leaf spot (%)	–0.127	0.040	0.669	–0.158
Fruit/plant (No)	0.283	–0.012	0.084	0.576
Fruit yield (g/plant)	0.157	0.337	–0.071	0.531
Eigenvalue	5.799	3.364	1.737	1.474
Variability (%)	41.420	24.027	12.406	10.531
Cumulative variance %	41.420	65.447	77.853	88.383

PC1: First principle component; PC2: Second principle component; PC3: Third principle component; and PC4: Four principle component.

a major danger for the survival and breeding of crop species (Olivera and Steffenson, 2009). Phenotypic data have been used to compare individual genotypes and populations of crop species with the aim of optimizing characterization, determining characters variations, associations and establishing genetic relationship within species. Variation in specific morphological traits targeted for their utility is required in tomato breeding program (Bhattarai et al., 2016). Significant variation of 14 quantitative traits in 20 tomato genotypes was documented in this study. These genotypes were selected to represent an important range of phenotypic diversity. Quantitative traits have been previously used for similar studies in tomato. As for example, Henareh et al. (2015) studied 21 quantitative traits in 97 tomato accessions from Iran and Turkey, Bernousi et al. (2011) surveyed 25 tomato genotypes with the help of 19 morphological traits; Bhattarai et al. (2016) analyzed 71 tomato genotypes with 8 morphological traits. All these studies revealed significant variation among the studied genotypes. Mean square values from the analysis of variance showed significant differences among the studied genotypes for all yield attributes, disease characteristics and growth features. Mohanty (2003), Golani et al. (2007), Bernousi et al. (2011), Henareh et al. (2015) and Bhattarai et al. (2016), also found significant differences between tomato genotypes with the help of morphological traits. Besides fruit yield, the other main objective in crop breeding remain the development of disease and pest resistances genotypes. Wild species of tomato were first used as source of adaptation to biotic stress including disease resistance (Stam et al., 2017). It is known that wild tomato plants exhibit great differences in morphological characters (Zhou et al., 2015). With important number of primary branches per plants and number of fruit per plant; with small pericarp thickness and significantly lower single fruit weight compared to hybrid and standard genotypes, Indigenous plants presented wild specifics characteristics and this likely explains the disease resistance of indigenous varieties.

Measurements of morphological traits provide a simple practice of assessing the genetic variation with simultaneous evaluation of genotypes performance under specific growing conditions although these morphological characters are generally influenced by the environment (Garcia, 1998; Fufa et al., 2005; Shuaib et al., 2007). Analysis of variance revealed significant differences among the studied genotypes for all the fourteen characters studied with essential quantitative characters such as fruit yield, number of fruit per plant and fruit weight exhibiting high coefficient of variation (43.36%, 45.14% and 31.03%, respectively). Similar results were reported by Reddy and Reddy (1992). The genotypic coefficient of variation (GCV) is seen as the real indicator of the extent of genetic variability in a population. GCV was high for all yield attributes, diseases characteristics and some growth features excluding time to 50% fruiting and time to 50% maturity. Heritability was observed high for eleven of the fourteen studied traits. High heritability associated with high genetic advance was observed in ten of the fourteen traits including fruit yield and yield attributes such as number of fruit per plant, single fruit

weight, fruit diameter and pericarp thickness. Similar observations associating high heritability and high genetic advance in yield components were reported by Vikram and Kohli (1998) with the study of twenty five tomato genotypes and Singh and Narayan (2004) with the investigation of ten tomato genotypes in India. This implies that the improvement of fruit yield, fruit weight, number of fruit per plant, fruit diameter and pericarp thickness can be achieved by simple selection process.

Although number of fruits per plant in indigenous tomatoes was higher compared to commercial hybrid genotypes, they, however, had lower yield. Similar results were reported by Agong et al. (2001) with Kenyan tomato genotypes. Fruit yield per plant showed significant positive correlation with single fruit weight. This is justified as single fruit weight looks like the fruit yield per plant at a small scale. As the number of days to 50% flowering, number of days to 50% fruiting and number of days to 50% maturity increases, fruit yield were found to be decreasing. This demonstrates that early maturing genotypes had better fruit yield. These observations were also recorded in the studies of Henareh et al. (2015) and Bhattarai et al. (2016) with the time to flowering and maturity negatively correlated with yield. This is expected as early maturing genotypes will have less exposure to tomato diseases with as consequence, a better yield resulting. A positive significant correlation was observed between single fruit weight and fruit yield, between number of fruits per plant and fruit yield per plant (Table 7). As the weight of a fruit is important and as a plant carries more fruit, it is expected to have important yield. This justifies these associations. These are in agreement with Ghosh et al. (2010) and Hidayatullah et al. (2008) who reported that fruit yield had positive and significant correlation with single fruit weight and the number of fruit per plant. Principal component analysis had been used to evaluate morphological variation and establish genetic relationship among germplasm of different plant species: as example PCA analysis was used in cowpea (Gerrano et al., 2015), tomato (Bernousi et al., 2011), and olive (Cantini et al., 1999). Results from PCA analysis showed that the first three principal components explained 77.85% of the total variation. Similar observation was reported with other studies on tomato: 71% (Bernousi et al., 2011), 71.6% (Henareh et al., 2015), 74.63% (Bhattarai et al., 2016), 78.54% (Zhou et al., 2015).

CONCLUSION

Genetic evaluation of crop germplasm is vital for the identification of potential parents and important traits of interest to be use in crop breeding. This study using fourteen quantitative traits revealed important genetic variability among the twenty genotypes of tomato cultivated in the western region of Cameroon. This important genetic variability was confirmed by genotype grouping and principal component analysis. Several significant character associations were found. Fruit yield correlated significantly with many other quantitative traits. Grouping analysis showed that indigenous genotypes are the most disease resistant and are having considerable fruit yield. The example being the genotype baptized local 2 that show an important fruit yield of 1576 g/plant. These indigenous tomato genotypes should be properly conserved; they should be promoted for cultivation and considered in tomato breeding.

Authors' contributions

EBK conceived and designed research. JRD and EBK conducted experiments, EBK and JDF interpreted the results. EBK analyzed data and wrote the manuscript. JDF reviewed the manuscript prior to submission and provided valuable comments on the presentation of results. All authors read and approved the manuscript.

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Received: January 3, 2018
Accepted after revisions: May 20, 2018