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Genetic Variability and Correlations in Rainfed Tomato (*Solanum spps.*) Accessions in Ibadan, Nigeria

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ABSTRACT

The extent of genetic variability among 19 accessions of tomato (*Solanum spp.*) was studied using genetic variability parameters as a basis for harnessing of the crop. Four weeks old seedlings were transplanted in a well levelled field with 0.6 x 0.6 spacing and replicated three times in randomized complete block design. High significant differences among the accessions for all attributes studied. Cluster analysis based on 37 agro-mophological attributes separated accessions into two distinct groups according to the fruit types i.e. cherry and classic fruit types. Values for genotypic and phenotypic coefficients of variation showed variability among the accessions. Correlation analysis showed fruit per plant is positively and significantly correlated to plant height, number of branches per plant and leaf length. Very high genetic advance and heritability estimates for leaf length, leaf width, days to flower, days to 50% flowering, number of fruits per plant, fruit length, fruit diameter, fruit weight and 1000 seed weight suggest simple inheritance system and thus amenability for these attributes to selection in tomato improvement.

INTRODUCTION

Tomato (*Solanumlycopersicon* L. *Syn. Lycopersiconesculentum*, Mill., *Lycopersiconlycopersicum*, (L.), Karsten ex Farw.), is one of the most important vegetable crops grown over the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. It is one of the most important vegetable crops grown in Nigeria and utilized in almost every household for preparation of several dishes. Tomato plays an important role in human nutrition by providing essential amino acids, vitamins and minerals (Sainju *et al.,* 2003). Its vitamin C content is particularly high (Kanyomeka and Shivute, 2005). It also contains lycopene, a very potent antioxidant that may be an important contributor to prevention of cancers (Agarwal and Rao, 2000).With production of over 150 million tons of fresh fruit on 3.7 million hectares tomato exceeds the production of all other crops, with the exception of the potato (*Solanumtuberosum*) and sweet potato (*Ipomea batatas*) (FAOSTAT, 2010). Production in Nigeria has more than doubled in the last 10 years with the production in 2001, amounting to about 879,000 tonnes (Akanbi and Oludemi, 2003). However, commercial tomato production in Nigeria relies mostly on exotic introductions. The production of which is essentially restricted to the Northern Guinea Savanna and the Sudan ecologies due to favourable climatic conditions, particularly high insolation and low relative humidity. In nearly three decades, no tomato variety has been released in Nigeria (NACGRAB and NASC, 2013). The need therefore, to explore the production capabilities and potentials of long forgotten indigenous land races and other ecotypes has never been more urgent.

The concept of heritability which specifies the proportion of the total variation among a species due to genetic components combined with genetic advance are good parameters for determining gene action involved in the inheritance of any trait and by extension help in deciding the best breeding method to apply for improving such trait. High heritability indicates less environmental influence in the observed variation (Songsri *et al*., 2008; Eid, 2009), while high heritability accompanied by high genetic advance is an indication of additive gene action for such trait, making it most amenable to selection (Tazeen *et al*., 2009). Determining the variability of yield and yield related components will enable the plant researcher to deduce the extent of environmental influence on yield, considering that yield and its components are quantitative characters and are affected by the environment. This study was carried out to determine the extent of genetic variation among available tomato accessions with the specific objective to use suitable genetic parameters such as phenotypic and genotypic variances, phenotypic and genotypic coefficients of variation and genetic advance as a basis for future breeding work in tomato.

MATERIALS AND METHOD

Nineteen (19) accessions of tomato held in National Gene bank at the National Centre for Genetic Resources and Biotechnology (NACGRAB) were planted for 2013 rainy season. The accessions were first planted in nursery trays after relevant seed treatment with Mancozeb®. Top soil was used for planting. Seedlings were transplanted at four weeks after planting (WAP) to NACGRAB research field, Moor Plantation (224m, 7^{o}23`, 3$^{o}$50`), Ibadan, Nigeria. Seedlings were transplanted unto a well ploughed, harrowed and levelled field. Inter- and intra-row spacing was 0.6 x 0.6m. Each treatment accession was in single 6 meter row plot. Total field size was 33m x 12m. The treatments were replicated thrice and laid out in a completely randomized block design. Recommended cultural practices were followed and irrigation was employed in the month of August when there was no rainfall. Data were recorded from five pre-tagged plants of each treatment. Attributes measured and recorded using descriptors for Tomato (*Solanum* spp.) (IBPGR, 1997) included: Leaf type, inflorescence type, stem pigmentation, stem pubescence, predominant fruit shape, colour of immature fruit, colour of ripe fruit, plant height (cm), number of branches per plant, leaf length (cm), leaf width (cm) number of leaflets, number of days to first flowering, number of days to first fifty per cent flowering, number of days to ripening of first fruit, number of days to maturity, number of fruits per inflorescence, number of fruits per plant, peduncle length (cm), fruit length (mm), fruit diameter (mm), weight per fruit (g), weight of 1000 seeds (g) and fruit yield per plant (g). Quantitative data obtained were subjected to Analysis of variance and significance means were separated using Fisher's least significant difference (LSD) using Software computer systems of SAS (SAS Institute, 2002). Mean values were used to estimate Genotypic and Phenotypic coefficients of variation as by Singh and Chaudhury (1985). The broad sense heritability and genetic advance were calculated as proposed by Johnson *et al*. (1955) and simple linear correlation coefficient was determined according to Snedecor and Cochram (1967). A correlation matrix was drawn up using the linear correlation coefficients. UPGMA cluster analysis was used to construct a dendogram to ascertain the genetic relationships among the tomato accessions.

RESULTS

Significant differences were shown among the accessions for the morphological characteristics measured, with genetic distance ranging from 0.30 to 0.49 (Fig. 1). In this study, the cluster analysis based on 37 agro-morphological attributes separated accessions into two distinct groups, which were according to fruit types – into cherry and classic fruit groups corresponding to varietal types (Fig 1). Cluster 1 included five accessions all of which are from south western Nigeria, while cluster 2 had 14 varieties from

South-West Nigeria, South-South Nigeria and Republic of Benin (Table 1).

Thirty- two of the 37 attributes recorded had morphological variation in 19 tomato accessions studied. The 20 qualitative attributes had two to nine numbers of observable types. Eight attributes (40%) had more than two types, of which fruit shape had the largest variation with six types (slightly flattened, flattened, cylindrical, rounded, ellipsoid and high rounded). There were no obvious differences for five attributes (leaf type, division of leaf blade, stem pigmentation, abscission layer and flower colour) among the accessions studied.

Genetic variability

Analysis of variance for the means of all the measured attributes showed significant differences ($P<0.001$) among the accessions (Table 2). Values of genotypic and phenotypic variances were lowest in peduncle length and highest in fruit yield per plant. Higher values of genotypic and phenotypic variances were observed respectively for plant height (21.89, 40.75), number of branches (319.60, 499.91), leaf length (31.08, 31.95), number of leaflets (203.41, 441.06), days to flower (33.23, 41.75), days to 50% flower (86.43, 105.79), days to fruit ripening(21.27, 36.65) fruit per plant (4349.08, 4826.12), fruit length (144.05, 149.06), fruit diameter(144.09, 160.49),weight per fruit (672.56, 772.6), day to maturity (28.07, 31.94) and fruit yield per plant (775796.12, 1049841.90).The genotypic coefficient of variation (GCV) ranged from 6.06 in days to fruit ripening to118.51 in fruit per plant. Similarly, PCV ranged from 7.96 (days to fruit ripening) to 124.84 (fruit per plant).

Estimates of broad sense heritability (H^2b) and genetic advance

Estimates of heritability in the broad sense were very high for leaf length (97%), leaf width (88%), days to flower (80%), days to 50% flowering (82%), fruit per plant (90%), fruit length (97%), fruit diameter (90%), fruit weight (100%) and 1000 seed weight (Table 3).Peduncle length (39%), number of leaflets per plant (46%) and number of days to fruit ripening (58%) had low to moderate heritability (Table 3). Very high genetic advance and heritability estimates were recorded for leaf length, leaf width, days to flower, days to 50% flowering, fruit per plant, fruit length, fruit diameter, fruit weight and 1000 seed weight.

Character association

Fruit yield per plant is positively and significantly ($P<0.05$) correlated to plant height ($r = 0.481$), number of branches per plant ($r = 0.471$) and leaf length ($r = 0.507$). Positive and significant association of number of fruits per plant with number of fruit per inflorescence ($r = 0.726$) is an indication of increased number of fruits with increased number of fruit bearing inflorescence. Weight per fruit which is a function of fruit size had predictably positive and significant association ($r = -0.582$) with fruit length and fruit diameter. In this work, number fruit per plant was negatively and significantly correlated with fruit diameter ($r = 0.582$). Number of branches had a significantly positive relationship with plant height ($r = 0.782$) and number of leaflets per plant ($r = 0.861$) while maintaining negative and significant relationships with days to flower ($r = -0.752$), days to 50% flowering ($r = -0.609$), days to fruit ripening ($r = -0.499$), and days to maturity ($r = -0.505$).

Table 1: Accession names and sources of accessions used for the study.

S. No.	Accession ID	Source	Region, Country
1	NG/SA/01/10/002	Quagbo market	Republic of Benin
2	NGHB/09/120	Agbo, Delta state	South-South, Nigeria
3	NG/AA/SEP/09/045	Igede, Ekiti state	South-West, Nigeria
4	NHGB/09/113	Agbo, Delta state	South-South, Nigeria
5	NG/AA/SEP/09/044	Igede, Ekiti state	South-West, Nigeria
6	L00170	Ido, Oyo state	South-West, Nigeria
7	NG/OE/MAY/09/019	Omi adio Oyo state	South-West, Nigeria
8	NG/AA/SEP/09/050	Ijeroekiti, Ekiti state	South-West, Nigeria
9	NG/SA/07/10/002	Quagbo market	Republic of Benin
10	NG/AA/SEP/09/040	Ikaejigbo, Osun state	South-West, Nigeria
11	NG/MR/MAY/09/005	Osiele, Ogun state	South-West, Nigeria
12	NG/AA/SEP/09/037	Osun state	South-West, Nigeria
13	NG/RM/JAN/10/001	Ido, Oyo state	South-West, Nigeria
14	NG/MR/MAY/09/006	Omida, Ogun state	South-West, Nigeria
15	NHGB/09/114	Sapele, Delta state	South-South, Nigeria
16	NG/AA/SEP/09/013	Osun state	South-West, Nigeria
17	NG/AA/SEP/09/042	Ilokoijesa, Osun state	South-West, Nigeria
18	L00169	Ido, Oyo state	South-West, Nigeria
19	NG/AA/SEP/09/053	Ojaoba ado, Ekiti state	South-West, Nigeria

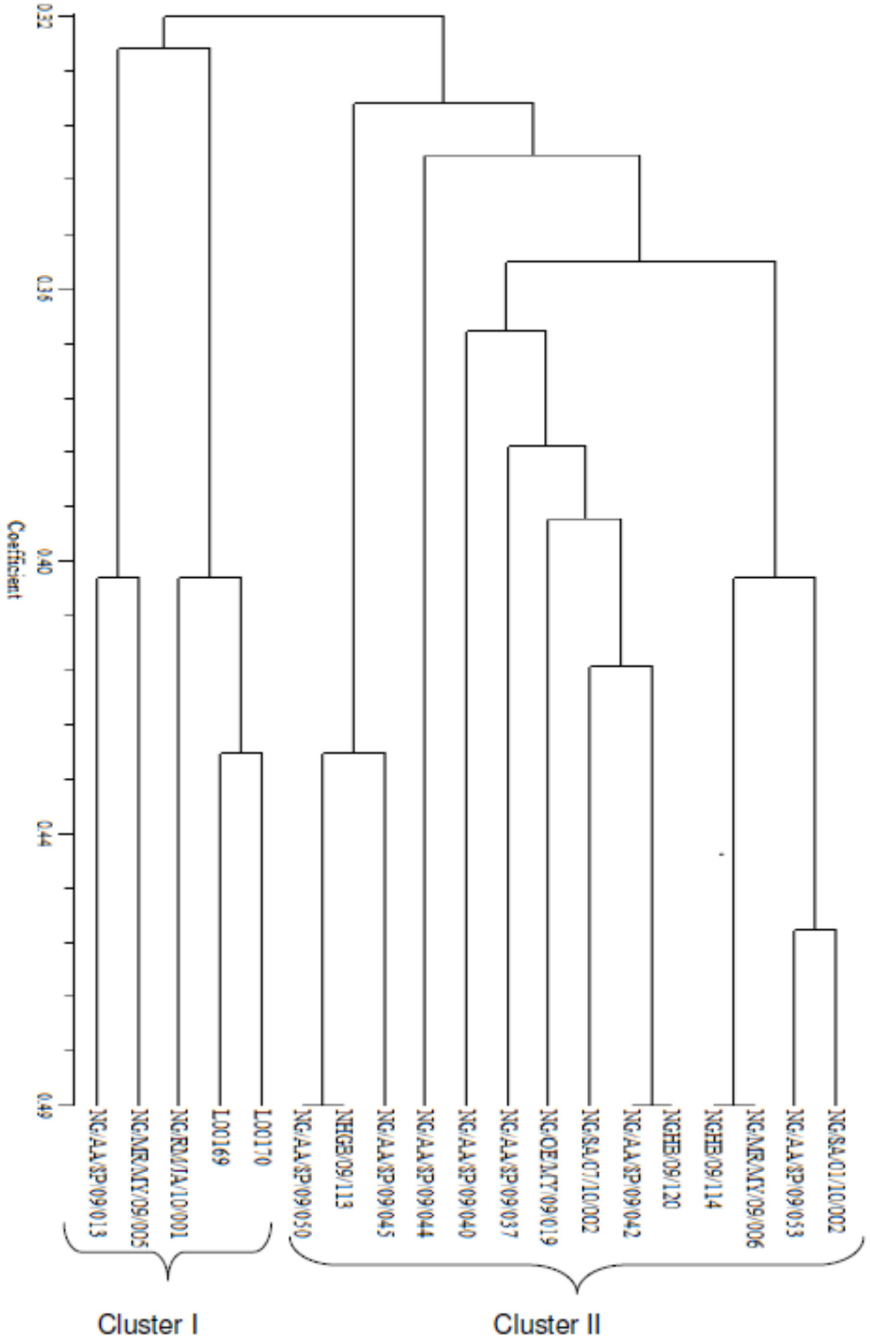

Figure 1: Dendogram of 19 tomato accessions based on 37 agro-morphological attributes and generated from average taxonomic distance matrix by UPGMA in NYSYSpc.

Figure 2: Genetic diversity as exhibited in fruits of 19 tomato accessions used for this study. 1-NG/SA/01/10/002, 2-NGHB/09/120, 3-NG/AA/SEP/09/045, 4-NHGB/09/113, 5-NG/AA/SEP/09/044.6-L00170, 7-NG/OE/MAY/09/019, 8-NG/AA/SEP/09/050, 9-NG/SA/07/10/002, 10-NG/AA/SEP/09/040, 11-NG/MR/MAY/09/005, 12-NG/AA/SEP/09/037, 13-NG/RM/JAN/10/001, 14-NG/MR/MAY/09/006, 15-NHGB/09/114, 16-NG/AA/SEP/09/013, 17-NG/AA/SEP/09/042, 18-L00169 and 19-NG/AA/SEP/09/053.

Table 2: Analysis of variance for different characters in tomato accessions.

Attribute	Accession mean	F - value	P-value ≤	Coefficient of variation
Weight/fruit (g)	36.74	21.26	0.001	27.16
1000 Seed weight (g)	2.29	16753.0	0.001	0.35
No of days to flowering	42.40	12.69	0.001	12.98
No of days to 50% flowering	49.40	14.39	0.001	8.79
No of days to fruit ripening	76.04	5.15	0.001	5.16
No of days to fruit maturity	78.65	20.96	0.001	2.54
Plant height (cm)	13.14	4.48	0.001	33.05
Number of leaflets	38.66	3.57	0.001	39.87
Number of branches	7.11	4.38	0.001	14.06
Peduncle length (cm)	0.51	2.95	0.05	22.97
No of fruit/inflorescence	5.14	11.79	0.001	14.06
Fruit length (mm)	35.98	87.20	0.001	6.22
Fruit diameter (mm)	38.01	27.35	0.001	10.66
No of fruit/peduncle	55.69	28.35	0.001	39.25
Leaf length(cm)	29.63	108.36	0.001	3.15
Leaf width (cm)	20.07	22.02	0.001	6.49
Fruit yield per plant (g)	1269.64	15.75	0.001	2.54

Table 3: Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), heritability (H^2b), genotypic and phenotypic coefficients of variability and genetic advance for various attributes of tomato accessions.

Attributes	σ^2g	σ^2p	σ^2e	H^2b (%)	GCV	PCV	GA
Plant height	21.89	40.75	18.86	54	35.60	48.58	53.75
No of branches/plant	319.60	499.91	180.31	64	17.68	22.11	29.12
Leaf length	31.08	31.95	0.87	97	18.82	19.08	38.23
Leaf width	11.89	13.55	1.70	88	17.18	18.37	33.11
Number of leaflets/plant	203.41	441.06	237.64	46	38.90	57.29	54.43
No of days to flower	33.23	41.75	8.53	80	13.59	15.24	24.98
No of days to 50% flowering	86.43	105.79	19.37	82	18.82	20.82	35.04
No of days to fruit ripening	21.27	36.65	15.39	58	6.06	7.96	9.52
No of fruit /inflorescence	1.88	2.40	0.52	78	26.67	30.15	48.60
No of fruit/plant	4349.08	4826.12	477.04	90	118.51	124.84	231.74
Peduncle length	0.01	0.02	0.01	39	18.54	29.53	23.98
Fruit length	144.05	149.06	5.01	97	33.36	33.93	67.55
Fruit diameter	144.09	160.49	16.40	90	31.58	33.33	61.64
Weight/Fruit	672.56	772.6	99.6	100	75.58	75.63	135.69
Days to Maturity	28.07	31.94	3.88	88	6.72	7.17	12.98
1000 seed weight	0.35	0.35	0.0	100	25.85	28.85	53.24
Fruit yield/plant	775796.12	1049841.90	274045.48	74	63.37	80.70	122.85

σ^2g = genotypic variance, σ^2g = phenotypic variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA= Genetic advance, H^2b = heritability in broad sense

Table 4: Correlation matrix for studied vegetative and reproductive attributes of tomato accessions.

	DTF	DTFR	DTM	PH	NOL	NOB	PDL	FPI	FL	FD	FPP	LL	LW	FYPP
W/F	.109	.191	.195	-.074	-.107	-.167	.509*	-.369	.576**	.872***	-.444	.206	.503*	.397
DTF		.720***	.693***	-.781***	-.856***	-.752***	-.186	.057	-.159	-.016	-.254	-.508*	-.259	-.368
DTFR			.878***	-.410	-.578**	-.499*	.182	-.164	.116	.154	-.309	-.228	.116	-.416
DTM				-.393	-.537*	-.505*	.092	-.110	.167	.193	-.383	-.114	.216	-.301
PH					.830***	.782***	.189	-.174	.314	.197	-.027	.724***	.540*	.481*
NOL						.861***	.099	-.188	.222	.086	-.040	.648***	.433	.363
NOB							.299	-.109	.115	.022	.095	.637**	.393	.471*
PDL								-.409	.414	.504*	-.218	.324	.539*	.141
FPI									-.299	-.639**	.726***	-.103	-.396	.061
FL										.530*	-.450	.381	.588**	.439
FW											-.582**	.343	.639**	.444
FPP												-.241	-.480*	.029
LL													.841***	.507*
LW														.412
FYPP														

W/F= weight per fruit, DTF= number of days to flower, DTFR= number of days to fruit ripening, DTM= number of days to maturity, PH= plant height, NOL= number of leaflets per plant, NOB= number of branches per plant, PDL= peduncle length, FPI= fruit per inflorescence, FL= fruit length, FD= fruit diameter, FPP= number of fruit per plant, LL= leaf length, LW= leaf width and FYPP= fruit yield per plant.

DISCUSSION

Genetic diversity can be estimated using measurements of morphological attributes. This is a simple technique for quantifying genetic variation and assessing genotype performance under appropriate growing environments (Fufa *et al*., 2005; Shuaib *et al*., 2007). The precise, fast and reliable identification of important plant varieties is essential in agriculture and plant breeding purposes (Weising *et al*., 2005). Clustering of accessions used in this study into cherry and classic fruit groups corresponding to varietal types was similar to the results of Kwon *et al*. (2009) who characterized 63 tomato varieties of Korea using SSR markers and morphological descriptors. Non-significant association between the clustering pattern and geographical origin of these materials is in agreement with the report by Hu *et al*. (2012) in their work with 67 argentine tomato varieties. Hu *et al.,* (2012) also reported that fruit shape had the most variable types (seven). The 19 accessions used for this study may be identified as distinct varieties. However, molecular characterization using SSR markers is on-going to ascertain this result.

Highly significant differences among the accessions for all attributes measured is an indication of enough genetic variability and diversity of the accessions hence the scope for improvement of this crop. Similar observations have been reported on 14 characters (Singh and Raj, 2004; Hidayatullah *et al.,* 2008) in tomato. Mohammed *et al*. (2012) also had similar findings of significant differences for all the traits they studied. Moreover, higher values of genotypic and phenotypic variances observed for plant height, number of branches, leaf length, leaf width, number of leaflets, days to flower, days to 50% flower, days to fruit ripening, fruit per plant, fruit diameter, fruit weight, day to maturity and fruit yield per plant indicate the existence of high magnitude of variability among the accessions with respect to these attributes.

Smallest differences observed between PCV and GCV values of attributes such as leaf length, leaf width, days to flower, days to 50% flower, days to fruit ripening, fruit length, fruit per inflorescence, fruit diameter, fruit weight, days to maturity and 1000 seed weight suggest lesser influence of environmental factors on their expression. Selection for improvement of tomato for these attributes is likely to be most effective. Relatively higher differences between PCV and GCV values recorded for plant height, number of branches, number of leaflets, fruit per plant, peduncle length and fruit yield indicate more influences of environmental factors than other attributes studied.

Very high heritability estimates for leaf length, leaf width, days to flower, days to 50% flowering, fruit per plant, fruit length, fruit diameter, fruit weight and 1000 seed weight indicate possibility of improvement through selection. Similar results have been reported by Tasisa *et al.* (2011) and Ulla *et al.* (2012). However, Parnse (1957) stated that greater usefulness of considering estimate of genetic advance as an effective selection tool lies in accompanied heritability estimates. Hence, very high genetic advance accompanied by high heritability estimates for leaf length, leaf width, days to flower, days to 50% flowering, fruit per plant, fruit length, fruit diameter, fruit weight and 1000 seed weight suggest simple inheritance system for these traits. Fehmida and Ahmed (2007) reported similar results for plant height, number of fruits per plant, fruit size and weight of 10 tomatoes.

Positive and significant association of fruit yield per plant with plant height, number of branches per plant and leaf length shows that taller plants, bearing more branches and longer leaves tend to yield higher as compared to shorter plants. This may be explained by the greater photosynthetic products available for partitioning to fruit production. Positive and significant association of number of fruits per plant with number of fruit per inflorescence is an indication of increased number of fruits with increased number of fruit bearing inflorescence. Weight per fruit which is a function of fruit size had predictably positive and significant association with fruit length and fruit diameter. Mohanty (2002) had reported positive and significant correlation of number of fruits per plant with fruit size and single fruit weight. More branching accessions of tomato tend to flower and mature late as shown in the negative and significant association of number of branches per plant with days to flower, days to fruit ripening and days to maturity. This may be due to the fact that much time is spent by the plant in growing more vegetative branches, hence extending its lifespan. Therefore, a breeder interested in improvement for early maturity in tomato may select plants with less number of branches.

CONCLUSION

The genetic parameters discussed here are functions of environmental variability, so estimates may differ in other environments. However, based on the high genetic advance accompanied by high heritability estimates for different attributes studied, especially, days to 50% flowering, fruit per plant, fruit length, fruit diameter, fruit weight and 1000 seed weight we could conclude that the determinant genetic effects of the phenotypic expression of these characters are fundamentally of the additive type. Hence, a highresponse should be achievable after several selection cycles.

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