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Genetic Diversity of Tomato Germplasm in Ghana using Morphological Characters

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Authors' contributions

Authors MKO, KOB and AA designed the study and performed the statistical analysis. Authors MKO and HSC wrote the first draft of the manuscript. Authors MKO and AA managed the analyses of the study. Authors KOB and HSC managed the literature searches. All authors read and approved the final manuscript.

Original Research Article

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ABSTRACT

Tomatoes constitute an important fruit vegetable crop in Ghana. However, its diversity is low and may be associated with numerous biotic stresses that pose serious threat to production.
Aim: To characterize 216 germplasm gathered from Korea (RDA), Taiwan (AVRDC), Burkina Faso and Ghana based on their morphological characters.
Study Design: An augmented randomized complete block design with six blocks and three checks.
Place and Duration of Study: Crops Research Institute, Kwadaso station, Kumasi-Ghana, from August 2012 to November 2012.
Methodology: Two hundred and sixteen tomato germplasm were planted in single rows at spacing of 100cm by 50cm. Each row had 12 plants per accession.
Data on morphological variables were measured using AVRDC descriptor list which was then subjected to multivariate analysis using Principal Component Analysis (PCA) and Clustering Criterion.
Results: Characters contributing most to variability were stem and fruit pubescence, leaf attitude, style, stamen length, colour of immature fruit, fruit skin colour, folia density, ease of fruit wall to peel and plant habit. Scores of the first principal component (PC-1)

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accounted for 11.88% of the total variation were highly correlated (correlation coefficient >0.3) to characters related in number of days to first flowering, number of days to 50% flowering and that of number of days to 100% flowering. The pruned dendogram generated through agglomerative hierarchical clustering based on the similarity matrix revealed two main groups according to the major morphological characters associated with them.

Conclusion: This study has shown that there is a wide variability in the accessions assembled. These can be used to breed high yielding varieties and/or screen for tomato fruits resistance to pest and disease infestation. The results of this study would be useful for conservation set up and genetic improvement, however, additional confirmation research is required using molecular tools to scrutinize the diversity detected.

Keywords: Tomato; diversity; germplasm; morphological characters; variability.

1. INTRODUCTION

Tomato is classified as the second most commonly grown vegetable crop in the world and forms an essential part of human diet [5]. It accounts for 14% of the world's vegetable production [over 100 million metric tons/year; $1.6 billion market [6]. The integral tomato fruit or vegetable is rich in micronutrients required in human diet and according to [15] and [11] it is an important vegetable crop in the West African sub-region. The main goal of tomato breeders is their ability to sustainably develop high yielding and high quality varieties which can resist continuous pest and disease infestation as well as environmental stresses (biotic and abiotic). The low diversity of tomato varieties, coupled with numerous pests and disease influx, poses a serious threat to tomato production in Ghana [10]. The increase in demand for high quality tomato products by consumers has resulted in the need to collect, characterize and evaluate unknown tomato germplasm. Tomatoes continue to play a key horticultural role in Ghana and its improvement would add to agricultural output, lessen poverty and facilitate food security. The ever increasing market value, as well as an increase in consumer demand makes the tomato fruit market-driven-intensification production process feasible. However, most of the tomato germplasm in the country is largely undocumented and has unidentified morphological, agronomic and biochemical attributes [10]. Tomato is grown in all the agro-ecological zones of Ghana where agriculture is viable. However, successive government policies geared toward cereal production (especially maize and rice) are among factors contributing to a decline in its production. This has resulted in the extensive cultivation of various tomato cultivars with unclear documentation.

The systematic study and characterization of tomato germ plasm is of great importance for current and future agronomists and genetic improvement specialists. Characterization therefore aids documentation of the genetic variability that exists in a population [13]. This is an important activity in crop improvement programmes because the amount of genetic diversity within populations determines the rate of adaptive evolution and extent of response to traditional breeding through selection. Furthermore, improvement programmes of evaluation is very important, in order to understand the genetic background and breeding value of existing tomato plants. Several research findings stress on the morphological, agronomic, and biochemical parameters that have been widely used in the assessment of various crops [14,8,8]. Morphological traits are important diagnostic features for distinguishing genotypes. These distinct morphological traits of genotypes facilitate the

selection process in crop improvement by serving as genetic markers. The usual approach to characterization and evaluation of populations involves cultivation of sub-samples by assessing their morphological and agronomic description [13]. Exploitation of such traits increases research findings and/or knowledge of the genetic variability available which facilitates breeding for wider geographic adaptability, with respect to biotic and abiotic stresses. Also, genetic diversity needs to be depicted and measured if it is to be successfully integrated into breeding strategies and management of plant genetic resources. The identification of variability among accessions is pivotal to the maintenance, utilization and acquisition of germplasm resources [9]. The International Plant Genetic Resources Institute (IPGRI) has developed descriptors for quantitative as well as qualitative characters to ensure precise, accurate and uniform identification of genotypes [4].

Principal component analysis (PCA) is a descriptive technique which reveals the pattern of character variation among individual accessions [9]. This brings a set of multivariate data into components that account for a meaningful amount of variation in a given population. Cluster analysis on the other hand decreases the number of individual variable units by classifying such variation into groups which are translated into a dendogram using the coefficient of similarity [16,17].

The objectives of this study therefore, are to characterize assembled tomato germplasm and examine variations in them based on their morphological traits with the ultimate aim of identifying potential accessions to improve tomato production. This would in the long term assist data generation in order to increase the understanding of the phylogeny of the Ghanaian tomato germplasm to that of Burkina Faso, Korea, and Taiwan.

2. MATERIALS AND METHODS

Tomato accessions collected from different parts of Ghana, Burkina Faso, Korea (RDA-NIHHS), and Taiwan (AVRDC) were studied. Germplasm collected from Ghana comprised mostly of landraces grown by small-scale farmers over several years. The areas from which data were collected differ greatly in their agro-ecological and ethnic compositions. Collections from Korea and Taiwan were delivered via postal mails. Compilation from Burkina Faso systematically covered mainly two districts (Kougoussi and Yako). A feasible timetable was organized for the collection of tomato germplasm in Ghana and Burkina Faso. The general logistics were taken care of as suggested by [6]. Using an augmented randomized complete block design (RCBD) with six blocks and three checks, a field experiment was established at Kwadaso (research station) in August, 2012. Two hundred and sixteen (216) tomato germplasm were planted in single rows at spacing of 100cm by 50cm. Each row had 12 plants per accession. Standard agronomic practices such as weed control, fertilizer application, staking and watering were adopted. An AVRDC descriptor list together with modified IPGRI descriptor lists was used in scoring characters [3]. The parameters scored included data on seedling, vegetative, flowering and fruiting stages (Table 1). The data were recorded either directly from the measurements using a scale of 1-7 or binary recording (1=present; 0=absent).

Table 1. Morphological traits used to describe tomato accessions

Code	Characters	Score Code- Descriptor State
1	Anthocyanin coloration of hypocotyls	0-absent 1-present x-mixture
2	Stem pubescence	0-absent 3-weak 5-medium 7-strong
3	Leaf attitude	3-semi erect 5-horizontal 7-drooping x-mixture
4	Intensity of greenback	0-none 3-slight 5-medium 7-strong x-mixture
5	Growth habit	1-dwarf 2-determinate 3-semi determinate 4-indeterminate x-mixture
7	Style type	1-inserted 3-same level as stamen 5-slightly exserted 7-highly exserted x-mixture
8	Exterior colour of immature fruit	3-light 5-medium 7-dark 9-very dark x-mixture
10	Blossom end shape	1-indented 2-flat 3-pointed x-mixture
11	Exterior colour of mature fruit	1-Green 2-Yellow 3-Orange 4-Red 5-Pink x-Mixture
12	Skin colour of ripen fruit	1-colorless 2-yellow x-mixture
13	Interior flesh colour intensity	3-light 5-medium 7-Dark x-mixture
14	Firmness	3-soft 5-medium 7-firm x-mixture
15	Predominant fruit shape	1-flattened 2-slightly flattened 3-round 4-high round 5-heartshaped 6-lengthened cylindrical 7-pearshaped 8-plumshaped
16	Fruit size variation within a plant	1-uniform 3-slight 5-medium 7-high
17	Radial cracking	0-none 1-corky lines 2-slight 5-medium 7-severe x-mixture
18	Transverse section	1-round 2-angular 3-Irregular x-mixture

All data were standardized and subjected to Euclidean method, average link cluster analysis as well as Principal component analysis (PCA) using Genstat discovery package [12] . Data from the PCA was used to generate Eigen values, percentage of the variation accumulated by the PCA and the load coefficient values between the original characters and respective PCA. The first principal components which explained the highest variation were used to plot two-dimensional dispersion or scatter diagram of the accessions. A similarity matrix was used to generate an agro-morphological distance plot among the accessions using Euclidean similarity coefficient. The hierarchical dendogram generated were used to study patterns of variance and relationships among the tomato accessions and accessions which are close genetically were positioned in closed proximity in the dendogram.

3. RESULTS AND DISCUSSION

3.1 Source of Tomato Germplasm

A total of 216 tomato accessions were assembled from four countries namely Ghana, Burkina Faso, Korea, and Taiwan (Fig.1).The highest and least collections were from Ghana and Burkina Faso. The evaluation of the tomato germplasm showed a large and significant variation in the quantitative traits between the accessions. This could be attributed to the fact that many areas covered in Ghana were weigh against Burkina Faso where only two districts

were visited for the germplasm collection. In Burkina Faso, most of the tomatoes grown are hybrids in view of the fact that the tomato industry are highly commercialized as compared to Ghana where a number of areas still use landraces and this permitted a lot more lines to be collected.

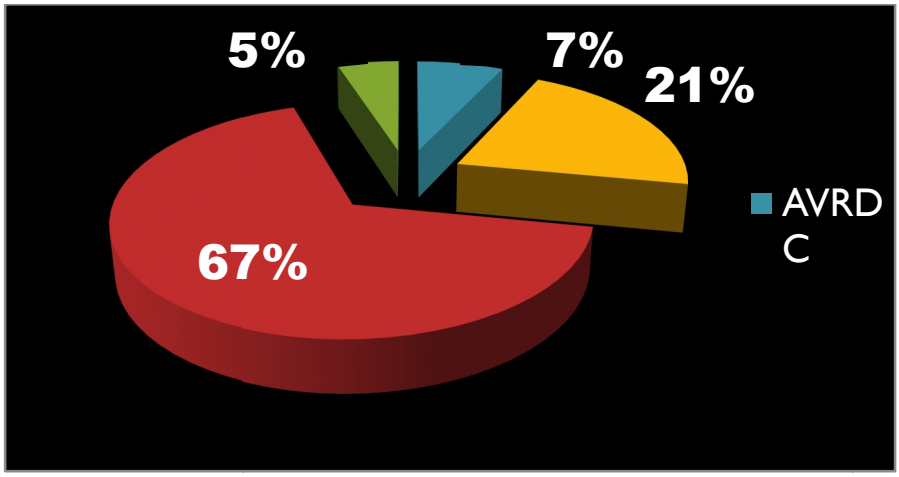

Fig. 1. Percentage of tomato germplasm assembled from different countries.

3.2 Principal Component Analysis (PCA)

The first five components with co-efficient values greater than 1.5 together explained 37.14% of the total variance present in the data set (Table 2). Scores of the first principal component (PC-1) accounted for 11.88% of the total variation were highly correlated (correlation coefficient >0.3) to characters related to number of days to that of first flowering, number of days to 50% flowering and number of days to 100% flowering (Table 3). The second principal component (PC-2) explained 8.5% of total variation and was highly associated with style length. The third component (PC-3) which explained 6.2% of the variation was mainly correlated to a character which is related to stamen length. The fourth component (PC-4) explained 5% of the variation and was determined by colour of immature fruit, plant size and leaf attitude. The fifth component (PC-5) was related to the stem pubescence. Principal component six (PC-6) was dominated by fruit skin, colour and folia density. The component explained a total of 4.6% of the variation. PC-7, PC-8, PC-9 and PC-10 explained an additional variation 4.4, 4.3, 3.9 and 3.7% of total variation respectively. PC-7 was correlated to characters related to colour of immature fruit and fruit pubescence. PC-8 was subjugated by characters that included style, hairness and fruit skin colour. PC-9 was also dominated by characters such as fruit easiness to detach and fruit wall to peel while PC-10 was correlated to characters such as fruit easiness to detach and fruit pubescence (Table 3). PC-11 and 12 variations were less than 3% and were considered to be less significance to the overall variability.

Table 2. Eigen values and the cumulative variability of the different PC for the traits among the germplasm of tomato studied

Principal component	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigen values	3.564	2.554	1.851	1.651	1.523	1.386	1.318	1.294	1.180	1.110
Variability (%)	11.88	8.51	6.17	5.50	5.08	4.62	4.39	4.31	3.93	3.70
Cumulative	11.88	20.39	26.56	32.06	37.14	41.76	46.15	50.46	54.39	58.09

Table 3. Correlations between variables and factors for the traits among the germplasm of tomato studied

Character	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Anthocyanin coloration	-0.206	0.019	0.002	-0.087	-0.273	0.060	-0.149	-0.429	0.182	-0.061
Stem pubescence	0.027	-0.017	0.090	0.139	0.492	-0.220	-0.205	0.006	-0.003	-0.223
Leaf attitude	0.197	-0.025	0.107	0.300	-0.155	0.012	0.216	-0.088	-0.195	-0.174
Intensity of greenback	0.007	0.290	-0.201	0.058	0.078	-0.138	-0.245	-0.173	0.138	0.225
Style length	-0.038	0.302*	0.239	-0.280	0.009	-0.285	0.133	-0.141	-0.003	-0.176
Sepal length	0.157	-0.262	0.254	0.076	0.008	0.149	0.047	0.072	-0.045	-0.005
Stamen length	0.046	0.115	0.524	-0.049	-0.090	-0.187	0.022	0.083	-0.138	0.038
Style hairness	-0.094	0.018	0.060	-0.072	0.104	-0.148	0.032	0.602	-0.085	0.113
Days to first flowering	0.388	-0.236	0.010	-0.067	0.145	-0.012	-0.056	-0.057	0.026	0.062
Days to 50% flowering	0.381	-0.211	0.150	-0.109	0.032	-0.113	-0.079	-0.132	-0.002	0.089
Days to 100% flowering	0.311	-0.237	0.106	-0.122	0.087	-0.074	0.072	-0.009	0.038	-0.146
Color of immature fruit	0.001	0.128	0.123	0.340	0.126	-0.152	0.435	0.179	-0.099	-0.043
Fruit easiness to detach	-0.141	0.091	0.201	-0.117	-0.185	-0.049	0.239	0.144	0.327	0.378
Fruit skin color	-0.029	-0.030	0.010	-0.111	0.002	0.338	-0.304	0.317	0.205	-0.085
Fruit pubescence	0.044	0.041	0.174	-0.114	-0.024	0.125	0.383	-0.079	-0.278	0.495
Folia density	-0.149	0.145	0.212	0.109	0.108	0.354	0.198	-0.166	0.006	-0.106
Ease of fruit wall to peel	-0.132	-0.123	0.030	-0.045	-0.286	0.197	-0.130	0.010	0.364	-0.041
Plant habit	-0.054	0.147	0.230	0.435	0.237	-0.151	-0.132	-0.134	0.038	-0.15

**Values in bold indicate the most relevant characters (>0.3) that contributed most to the variation of the particular component*

Multivariate analysis assumes inclusion of genotypes with maximum genetic divergence (2). Variability was obtained in majority of the measured characteristics indicating presence of a high degree of morphological polymorphism among the cultivated varieties of tomato assembled in Ghana. This indicates the presence of diverse morphotypes at the individual genotype level pointing to ample possibilities of obtaining desirable trait combinations in specific cultivars. This would be crucial in meeting the diverse demands of farmers, researchers and consumers of tomato. Substantial morphological variation within and between the various accessions especially those from Ghana may be attributed to segregation and perhaps mutation followed by intensive selection by isolated human communities in diverse environments. The distribution of variates based on the PC-1 and PC-2 shows the phenotypic variation among the accessions and how widely dispersed they are along both axes (Fig. 2). The two components explain a cumulative variability of 20.39%. Based on the distribution of variates, 169 (AVT-3) is the most distantly related to the group while the second group indicates accessions 71 and 141 to be least similar to the group. The most distant in the third quarter is made up of 43 and 7. The last quarter is made up of 8 and 150 that are least similar to the group (Fig. 2).

The agglomerative hierachical clustering dendogram illustrates the relationship among the accessions (Fig. 3). At 0.925 similarity level, almost all the 216 tomato accessions were distinct from each other while between 0.900 and 0.850, almost half of the accessions were similar to each other. The cluster analysis separated the 216 tomato accessions as different genotypes with Euclidean similarity distance ranging from 0.900 to 0.800. The pruned dendogram at similarity distance=0.806 identified two main clusters A and B according to the major morphological characters associated with them. From the dendogram, it was not possible to group all the tomato accessions from the different collection sites or location into their specific groups but it was clear the greater part are quite related. It is also likely that continuous recycling of tomato seeds by farmers and selections leading to massive segregation have contributed to the wide phenotypic variability of the tomato crop. The analysis also suggests that most local names of the germplasm from Ghana represented same cultivars (Table 4).

The clustering patterns using principal components analysis and dendrogram generated exemplify genetic relationship among the accessions. All in all, thirty-two tomato accessions were selected. These were based on fruit shape, fruit size, fruit surface, fruit colour and pests and diseases resistance. Divergent accessions may have good breeding values and accessions in the same cluster may represent members of one heterotic group. According to (2) the maximum variability for segregation in a segregating population may be achieved by utilizing accessions from different clusters as parents of crosses.

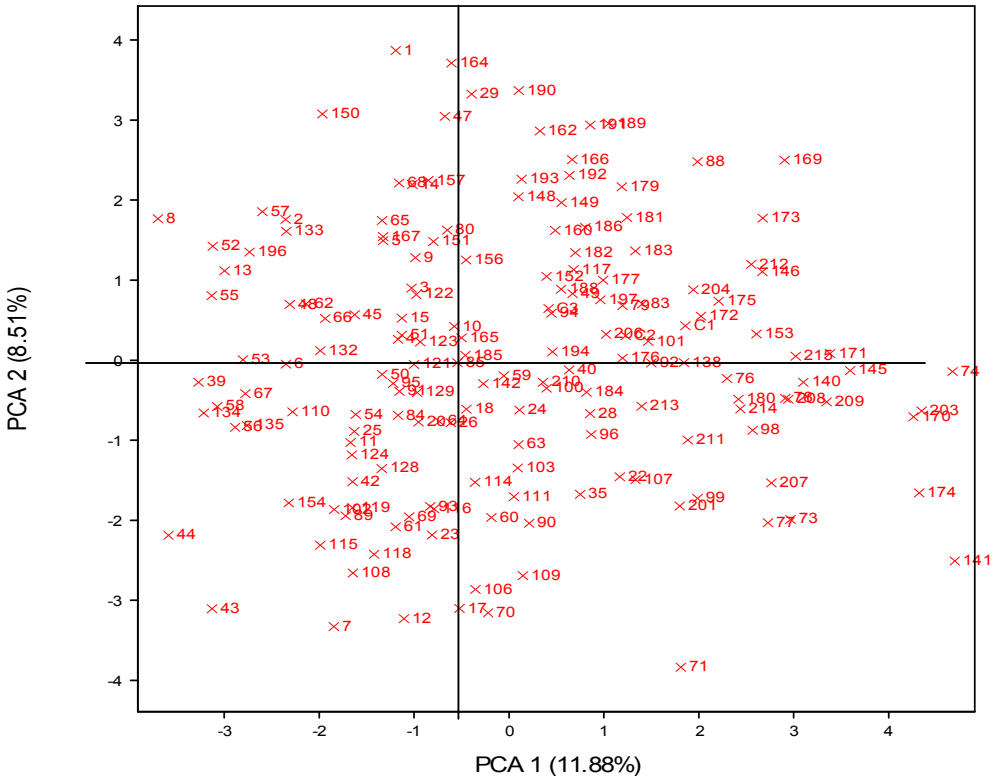

Fig. 2. Distribution of variates among accessions in PCA1 and PCA2.

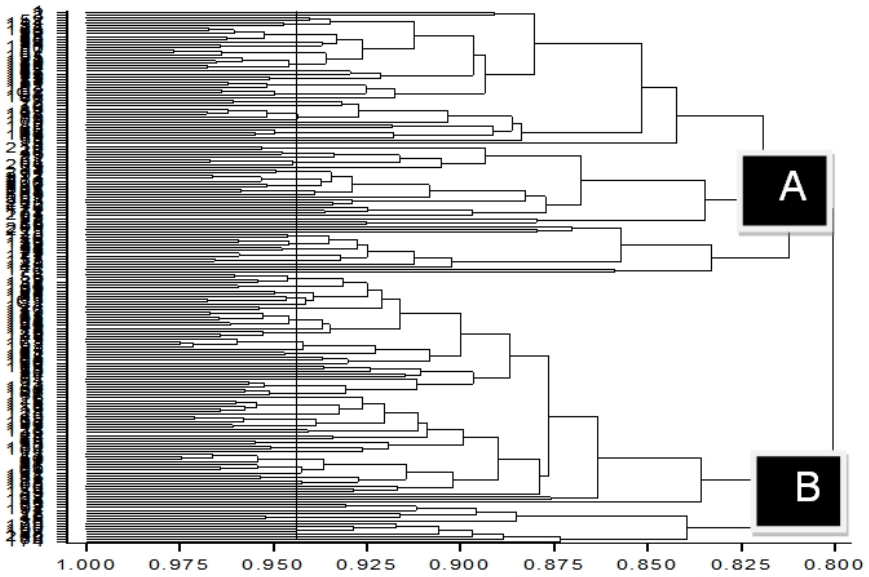

Fig. 3. Dendogram based on agro-morphological characters of tomato germplasm assembled.

Table 4. Key local names of tomato germplasm characterized

Code	Local name/ Accession	Code	Local name/ Acession	Code	Local name/Accession	Code	Local name/Accession	Code	Local name/Accession
1	Fadebegye 1	21	Lorry Tyre	41	Tomatose17	61	Fadebegye10	81	18(L)
2	Fadebegye 2	22	Tomatose 4	42	Tomatose18	62	Fadebegye11	82	4(0)
3	Tomatose 1	23	Tomatose 5	43	Tomatose19	63	Fadebegye12	83	6(A)
4	Tomatose 2	24	Local1	44	Tomatose20	64	Ataamba1	84	1R
5	Petomech	25	Mixed	45	Tomatose21	65	Ataamba2	85	21(B)
6	Power Rano	26	Lorry Tyre	46	One Man thousand1	66	Fadebegye13	86	9(W)
7	RASTER	27	Local2	47	One Man thousand2	67	Koforidua tomato	87	5(K)
8	Mmoboboye 1	28	Local3	48	Adwoba1	68	Fadebegye14	88	Bindurii local 1
9	Mmoboboye 2	29	Tomatose6	49	Asante tomato1	69	Local 1	89	Bindurii local 2
10	Ntose 1	30	Tomatose7*	50	Asante tomato2	70	Local 2	90	Bindurii local 3
11	Ntose 1	31	Tomatose8	51	Asante tomato3	71	Local 3	91	Bindurii local 4
12	Abrewabrewa	32	Local4	52	Adwoba2	72	Local 4	92	Bindurii local 5
13	Burkina	33	Tomatose9	53	Fadebegye3	73	Local 5	93	Bindurii local 6
14	Tomatose3	34	Tomatose10	54	Fadebegye4	74	Local 6	94	Bindurii local 7
15	Mixed Local	35	Tomatose11	55	Fadebegye5	75	Local 7	95	Bindurii local 8
16	Dorgobom	36	Tomatose12	56	Fadebegye6	76	Local 8	96	Bindurii local 9
17	Amo	37	Tomatose13	57	Fadebegye7	77	Local 9	97	Bindurii local10
18	Amoako	38	Tomatose14	58	Fadebegye8	78	Local 10	98	Nav local 1
19	Lorry Tyre	39	Tomatose15	59	Local	79	Local 1	99	Nav local 2
20	Haly	40	Tomatose16	60	Fadebegye9	80	2(V)	100	Nav local 3

Code	Accession/LN	Code	Acession/LN	Code	Accession/ LN	Code	Accession/LN	Code	Accession/ LN
101	Nav local 4	126	Agogo Local 3	151	IIVT-3	176	10CH-17-6	201	AVTO 0101
102	Nav local 5	127	Powerano	152	IIVT-4	177	IICH-Z	202	AVTO 0102
103	Nav local 6	128	Akoma	153	IIVT-5	178	IICH-5	203	AVTO 1003
104	Hian local 1	129	Pectofake	154	IIVT-6	179	IICH-7	204	AVTO 1004
105	Bolga local 1	130	Dormaa local 1	155	IIVT-8	180	IICH-10	205	AVTO 1006
106	Bolga local 2	131	Dormaa local 2	156	IIVT-9	181	IICH-11	206	AVTO 1008
107	Kun local 1	132	Dormaa local 3	157	IIVT-10	182	Kyapirang	207	AVTO 1009
108	Kun local 2	133	Shavini local 1	158	IIVT-11	183	Pingkeutap	208	AVTO 1010
109	Kun local 3	134	Fadebegye A	159	IIVT-12	184	Bigdena	209	AVTO 1020
110	Kun local 4	135	Pimplifolium	160	IIVT-13	185	Bakkeoseu	210	AVTO 0201
111	Kun local 5	136	Fadebegye B	161	IIVT-14	186	Superdotaerang	211	AVTO 9802
112	Nav local 1	137	Fadebegye C	162	IIVT-15	187	Rapsody	212	AVTO 9803
113	Pwu local 1	138	BK-Koly zy	163	IIVT-16	188	Madiso	213	AVTO 9804
114	No name	139	BK-Local 1	164	IIVT-17	189	Rikopim-9	214	AVTO 9001
115	Asante tomatoes 1	140	BK-Kong Roma 2	165	IIVT-18	190	Orange carl	215	AVTO 9601
116	Asante tomatoes 2	141	KK-Koly Local 8	166	IIVT-19	191	Dyune	216	AVTO 1173
117	Asante tomatoes 3	142	BK-FBTS INERA	167	IIVT-20	192	Solution		
118	Rano 1	143	BK-Kong L3	168	IIVT-21	193	B-Blocking		
119	Rano 2	144	BK-Dotvert Yako	169	AVT-3	194	Magmet		
120	Rano 3	145	BK-Kong L2 XLYS	170	IIAVT-4	195	Heat Tolerant		
121	Afua 1	146	BK-Kong-L6	171	IIAVT5	196	Pimplifolium		
122	Afua 2	147	BK-Kong-Trop	172	IIAVT10	197	REX		
123	Power	148	BK-Yako Kabacci	173	2011-893	198	T-245		
124	Agogo Local 1	149	IIVT-1	174	Maereuk	199	King		
125	Agogo Local 2	150	IIVT-2	175	Tamina	200	2001heat tolerant		

4. CONCLUSION

Complementary studies, for example using genetic characterization are needed to further identify and classify the major tomato accessions grown in Ghana. In many cases crop germplasm resources are threatened with loss through genetic erosion due to environmental, social, political and economic challenges in Ghana. Genetic conservation and improvement based on selected materials should be encouraged with an aim to prevent and/or reverse erosion while these activities could maximize the use of the resources identified.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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