Characterization of Some Selected Nigerian Indigenous Tomato Accessions (Morphology, Molecular and Yield).

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Abstract

This study aimed to develop a morpho-molecular and yield-based screening system to identify the best tomato genotypes in Nigeria. Conducted at the National Biotechnology Development Agency (NABDA) in Abuja, the experiment used twelve tomato accessions from the National Center for Genetic Resources and Biotechnology (NACGRAB). Five seeds per accession were sown in a Randomized Complete Block Design (RCBD) in rich loamy soil. Morphological and yield parameters were monitored, revealing significant differences ($p<0.05$) among the accessions at week 8. Accession NW1 demonstrated superior traits in plant height, number of branches, leaflets, flowers, and fruits per plant but had the lowest fruit weight due to smaller fruit size. Molecular analysis using RAPD-PCR with ten primers identified 28 polymorphic fragments, showing genetic variability among the accessions. Combining molecular and morphological traits proved reliable for selecting improved tomato genotypes but traits such as fruit weight, number of flowers, and number of fruits per plant were positively correlated with yield and can serve as selection indices for breeding programs. This research provides valuable insights for enhancing tomato breeding and yield in Nigeria.

Keywords: Morphology, Molecular, Accessions, Yield, Genotypes, Breeding.

Introduction

Tomato (*Solanum lycopersicum* Linn.), a member of the Solanaceae family, is an economically significant vegetable cultivated globally for both fresh consumption and processing. Originating from the Andean region, the domestication of tomatoes has resulted in a variety of cultivated forms with significant genetic diversity (Albrecht *et al*., 2010). In Nigeria, tomatoes are a staple, accounting for about 48% of daily vegetable consumption (Olajide and Oladiran, 2014). The improvement of tomato varieties through breeding programs has traditionally relied on morphological, biochemical, and molecular markers. Among these, molecular markers such as Randomly-Amplified Polymorphic DNA (RAPD) have proven invaluable for evaluating genetic relationships and identifying superior genotypes (Bai and Lindhout, 2007). Despite challenges
with reproducibility (Samia *et al*., 2015), RAPD remains a costeffective and time-efficient tool in the absence of more advanced techniques.

This study aims to develop a morpho-molecular and yield screening system to identify the best tomato accessions in Nigeria, addressing the need to trace phenotypic, yield and genotypic relationships using characters from locally available tomato fruits. By combining morphological, yield and molecular analyses, this research seeks to enhance the selection process for improved tomato genotypes, ultimately contributing to higher yield and better quality in tomato production.

Method

Sample Collection: Twelve accessions of Indigenous tomato samples were collected from the National Centre for Genetic Resources and Biotechnology (NACGRAB), with detailed information documented:|NGB 01232 - NC1 - North Central, NGB 01301 - NC2 - North Central, |NG/RM/01/01/01- NW1- North West, NGB 01237 - NW2 - North West, NGB 01302 - NE1 - North East, NG/SA/07/10/002- NE2 - North East, NGB 01207 - SE1- South East, NGB 01209 - SE2 - South East, NG/MR/01/005 - SW1 - South West, NG/AA/09/037 - SW2- South West, NHGB/09/113 - SS1- South South, NHGB/09/114 - SS2 - South South (Source: NACGRAB).

Viability Test: Seeds from each accession were tested for viability using the floating technique (Falusi *et al*., 2012). Viable seeds (those that settled at the bottom) were selected for planting.

Experimental Design: The experiment was conducted in a screen house facility at the National Biotechnology Development Agency (NABDA), Abuja, using a Randomized Complete Block Design (RCBD) with five replicates per accession (Nwosu *et al*., 2014). Five seeds of each accession were sown in pots filled with rich loamy soil and irrigated twice daily.

Evaluation: Growth Monitoring: Emergence days and plant heights were recorded every two weeks. The number of leaves, leaflets, and branches was also noted.

Yield Parameters: Data on flower set (days to flower emergence, days to flower opening), fruit set (number of buds, aborted buds, fruits per plant), and fruit characteristics (size, shape, color, weight of 10 fruits) were collected (Falusi *et al*., 2012).

Molecular Characterization: DNA Extraction: DNA was extracted using the Sarkosyl Nitrogen Method from 0.5g of fresh apical leaves. The extracted DNA was quantified using a NanoDrop spectrophotometer.

Primers Screening: Twelve arbitrary decamer primers were screened, with those showing high polymorphism used for RAPD-PCR analysis.

PCR Amplification: DNA was amplified using standard PCR conditions with a set of RAPD primers. The PCR products were analyzed using agarose gel electrophoresis, visualized with ethidium bromide, and documented (Samia *et al*., 2015).

Data Analysis: Data were analyzed using ANOVA and DMRT at P< 0.05 with SPSS 16.0. Molecular data were processed using RAP Distance Package Software and NTSYS-pc to construct dendrograms using UPGMA.

Results and Discussion

Morphological Parameters.

Table 1: *Analysis of variance for the mean of morphological parameters in tomato accessions.*

Accession Symbol	No. of Days to emergence	No. of Leaflets/plant	No. of leaves/ plant	No. of branches/ plant	Plant height (cm)
NC1	9.00±0.40^{ab}	29.4±18.9^{b}	7.87±4.90^{a}	4.25±1.11^{a}	8.10±5.12^{b}
NC2	10.00±0.40^{b}	20.2±10.1^{a}	6.47±2.86^{a}	4.25±1.11^{a}	6.93±3.46^{a}
NW1	8.00±0.20^{ab}	64.4±40.5^{c}	12.7±6.81^{d}	5.65±1.38^{b}	11.2±6.22^{d}
NW2	8.00±0.75^{ab}	47.9±27.8^{b}	10.3±5.09^{b}	4.35±1.10^{a}	10.8±5.00^{c}
NE1	7.00±0.55^{a}	48.4±30.4^{b}	9.00±4.08^{ab}	4.40±1.16^{a}	10.4±4.67^{c}
NE2	6.00±0.60^{a}	33.4±14.2^{ab}	9.93±4.02^{ab}	4.30±1.14^{a}	16.1±5.36^{f}
SE1	9.00±0.25^{ab}	31.5±16.0^{ab}	8.13±3.51^{ab}	4.35±1.20^{a}	9.65±4.57^{bc}
SE2	6.00±0.40^{a}	36.3±18.1^{ab}	7.73±2.70^{a}	4.05±1.11^{a}	8.92±3.78^{b}
SW1	6.00±0.0^{a}	38.9±19.7^{ab}	8.80±3.80^{ab}	4.15±1.24^{a}	14.6±6.89^{e}
SW2	7.00±0.25^{a}	48.5±24.6^{b}	11.1±5.09^{c}	5.15±1.38^{b}	9.38±4.10^{bc}
SS1	8.00±0.63^{ab}	49.1±29.1^{b}	10.4±4.80^{b}	4.25±1.11^{a}	11.6±5.44^{d}
SS2	7.00±0.20^{a}	65.5±35.9^{c}	10.9±5.15^{b}	5.00±1.29^{b}	12.3±5.05^{e}

Yield parameters

Flower Set and Fruit Set Analysis

Table 2: Analysis of variance for the mean of the flower set and Fruit set

Acces. fruit formed symbols	No. of days to flower emergence	No. of days to opening flower/plant.	No. of flower Buds formed.	No. of flowers Buds	No. of aborted.
NC1	63.0±0.40c	67.0±0.40c	17.0±0.70b	4.00±0.32ab	13.0±0.95b
NC2	63.0±0.37c	66.0±0.37c	12.0±1.56a	4.00±0.60ab	9.0±1.03a
NW1	58.0±1.32ab	64.0±1.56b	61.0±15.4e	18.00±4.98d	43.0±10.4e
NW2	60.0±1.16b	64.0±1.80b	22.0±2.98c	4.00±1.03ab	17.0±2.13c
NE1	61.0±0.74b	64.0±00b	12.0±1.58a	3.00±0.75a	9.0±1.21a
NE2	61.0±0.63b	66.0±0.68c	11.0±2.91a	3.00±0.86a	8.0±2.28a
SE1	60.0±1.08b 10.0±0.68ab	63.0±1.11b	12.0±0.84a	2.00±0.25a	
SE2	60.0±0.45b	63.0±0.89b	23.0±2.65c	6.00±0.80b	17.0±2.18c
SW1	54.0±2.10a 15.0±1.46bc	58.0±1.90b	19.0±1.66b	4.00±0.60ab	
SW2	59.0±1.02ab	63.0±0.89b	24.0±2.92cd	5.00±0.81ab	18.0±2.25c
SS1	58.0±1.32ab 20.0±2.69cd	61.0±1.29ab	28.0±3.98d	8.00±1.56c	
SS2	54.0±1.67a	55.0±1.10a	28.0±4.63d	6.00±1.28b	22.0±3.41d

Values are means ± SE, values followed by different superscript (s) across the column are significantly different at p<0.05.

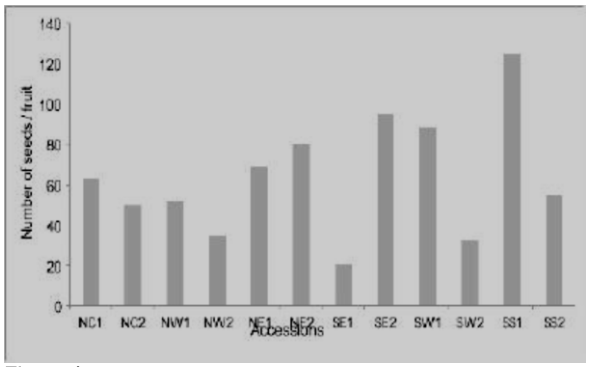

Figure 1: Number of seeds per fruit of each accession

Fruit Phenotypic Variance

The fruits obtained from the different accessions were phenotypically different from one another.





DNA Quantification

The result shows that the entire DNA extracted was of good quality because their purity was up to 1.5 and above, with concentration(ng) and purity(µl) ranging from SS1 112.1 / 1.53 to NW2- - 412.4 / 1.63.

Table 3: DNA Quantification

Accessions	concentration / ng/µl	purity
NC1	185.9	1.51
NC2	175.6	1.54
NW1	382.7	1.72
NW2	412.4	1.63
NE1	341.9	1.72
NE2	132.5	1.55
SE1	398.7	1.76
SE2	287.7	1.52
SW1	121.1	1.61
SW2	222.4	1.66
SS1	112.1	1.53
SS2	289.8	1.53

DNA fingerprinting of the Tomato Accessions

The primers that were used in this have been useful for assessing variabilities among the tomato accessions. The number of amplification products obtained was in the range of 2-8, and the primer OPA-18 produced the highest (83%) polymorphic information content (PIC), followed by OPA-02 with (80%) PIC. This is an indication that these primers are the best for determining variability in tomatoes. The polymorphic band range from 1 to 5 bands and the polymorphic percentage range from 25 to 85%.

Conclusion

Determining the variability of yield and yield-related components will enable the plant breeders to infer the extent of environmental influence on yield; since yield and its components are quantitative characters that are affected by the environment. This research is useful for the selection of improved tomato genotypes for maximum yield production. Conclusively traits like; fruit weight, number of flowers per plant and number of fruits per plant showed a positive relation with yield as well and they have a direct effect on yield. These can be used as selection indices in tomatoes to bring about an improvement in fruit yield. The fruit and flower set parameters are yield characters too. These characters could be used as selection indices in Nigerian tomatoes to bring about an improvement in fruit quality and quantity.

Declaration of interest

The authors declare no conflict of interest.

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