Characterization of eggplant (Solanum species) seedlings using quantitative trait analysis

C.U. Aguoru1*, L.O. Omoigui2, J.O Olasan3

1Department of Biological Sciences, University of Agriculture, Makurdi. Nigeria
2Department of Plant breeding and Seed Science, University of Agriculture, Makurdi, Nigeria

Abstract: Quantitative trait analysis of eggplant seedlings (Solanum species) was undertaken in the North Central zone of Nigeria with a view to revealing the level of diversity and taxonomic relationships of the collected species. 60 seeds of the various eggplant accessions were randomly collected and planted in a controlled screen house environment. A total of 52 accessions were characterized using sixteen (16) quantitative characters between day 4 to 31 of planting. In each accession, five (5) seedlings were phenotypically investigated and the mean value of the variables was noted. Data of quantitative characters were analyzed using the SPSS (Statistical Package for the Social Scientists) software programme (20.0 versions). Cluster analysis was performed using the Average Linkage (between group) method based on Euclidean distance which generated a dendrogram for the accessions. Histograms and normal distribution curves were generated which revealed the mean values and deviations of the characters. Degree of relationships amongst the variables was determined through the Pearson’s Product Moment Correlation. The results revealed substantial variations in most of the quantitative traits. Emergence of first seed leaf varied between day 4 to day 9 of planting while the percentage of germinated seeds ranged from 3.3% to 98.3% amongst the accessions. Clustering patterns which revealed a high level of intraspecific and interspecific variability were of two types: Location dependent and location independent. Interspecific similarity was also observed which indicates a common ancestral relationship of the species. Plant height was positively correlated with petiole length (0.754), plant total weight (0.903) and number of leaves (0.738). This quantitative approach of combining morphological and embryological taxonomic evidence has made available detailed taxonomic relationships information of eggplant seedlings in Nigeria due to the dearth of such information. The implication of the findings is to ease breeding efforts where some accessions of known qualities could be selected for commercial farming. Therefore, the valuable information provided may be useful in the development of breeding, crop improvement and conservation programme of the named germplasm.

Keywords: quantitative traits, seedlings, germination, variability, breeding, germplasm

INTRODUCTION

Eggplants (Solanum species) belong to the family Solanaceae and consist of about 1500 morphologically diverse species[1-2]. According to many authors[3-6] taxonomic confusion and complications exist within this genus due to the varied morphology, wide ecogeographical distribution and presence of different hybrids in eggplants. Basically, among the commonly reported species include: S. melongena, S. macrocarpon, S. aethiopicum, S. incanum, S. scabrum, S. dasysthyllum, S. erianthum [2, 3, 7-9] while many species are yet to be identified, named and classified systematically[3] S. aethiopicum further grouped into different ecotypes which are: Aculatum, Gilo, Kumba and Shum group as revealed by similarities in genotypic characterization though varied phenotypes exist[1].

Though no statistics is officially available or reportedly published on the volume of eggplant produced in Nigeria, the crop is intensively cultivated in the country for its benefits. The production of eggplant is highly concentrated, with 90% of world output coming from five countries. China is the top producer (58% of world output) and India is second (25%), followed by Iran, Egypt and Turkey. More than 4,000,000 acres (1,600,000 ha) are devoted to the cultivation of eggplant in the world [10]. The crop is commonly cultivated all over the world and it is known for its nutritive values, therapeutic benefits among other uses. Hence, it has dual status of being a vegetable crop on one hand and a fruit crop on the other hand.

Assessment of the diversity and relationships of the cultivated species facilitates the establishment of conservation strategies, the use of genetic resources in breeding programmes, and the study of the crop...
evolution [11]. The evaluation of genetic resources is therefore crucial for breeders to produce new cultivars or to further improve the existing ones according to changing consumer demands or overcoming challenges during plant growth such as pest and disease resistance[4,7] morphologically characterized African eggplants using twenty-eight accessions from three species of Solanum aethiopicum (16), Solanum macrocarpon (9) and Solanum anguivi (3). Their results indicated distinct and wide variations between the three Solanum species with a lot of similarities between the S. aethiopicum and S. anguivi lines. Morphological and agronomical characterization of eggplant genetic resources was carried out [12]. In their report, some genotypes were more productive and produced fruit faster than others. In Spain, conventional descriptors and the high-throughput phenomics tool of Tomato Analyzer for characterizing 63 accessions of eggplant complexes with substantial level of variations reported[9]. Different molecular markers have also been employed by authors to study the diversity of the crop and other crops across the world[2, 13-15].

However, there is dearth of information on its diversity using seedlings as embryonic evidence as most studies have confirmed the fact that taxonomic relationship is difficult to establish in the crop due its varied characters. On this note, this study was carried out on the growing seedlings by employing quantitative trait approach to reveal information on its germination and diversity. The overall aim was to investigate the level of diversity and taxonomic relationships or otherwise among the species.

MATERIALS AND METHODS
This study was carried out across 52 north central locations in Nigeria, tropical West Africa. 60 seeds each of the various eggplant accessions were randomly collected and planted in green rounded plastic pots of equal sizes (23cm in diameter, 8.5cm in height) arranged under a controlled screen house system. All pots contained the same quantity of fertile soil and maintenance was equally apportioned. Equal depth was used in planting. A total of 52 accessions were characterized using sixteen (16) quantitative characters between day 4 to 31 of planting. In each accession, five (5) seedlings were phenotypically investigated and the mean value of the variables was noted. Meter rule was used in measurement of length, breadth, and height while electronic weighing balance with tarring function was employed in weight measurements. Number of seeds planted in relation to the proportion that germinated was physically counted. Data of quantitative characters were analyzed using the SPSS (Statistical Package for the Social Scientists) software programme (20.0 versions) following the method of Oboh et al.[16]. Cluster analysis was performed using the Average Linkage (between group) method based on Euclidean distance which generated a dendrogram for the accessions. Histograms and normal distribution curves were generated to reveal the mean values and deviations of the characters. Degree of relationships amongst the variables was determined through the Pearson’s Product Moment Correlation.

RESULTS AND DISCUSSION
The diversity, taxonomic relationship and information on eggplant germination have been revealed in this study. Dendrogram(figure 1) has revealed 2 main clusters. Cluster 1 consists of 2 sub clusters where four accessions from Nasarawa state were grouped on the basis of location indicating a strong relationship between them. Other accessions in these two sub clusters were grouped together but not strongly tied to their location and this indicates similarities on one hand as well variations on the other hand. They include but not limited to: S. aethiopicum Gilo (PL3), S. anguivingmedium (NG2A), S. aethiopicumgilo (NG2B), S. aethiopicum Slum (PL1B) and S. aethiopicumShum (KG2B). However, S. anguivinginty (BN7) was semi divergent within the groups therefore reflecting a variation from the S. aethiopicum line. The fruit and seeds of BN7 were noted for their small size and high germination rate respectively. Cluster 2 consists of three sub clusters whose accessions display much interspecific and intraspecific similarity. For instance, BN2B and BN1B are both S. aethiopicumgilo while PL1A and PL4B are S. aethiopicum gilo and S. aethiopicum Kumba respectively. FCT2 and FCT3 are also S. aethiopicum Kumba. This shows similar characteristics among the S. aethiopicum groups but differ intraspecifically from S. aethiopicumgilo of NG2A and S. aethiopicum Shum of KG1B in cluster 1. Attention is particularly drawn to accession BN6 (S. macrocarpon) noted for its large fruit sizes which diverged from the rest S. aethiopicum group. In spite of this difference, it is suggested that S. macrocarpon and other groups of S. aethiopicum in this group are related. This finding is in agreement with reports from several authors[2, 14, 17, 18] that these species have a common progenitor in their phylogenetic history, hence their relationship. This notion of common ancestral linkage is further established by BN2B (S. aethiopicum Gilo and KG6 (S. macrocarpon) forming a tied cluster together.

However, there is a strong relationship between BN1D (S.aethiopicum Gilo and FCT 2 (S. aethiopicum Kumba). Also BN1F (S.aethiopicum Gilo) and NS7 (S.aethiopicum Kumba) are also strongly tied together. This may be due to their specific relationship in most of the characters. The fruits of both sub groups of S. aethiopicum are similar except that the Kumba group has grooves longitudinally along its surfaces. The result obtained from morphological characterization in this study also aligns with the work of Osei et al. [7] who morphologically characterized African eggplants using twenty-eight accessions from three species of Solanumaethiopicum (16), Solanummacrocarpon (9) and Solanumanguivi (3) Their results indicated distinct
and wide variations between the three *Solanum* species with a lot of similarities between the *S. aethiopicum* and *S. anguivi* lines. It has further been confirmed that Statistical Correlation is a true measure of relationship. The high positive correlation between KG1A and BN1F (+0.999) indicates that they are both *S.aethiopicum* Gilo showing high affinity in their quantitative characters. PL2A (*S. aethiopicum* Kumba) and BNIE (Kumba complex) also shows high proximity by +0.997. Correlation how ever however contrasts the view of Nunome *et al.*, [15] and Mariola *et al.*, [9] who suggested that the sub groups in *S. aethiopicum* be treated as different species since they all display varied phenotypes and genotypes using a combination of molecular markers. As illustrated in figure 2a-d, the accessions that are very fast in producing their first cotyledon within four days of planting include: NSID, NS5, NS7, KG2B, BN1A, BNIE, BN1F, BN2A, BN5, BN6, FCT2, NG2A, PL1B and PL1C among others with an overall mean value of 6.12 days. Plant height was symmetrically distributed with a mean value of 7cm. Ripe fruit weight ranged from 5.32g in BN7 (*S. anguivi* tiny) to 139.34g in BN6 (*S. macrocarpon*). Table 1 indicated that FCT5 (*S. aethiopicum* gilo) yielded the least number of germinated seeds after 30 days of planting (2 seedlings) while high number of germination was recorded in BN1A (Striped Gilo Kumba complex) yielding 59 seedlings. KG2A (*S. aethiopicum* Kumba) and BN7 (*S. anguivi* tiny) also recorded high number of seedlings, 58 each. However, there was no relationship between fruit weigh and germination (0.339). Since environmental effects are excluded in these differences by using a controlled system, the variation observed in seed germination might reflect the genetic constitutions of the species [3, 16] (irrespective of their fruit sizes).

**Fig-1: Dendrogram of the phenotypic quantitative characters in 52 accessions of eggplant**
Aguoru CU et al.; Sch J Agric Vet Sci 2015; 2(1B):54-60.

Fig-2a: Distribution curve of plant height (PLH)

Fig-2b: Distribution curve of percentage of plants that germinated in day 30 (%GP)

Fig-2c: Distribution curve of ripe fruit weight

Fig-2d: Distribution curve of number of days for the emergence of first cotyledon

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Table 1: Quantitative characters

<table>
<thead>
<tr>
<th>ACCESSION</th>
<th>RFW(g)</th>
<th>NSP</th>
<th>DSWg/seed</th>
<th>GP@30days</th>
<th>%GP</th>
<th>PLH(cm)</th>
<th>STD(cm)</th>
<th>STH(cm)</th>
<th>PTL(cm)</th>
<th>LFL(cm)</th>
<th>LFB(cm)</th>
<th>FLWg/4lvs</th>
<th>PTW(g)</th>
<th>SHW(g)</th>
<th>NoL</th>
<th>1st cotyl. (days)</th>
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The environment variations among the accessions may be due to the fact that quantitative traits are determined by the interaction between the polygenes coding for these characters or interactions between polygene and the environment.

### Variables

- **KG4**: 0 60 0.003 49 81.7 6.9 0.25 1.2 0.4 2.4 1.5 0.24 0.8 0.64 4 7
- **KG5**: 82.7 60 0.0026 30 50 5.9 0.1 1 0.3 2 1.5 0.26 0.52 0.26 4 7
- **KG6**: 101.8 60 0.0028 42 70 6.8 0.1 1.9 0.4 2.2 1.8 0.29 0.87 0.58 4 8
- **BN1A**: 111.42 60 0.0036 59 98.3 9 0.15 2.3 0.5 2 1.1 0.34 1.16 0.82 6 4
- **BN1B**: 94.68 60 0.0028 38 63.3 8.2 0.1 2 0.5 2.2 1.5 0.35 1.14 0.79 6 4
- **BN1D**: 98.72 60 0.003 20 33.3 6.4 0.1 1.8 0.5 1.8 1.4 0.26 0.82 0.56 4 7
- **BN1E**: 100.41 60 0.0036 51 85 8.1 0.1 2.1 0.6 2 1.2 0.32 1 0.68 4 4
- **BN1F**: 74.28 60 0.0038 28 46.67 8.5 0.1 2.5 0.6 2.1 0.8 0.27 0.92 0.65 6 4
- **BN2A**: 108.43 60 0.026 39 65 8 0.2 1.9 0.6 2.5 1.7 0.28 0.94 0.66 6 4
- **BN2B**: 98.91 60 0.0022 41 68.3 6.4 0.1 1.8 0.5 1.5 1 0.18 0.54 0.36 4 7
- **BN3A**: 0 60 0.0036 14 23.3 5.2 0.1 2.2 0.3 1.6 1 0.18 0.5 0.32 4 8
- **BN3B**: 0 60 0.0036 28 46.67 7 0.1 2.5 0.3 1.6 1.1 0.15 0.71 0.56 6 7
- **BN4**: 0 60 0.0028 6 10 6.9 0.1 1.7 0.4 1.6 1.2 0.2 0.66 0.46 4 7
- **BN5**: 94.8 60 0.003 41 68.3 9.1 0.1 2.2 0.7 3.4 2 0.4 1.2 0.8 6 4
- **BN6**: 139.34 60 0.0036 40 66.7 9.5 0.2 2.7 0.6 3.9 2.3 0.43 1.43 1 6 4
- **BN7**: 5.32 60 0.00034 58 96.7 7.6 0.1 1.9 0.5 1.5 1.7 0.2 0.98 0.78 4 7
- **BN8**: 72.4 60 0.003 23 38.3 7.5 0.15 2.5 0.4 2 1.1 0.25 1 0.75 4 7
- **FCT2**: 100.83 60 0.0036 19 31.7 7.5 0.2 1.5 0.3 1.3 1.1 0.19 1 0.81 4 7
- **FCT3**: 94.3 60 0.003 21 35 8 0.25 2 0.5 2.5 1.5 0.21 0.82 0.61 6 7
- **FCT4**: 0 60 0.0034 45 75 4.8 0.2 2 0.4 1.3 0.6 0.18 0.39 0.21 3 9
- **FCT5**: 52.8 60 0.0028 2 3.3 5.5 0.2 1 0.2 1.5 1.2 0.18 0.52 0.34 4 7
- **FCT6**: 50.4 60 0.0036 23 38.3 5 0.1 1.3 0.3 1.2 1 0.15 0.53 0.38 4 7
- **NG1B**: 0 60 0.0038 2 3.3 7.4 0.1 2.4 0.2 1.9 0.9 0.21 0.89 0.68 4 8
- **NG1C**: 0 60 0.0032 43 71.67 6.9 0.1 3 0.3 1.7 1.2 0.17 0.78 0.61 4 7
- **NG2A**: 9.66 60 0.0036 32 53.3 8.1 0.1 2.3 0.4 2 1.1 0.22 0.88 0.66 6 4
- **NG2B**: 17.58 60 0.0028 37 61.7 5.4 0.1 1.8 0.2 1.5 0.8 0.19 0.55 0.36 4 7
- **NG3B**: 64.18 60 0.0033 22 36.7 7.3 0.2 2.6 0.3 1.2 1.1 0.33 0.8 0.47 4 8
- **NG3C**: 50.1 60 0.0032 14 23.3 5 0.1 1.2 0.2 1.5 1.3 0.18 0.5 0.32 3 8
- **PL1A**: 79.8 60 0.003 38 63.3 5 0.1 1.5 0.3 1.5 1 0.17 0.62 0.45 4 7
- **PL1B**: 29.2 60 0.0034 34 56.7 8.2 0.1 2 0.6 3.1 2.3 0.36 0.9 0.54 6 4
- **PL1C**: 24.8 60 0.003 21 35 7.8 0.1 1.5 0.6 2.8 2.2 0.31 0.88 0.57 6 4
- **PL2A**: 97.3 60 0.0021 56 93.3 4.4 0.25 1 0.2 1.5 1.5 0.19 0.6 0.41 4 5
- **PL2B**: 65.6 60 0.003 38 63.3 3.4 0.05 1.3 0.2 1 0.6 0.16 0.39 0.23 4 7
- **PL3**: 9.67 60 0.0034 4 6.7 6.2 0.1 1.9 0.4 2.5 2 0.28 0.59 0.31 4 7
- **PL4A**: 30.4 60 0.0036 16 26.7 7.7 0.1 1.8 0.4 1.9 1.1 0.21 0.85 0.64 4 7
- **PL4B**: 80.2 60 0.0036 41 68.3 8.5 0.2 2 0.5 1.9 1.4 0.2 0.91 0.71 6 4

**Definitions**

- **RFW(g)**: ripe fruit weight
- 0g of RFW= only dry seed collected (not ripe fruit)
- **NSP**: number of seed planted
- **DSW**: dry seed weight= x/50 seeds
- **DSW**: dry seed weight= x/50 seeds
- **GP@30days**: germinated seeds in day 30
- **%GP**: percentage of germination
- **PLH**: plant height
- **STD**: stem diameter
- **STH**: stem height
- **PTL**: petiole length
- **LFL**: leaf length
- **LFB**: leaf breadth
- **FLW(g)/4ls**: total fresh leaf weight/plant
- **PTW(g)**: plant total weight
- **SHW(g)**: Shoot weight (PTW-FLW)
- **NoL**: number of leaves per plant/accession
- 1“cotyl (days)= number of days for the emergence of first cotyledon

### Conclusion

In conclusion, the establishment of continuous variations among the accessions may be due to the fact that quantitative traits are determined by the interaction between the polygenes coding for these characters or interactions between polygene and the environment.
which cannot be totally excluded in phenotypic differences[19-20]. Since variability is a template for breeding programmes and crop improvement[21], accessions that display quality characters in their germination may be selected and exploited for commercial horticulture. However, further studies are recommended using larger sample size a combination of many types of molecular markers to fully substantiate these findings.

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