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Interrelationships of Sweet Potato Varieties and their Characters for Yield Determination

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Abstract

Seven sweet potato varieties were evaluated for their relationship (similarity and differences) in southern and eastern zones of Tigray, Ethiopia in 2012. Randomized complete block design with three replications was used for the experiment. Cluster analysis based on ward's method using Squared Euclidian distance was performed for clustering the varieties. Moreover, all characters were standardized before the distance matrix is done due to variables are in different units of characters and to minimize the effect of scale differences. The combined analysis of variance across locations showed significant variation among genotypes, locations and the genotypes by locations interaction..The superior mean total root yield (26.82 t/ha) was obtained at Kukufto testing location while the inferior yield (13.45 t/ha) was at Rarhe. Similarly, genotype LO gave the highest mean total root yield (30.9 t/ha), but bellela gave the lowest (7.78 t/ha). The AMMI analysis also showed highly significant difference for genotypes, locations and the genotypes by locations interaction. The genotype main effect contributed more to the total variability (54.1%) indicating that the variation was largely due to the inheritance of genotype effect. The genotype by location interaction was further partitioned using AMMI model and the first two principal components explained 100% of the total variability. AMMI biplot view of this study identified kukufto as best testing location and LO, Tulla and Kulfo as best genotypes for south and south east zones of Tigray region.

Key Words: Characters; Sweet potato; Yield; Varieties.

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1. Introduction

Sweet potato [*Ipomoea batatas* (L.) Lam] belongs to convolvulaceae family. According to [1] Sweet potato is the world's seventh major food crop after maize, wheat, rice, potato, barley and cassava, and is mainly grown for its edible roots which are high in dietary energy. It grows around the world in diverse environments, often by small farmers in marginal soils, using few inputs [2]. Likewise, this crop is one of the root and tuber crops grown in Ethiopia, and it is the third important root crop next to Enset and Potato [3].The area covered and production of sweet potato in Ethiopia increases from time to time. However, not only the sweet potato research but also its production is very limited to specific regions, like that of South Nation Nationalities and Peoples, Oromia, Harerghe and Amhara regions. In Tigray region, sweet potato is grown mainly in the lowlands and medium altitude areas. Currently, the area coverage of the crop in the region is increasing from time to time. Despite the crop potential, lack of improved sweet potato varieties suitable for different agro-ecologies and resistant to insect pests are some of the factors that hider the crop expansion. Reference [4] pointed out the importance of studying genotype by location interaction not only from the genetic and environmental point of view but also its relevance to the production problems of agriculture in general. The importance of any variety testing program is to obtain the most accurate estimate of variety performance that is possible within the limitations imposed by the environmental growing conditions [5]. Farmers are basically interested in superior and specifically adapted varieties to their condition and with a high degree of stability over time [6],. Hence, the study of multi-location variety trial is particularly relevant to countries that have diverse agro-ecologies, as is the case in Ethiopia. The well performing ability of sweet potato over wide range of environments is of major interest to plant breeders [7]. Due to the higher productivity and drought tolerance of the crop, it can play vital role in achieving food self sufficiency of the region. Even though Tigray region has wider agro-ecological zones and suitable for sweet potato production, unavailability of improved sweet potato varieties that can give high yield and tolerance for diseases and insect pests is a major problem in most sweet potato growing areas of Tigray. Moreover, despite of the diverse agro-ecologies of the Tigray region, multi-location trials have not been conducted for sweet potato varieties and/or genotypes.

A more recent development in measuring genotype adaptability over locations is the application of a multiplicative interaction models such as Additive Main Effects and Multiplicative Interaction [8]. AMMI analysis permits estimation of interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations [9;10;11]. AMMI combines the analysis of variance of genotypes and the location main effects with principal component analysis of the G x L into a unified approach [8]. It uses ordinary ANOVA to analyse the main effects (additive part) and Principal Component Analysis (PCA) to analyse the non additive residual left over by the ANOVA. The results can be graphically represented in an easily interpretable and informative bi-plot that shows both main effects and G x L interaction. The objective of the study was to evaluate the yield performance of the sweet potato genotypes across different locations of the Tigray region

2. Materials and methods

The experiment was carried out in three locations of South and South Eastern zones of Tigray region, Ethiopia.

These locations were Illala, Kukufto and Rarhe and the materials used in this trial were Bellela, Kabode, Kulfo, LO, Temesgen, Tulla and Vitae. The experiment was arranged in Randomized Complete Block Design (RCBD) with three replications and the materials were planted under rain fed condition in 2012. Plot size of 2.4 meter by 4.2 meter with a respective inters-and intra row spacing of 0.60 and 0.30m were used. The Net harvestable plot was 2.4m x 3m (7.2 m^2). Total storage root yield data was taken during the study and the central five rows were harvested from each plot leaving border rows to avoid border effects.

Statistical Analysis: Combined analysis of variance (ANOVA) for yield and yield component characters of the varieties tested across locations was performed using the GenStat [12] statistical package. Before running data analysis, the data were first tested for normality with Shapiro Wilk test method.

Accordingly, all data set showed normal distribution. The pooled ANOVA was used to evaluate the presence of genotype by location interaction and to partition the variation due to variety, location and genotype by location interaction. Since the pooled analysis of variance considers only the main effects, the additive main effect and multiplicative interaction model (AMMI) was computed.

The AMMI method used the standard ANOVA procedure, where after, the AMMI model separates the additive variance from the multiplicative variance (interaction), and then used Interaction Principal Component Analysis (IPCA) to explain the pattern in the genotype by location and residual matrix and also to extract a new set of coordinate axes [13]. The AMMI model is expressed as the following model for the observation Yij on Genotype i in Environment j:

$Y_{ij} = \mu + G_i + E_j + \sum \lambda_k \alpha_{ik}\gamma_{jk} + \varepsilon_{ij}$ where,

Yij is the observed mean yield of the *i*th genotype in the *j*th environment,

μ is the general (Grand) mean)

Gi and *Ej* represent the effects of the genotype and environment respectively,

λ*k* is the singular value of the *k*th axis in the principal component analysis,

α*ik* is the eigenvector of the *i*th genotype for the *k*th axis,

γ*jk* is the eigenvector of the *j*th environment for the *k*th axis, *n* is the number of principal components in the model, and

ε_{ij} is the average of the corresponding random errors.

Based on the results obtained from combined ANOVA, adaptability analysis for sweet potato varieties and traits was determined by AMMI model using GenStat [12]. In addition, Environment mean, Environment index and AMMI Stability Value (ASV) were also used to determine the genotype adaptability in the location

3. Results and discussion

3.1 Grouping of Varieties

The varieties in each cluster are similar to one another with respect to different characters (Figure 3 and Appendix 8) but that the two clusters are quite distinct from each other.

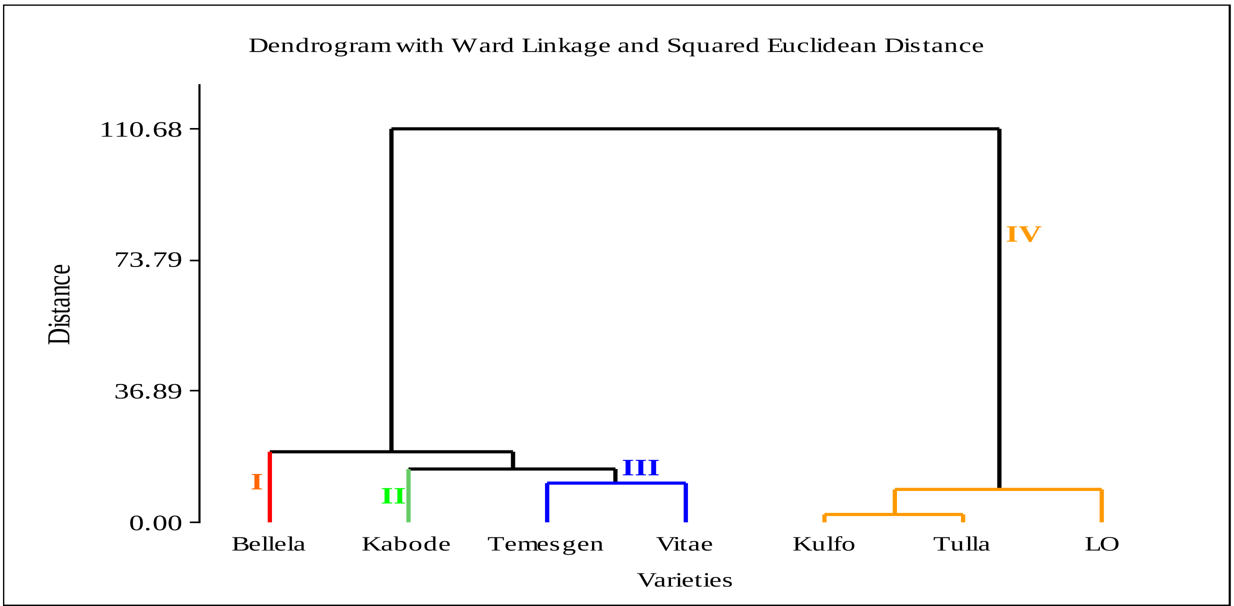

Figure1: Tree diagram of 7 varieties using hierarchical CA (Ward's method and Squared Euclidian distance)

Cluster analysis based on squared Euclidean distance and ward's method [14] categorized the varieties (genotypes) into four groups (clusters). Based on this, cluster I, II, III and IV has 1, 1, 2 and 3 varieties with their ratio of 14.29, 14.29, 28.57 and 42.86%, respectively. Based on Figure 3 and Appendix 8, the result was summarized as follow:

Cluster Variet Characteristics

Cluster 1: Bellela Longest in plant height (larger than the total mean), lowest in total storage root yield (both marketable and unmarketable yields) and poor stand percent at harvest. Moreover, as evaluated at field condition, this cluster (variety) was highly infested with viral disease at all locations as compared with others.

Cluster 2: Kabode Highest in above ground fresh biomass weight but lowest in total storage root number (both marketable and unmarketable). As observed at field condition, pinkish skin color and irregular root shape (most roots curved) were typical features of this variety (cluster).

Cluster 3: Temesgen and Vitae: Above ground fresh biomass weight and root girth was lowest but storage root length, root dry matter content and unmarketable root yield (almost all were less than 100 gram) of this cluster were highest as compared to others. Cluster 4: Tulla, Kulfo and LO: Storage root girth, storage root numbers per plant, root weight, total root numbers and root yields (both marketable and unmarketable) and stand count at harvest were highest for this category but lowest in root length and root dry matter content As observed at field, all the varieties had similar phonological shoot structure (leaf color, shape and size) and were free of diseases. In addition, most of the unmarketable root number of this group was due to its over sized (greater than 500 gram). Based on the CA, it is possible to improve different yield components of varieties. For instance, despite the highest total root yields of cluster IV, its root dry matter content was lower (Figure 2). Similarly, the reverse is true for cluster II. Therefore, it is possible to improve poor character of a member's variety through crossing.

3.2 Principal Component Analysis

Principal Component Analysis (PCA) uses in identifying hidden patterns in the data and was performed to obtain more reliable information on how to identify groups of genotypes that have desirable yield traits for breeding. Eight components were extracted from the 14 studied traits by PCA analysis. But, based on Diana [15] as cited from Kaiser (1960), factors to be retained should have more than 1 eigenvalues, at least 5% variance explained for each component, and/or more than 70% cumulative proportion of variance explained. Accordingly, the first three components that explained 92.3 % of total variation were used for displaying characters. In the first principal component, SRW, MKSRY, TSRY, MKSRN and UMKSRY were the most important traits contributing more to the variation and this component was more associated with the high values of the above traits positively. The sign indicates the direction of the relationship between the components and the characters [16]. Due to more variation explained by the PC 1 (Table 1), its scores could effectively represent the variety effect [17]. In the second principal component, the observed variation (12.9%) was caused mainly by UMKSRN, SRL, VL SRG and AGFBW of which, the latter three traits had negative relationship with this PC. On the other hand, AGFBW, VL and UMKSRN constituted large part of the total variation (8.7 %) explained by the third principal component (Table 1).

Table 1: Eigenvalues, total variance and cumulative variance for 13 quantitative characters in sweet potato varieties

Characters	PC 1	PC 2	PC 3
VL	-0.1296	-0.7581	-0.5262
AGFBW	0.3639	-0.3608	0.6978
SRL	-0.7584	0.5083	0.2744
SRG	0.8891	-0.3937	0.1636
SRN	0.9508	0.2541	-0.1333
SRW	0.9856	-0.04724	0.06602
MKSRN	0.9772	0.07288	0.1125
UMKSRN	0.5916	0.5344	-0.3955
TSRN	0.9231	0.3068	-0.1183
MKSRY	0.9825	-0.06697	0.1009
UMKSRY	0.959	0.1736	0.03949
TSRY	0.9803	0.04134	0.0735
DMC	-0.9001	-0.7581	-0.5262
Eigenvalues	9.20334	1.67646	1.12547
% of total variance	70.795	12.896	8.657
% Cumulative variance	70.795	83.691	92.348

**VL: Vine Length (cm); AGFBW: Above Ground Fresh Biomass Weight (t/ha); SRL: Storage Root Length (cm); SRG: Storage Root Girth (cm); SRN: Storage Root Number per plant, SRW: Storage Root Weight (g/root); MKSRN: Marketable Storage Root Number Per Plot; MKSRY: Marketable Storage Root Yield (t/ha); UMKSRN: Unmarketable Storage Root Number Per Plot; UMKSRY: Unmarketable Storage Root Yield (t/ha); TSRN: Total Storage Root Number Per Plot; TSRY: Total Storage Root Yield (t/ha); DMC: Root Dry-Matter Content (%)*

The first two component scores were plotted to aid visualization of the overall variability among the populations. Hence, Figure 4 showed that there was a positive relationship between total storage root yield (TSRY) and UMKSRY, UMKSRN, TSRN, SRN, MKSRN, MKSRY, SRW SRG and AGFBW whereas SRL and DMC were negatively correlated to the total root yield. Other researchers [17] ; [18] and [19] used PCA to explain variation among genotype characters and reported the relationship that existed between yield and yield components of different crops. Varieties, Tulla, Kulfo and LO varieties had low values (Figure 2) with respect to SRL and DMC but high value relatively with other yiled components. This contributed to the variations in the first and second principal components. On the other hand, Temesgen and Vitae (group 3) and Kabode (group 2) had more SRL and DMC. In general, this PCA allowed comparative evaluation of varieties for yield components and total storage root yield and helped to identify varieties that were desirable relative to several traits.

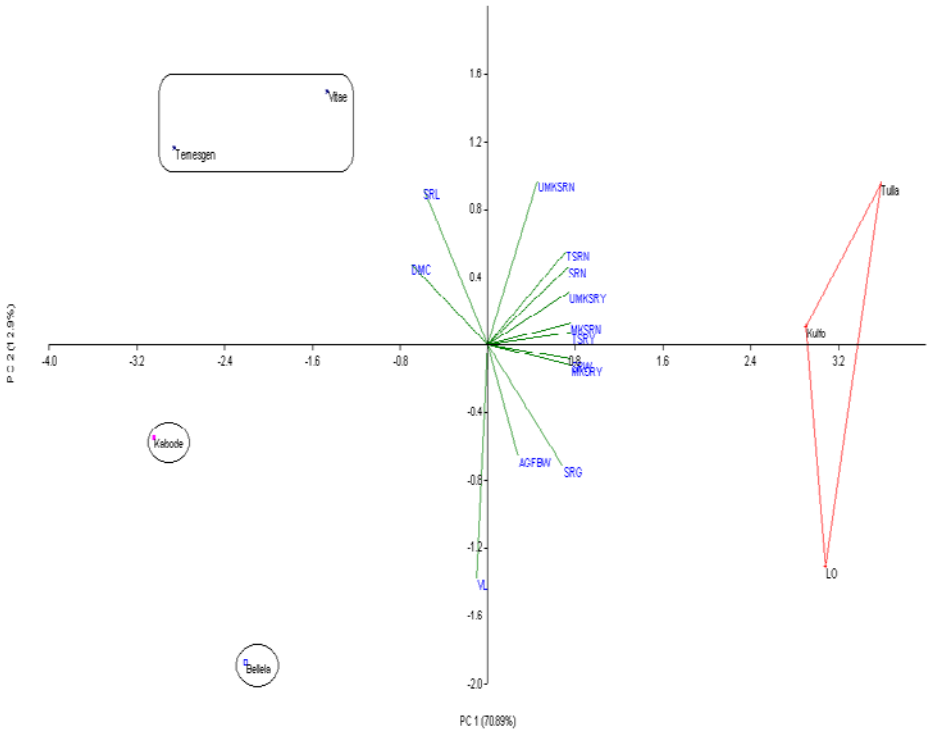

Figure 2: PCA scatter diagram of sweet potato varieties and their yield components

3.3 Association of Total Storage Root Yield with other Yield Components

Phenotypic correlation coefficient of total storage root yield with other characters is presented in Table 10. Total root yield had positive phenotypic correlation with all the other traits but has negative relationship with storage root length and root dry matter content. This negative relationship of the total root yield with root length (r = **-**0.651) and root dry matter content (r = **-**0.851) was highly statistical significance. This result was in contradiction with [20] but in agreement with the findings of [21,22,23] .

They indicated the presence of negative and highly significant associations between dry-matter content of the root and total storage root yield. Therefore, these traits could not be improved with total storage root yield in positive direction since selecting higher values of these traits would lead to reduced total storage root yield. In addition, the total root yield has highly positive significant association with the characters of storage root number per plant, average root weight, marketable and unmarketable root numbers and yields.

The existence of positive and significant association between total storage root yield with unmarketable root yield, marketable root number, marketable root yield, the root number per plant, and root weight indicates choice based on the characters improve the total yield. The magnitude of these traits for the contribution of positive and highly significance association was r = 0.989, 0.953, 0.993, 0.911 and 0.945**,** respectively.

These traits are the most important components to have acceptable total storage yield and a variety to be selected. On the other hand, the total root yield correlated positively but non-significantly with above ground fresh biomass weight. The non-significant association between these traits and total storage root yield indicates that a researcher may not be possible to select high yielding varieties (genotypes) based on these characters. A number of findings indicated that there was non-significant and/or negative association between vine length trait and total root yield.

Studies conducted by [24] on assessment of agro-morphological variability and yield components among sweet potato landraces has shown non-significance correlation among root yield and stand count at harvest. The study carried out by [25] revealed that in sweet potato cultivars with large shoot growth resulted to more competition with storage root growth for assimilates.

This was practically observed at Rarhe location where highest shoot biomass weight was recorded. The present result was in agreement with [20], who observed non-significance association between total storage root yield and other traits, such as fresh top weight and vine length at three locations of southern Ethiopia.

According to [24] as cited in Grafius (1959), increasing total root yield would be made easier by selecting for components because components are more often easily inherited than total yield itself.

Table 2: Phenotypic Correlation coefficient among sweet potato traits

	VL	AGFBW	SRL	SRG	SRN	SRW	MKSRN	UMKSRN	TSRN	MKSRY	UMKSRY	TSRY
VL	1											
AGFBW	**-0.012**	**1**										
SRL	**-0.359**	**-0.250**	**1**									
SRG	**0.157**	**0.421**	**-0.838****	**1**								
SRN	**-0.260**	**0.188**	**-0.66****	**0.811****	**1**							
SRW	**-0.016**	**0.377**	**-0.661****	**0.943****	**0.741****	**1**						
MKSRN	**-0.278**	**0.388**	**-0.704****	**0.88****	**0.945****	**0.847****	**1**					
UMSRN	**-0.134**	**-0.030**	**-0.270**	**0.426**	**0.765****	**0.299**	**0.541****	**1**				
TSRN	**-0.249**	**0.237**	**-0.588****	**0.776****	**0.986****	**0.693****	**0.913****	**0.837****	**1**			
MKSRY	**-0.123**	**0.412**	**-0.711****	**0.959****	**0.886****	**0.961****	**0.955****	**0.481**	**0 .853****	**1**		
UMKSRY	**-0.249**	**0.269**	**-0.567****	**0.878****	**0.925****	**0.907****	**0.935****	**0.623****	**0.909****	**0.965****	**1**	
TSRY	**-0.180**	**0.35**	**-0.651****	**0.930****	**0.911****	**0.945****	**0.953****	**0.550****	**0.885****	**0.993****	**0.989****	**1**
DMC	**-0.082**	**-0.182**	**0.922****	**-0.919****	**-0.815****	**-0.847****	**-0.863****	**-0.350**	**-0.73****	**-0.882****	**-0.796****	**-0.851****

** significance at 1% probability levels; ¥ Figures in parenthesis indicate the degree of freedom

3.4 Correlation between Sweet Potato Characters

In the present investigation many of the characters were positively and negatively correlated with each other. However, in most cases, the correlations between pairs of characters were non-significant at phenotypic level (Table 2). Among associations exhibited between pairs of characters at phenotypic level, vine length was found to be negative but very non significantly correlated with above ground fresh biomass weight (r = -0.012) but positive with stand count at harvest (table not shown). This indicates that an increase in vine length does not necessarily lead to an increase in biomass weight. But the vine length associated negatively but non-significantly with storage root length, average root weight, unmarketable root number and root yield. Similarly, it correlated negatively and non significantly with the average root number per plant, marketable root number and root yield as well as with root dry matter content. Above ground fresh weight showed highly significant positive relationship only with the stand count at harvest and negatively non significance only with the root length, unmarketable root number and root dry matter. It correlated positively but non-significantly with the remaining characters.

Likewise, the total storage root number correlated in a highly significant and positively approach with unmarketable and marketable storage root numbers and root yields but negatively with the root dry matter. Similar results were obtained by [26] though non- significance for the marketable and unmarketable yield components. Even if the total storage root number was negatively correlated with root length, it was significant. The negative relationship of total root number with root length and dry-matter content of the root is supported by other findings [22,27].

Root length and root diameter had shown highly significance negative correlation (r = -0.838). Though, this finding contradicted with the result of [24], it is concurred with the result done by [28]. However, highly Significant positive correlations was attained within root girth and average storage root weight (r = 0.943). This suggested that improvement aimed at any of the character would automatically lead to improvement in the other. The work of [21] also linked an increase in storage root diameter within an increase in individual storage root weight. Plants that have smaller root size could have light weight as supported by the result obtained from different authors [29,22]. They identified highly significant positive association between these traits. On the other hand, most of the association of average storage root weight and other characters was positive and highly significant, such as with root yields and marketable root number but negative and relatively higher relation observed with root length and root dry matter content. Smaller and positive magnitude of relationship was found between average root weight with unmarketable root number, stand count at harvest, root length and green top fresh biomass weight.

As indicated in Table 2, the marketable storage root yield correlated negatively with the root length and the root dry matter in significant manner. This implies, more and more length in the root resulted in more thinly and fibrous roots that may not end with desired marketable storage roots, i. e, round healthy, neither over sized nor under sized, weighing 100g - 500g as suggested by[30]. On the other hand, more marketable root yield leads to lower dry matter content as fresh root yield holds more water content and relatively lower dry matter [31]. As explained earlier, marketable root yield positively correlated with all the characters except the vine length, root length and root dry matter. However, it had shown very highly relationship with marketable root number (r = 0.955), and average root weight (r = 0.961) and very small with the above ground fresh biomass weight (r = 0.412).

In similar manner with the marketable root yield, the unmarketable storage root yield also showed positive correlation with all the traits but negatively with the root length, vine length and root dry matter. It had highly significant positive association with marketable and unmarketable root numbers (total root numbers), average storage root weights but non-significant positive with the fresh shoot weight and stand count at harvest. As described by [32], the positive association of unmarketable storage root yield with the traits suggested that selection of one of the traits would lead to the improvement of unmarketable storage root yield in a similar direction. On the contrary, unmarketable storage root yield was significantly but negatively correlated with root length and dry-matter content of the root. These would lead to the selection of one trait in undesirable direction if we perform selection for higher values of the other traits.

Except storage root length, none of the traits was positively correlated with root dry matter content (Table 2). Similarly, none of the traits was negatively associated with stand count at harvest except unmarketable storage root number and root dry matter. The root dry matter content correlated negatively and non-significantly only with three traits (plant height, above ground fresh biomass weight and unmarketable root number). But it associated highly and significantly with the other characters negatively except root length (positive). Most of the characters examined by [30] were in agreement with this correlation result of root dry matter content correlation. On the contrary, the character of stand count at harvest had non-significant relationship with all the traits except vine length and biomass weight. Additionally, unlike with the unmarketable storage root number and root dry matter (negative), the stand count at harvest was correlated with all the other characters positively. From this statistics, one can understand that, as the number of plant population increased in the harvestable plot, above ground fresh biomass weight also increased.

4. Summary and Conclusion

Based on the combined mean total root yield of locations and different yield evaluation methods, high yielding varieties were identified. Accordingly, LO and Tulla varieties gave highest root yield per unit area at all locations, followed by Kulfo. Therefore, these varieties can play a vital role in food self sufficiency and food security of Tigray. Moreover, LO, Tulla and Kulfo are early maturing, drought and disease tolerant varieties and thus, they can be appropriate varieties for the dry land areas of the region. Not only higher productivity and drought tolerance, but also they are orange fleshed varieties which contribute in the reduction of vitamin A and C deficiency. Therefore, these varieties should be widely distributed to farmers of the testing locations and similar areas of the region. The presence of significant genotype by location interaction effect shows that some varieties adapted to wider locations, whereas others to specific locations. Based on this, genotype Kabode has shown less V x L interaction and it is more stable across locations. Despite of its consistence (wider adaptability), the root yield obtained from this genotype was below average. On the other hand, it gave better above ground fresh biomass weight and hence, good for animal feed. In this study, Temesgen, Vitae, and Bellela varieties gave below average total root yield and their roots were mostly under sized (less than 100 gm).

5. Recommendation

Based on the overall mean tuber yield and yield components of this multi-location trial, varieties Kulfo and Tulla could be scaled out to farmers of the growing areas and its similar characteristics. Likewise, the experiment needs to be repeated over several locations and years to understand the interrelationships of the sweet potato varieties and their characters**.** Root diameter and average storage root weight should also be given due consideration during selection for improved total storage root yield of sweet potato crop in general.

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