Variability and Association of Traits in Sweet Potato *Ipomoea Batatas* Accessions at Haramaya, Eastern Ethiopia

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ABSTRACT

Sweet potato (*Ipomoea batatas* (L.) Lam.) belongs to the convolvulaceae family. In Ethiopia, sweet potato has been cultivated for the last several years. By considering its prominence, it is important to increase its productivity through genetic manipulation. Thus, this study was

undertaken, to estimate the extent of variability in accessions, heritability and genetic advance for yield and yield related traits. The experiment carried out 2014/2015 cropping season using 25 accessions with two released varieties. Randomized Complete Block Design (RCBD) with three replications where used. Data was collected on both plants and plot basis. The mean squares due to accessions were highly significant ($p<0.01$) for all traits studied, except storage root length ($p<0.05$) this indicates the existence of sufficient genetic variability among the accessions. For all characters PCV value greater than GCV but the two values different in narrow. PCV ranges (6.72% DPM-73.14% MSRY) and GCV ranges (5.12% DPM-66.72 AMSR). High PCV and GCV can offer opportunity for selection of superior genotypes with respect to character of interest. All the traits considered in the study exhibited high heritability ranged (13.79 GC-99.18% MSRY) it indicated additive and non-additive genetic variances with lesser influence of the environment.

Keywords: Accessions; Genetic advance; Heritability; Sweet potato; Yield related traits

INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a root crop belongs to the convolvulaceae family. This family includes about 55 genera and more than 1000 species. It is hexaploid (6x=90) and usually considered the only species of Ipomoea of economic importance which support millions of people throughout the tropical regions. In Africa it was introduced by explorers from Spain and Portugal during the 16th century [1]. Based on the presence of large numbers of varieties, East Africa is one of the areas suggested as secondary center of diversity for sweet potato [2].

In Ethiopia, agriculture is the main source of livelihood for about 80% of the population which it contributes to 42% of Ethiopia's gross domestic product [3]. Sweet potato has been cultivated for the last several years and over 95 % of the crop is produced in the southwest, eastern and southern parts. It is one of five most important crops, in terms of production, economic value, and contribution to calories and proteins. But the productivity of sweet potato is limited to both abiotic and biotic constraints, leading to poor yields and quality at

farm levels. The crop has a potential of giving over 50 to 60 tons/

ha in Ethiopian conditions, however, yield obtained from farmer's field is lower than 6 to 8 tons/ha. Thus the yields are ten times lower than the potential sought. One of the main reasons is shortage of improved varieties planting materials in addition to other factors [4]. Despite its importance, there have been few genetic studies on sweet potato, probably due to its self-incompatibility and high level of cross incompatibility, polyploidy level hexaploid (2n=6x=90) and large chromosome number [5]. This may be the reason that sweet potato is one of the most under exploited in the developing worlds as compared to major crops [6]. Considering the importance of sweet potato as one of the potential crops for both domestic consumption as well as export markets, it is important to increase its productivity along with desirable attributes through genetic manipulation. However, genetic information with respect to the nature and magnitude of variability and relationship between root yield and yield related traits are not generated on sweet potato genotypes maintained under Ethiopian conditions. Such information is absolutely essential to design effective breeding strategies for genetic improvement of this crop. Thus, this study were undertaken to determine interrelationships among yield and yield related characters so as to identify component characters whose

selection lead to improvement in storage root yield. Moreover, this study was there for involve the evaluation of variable sweet potato collections with different yield potentials and qualities and selection of superior genotypes for future use and improvement. Therefore, the objectives of this study are; to estimate the extent of variability, to estimate heritability and genetic advance for yield and yield related traits and to estimate the degree of association among yield and related traits.

MATERIALS AND METHODS

The field experiment was carried out during 2014/2015 cropping season at Haramaya University research field. The area receives an annual rainfall of 760 mm and average maximum and minimum temperatures respectively. Twenty five sweet potato accessions along with two released varieties (Table 1) were used to assess the information on variability and association of the characters which determine yield and other quality attributes. The accessions were selected among 116 local and international collections maintained at Haramaya University based on the evaluation and characterization made in 2012/13 cropping season. The selection of the accessions was made on the performance of genotypes which were performing better. Eleven accessions were introduced from abroad (6 and 5 from Asian and Nigeria vegetable center, respectively), 10 accessions were collected from Hararghe, one each from central and southern Ethiopia, while the two released varieties were introduced from Cuba.

Table 1: List of accessions used.

S.No.	Accession code	Collection source	Days to physiological maturity
1	CN-2065-15	Asian Vegetable Center	185
2	CN-1753-11	Asian Vegetable Center	163
3	CN-1753-18	Asian Vegetable Center	176
4	CN-1752-5	Asian Vegetable Center	160
5	CN-2059-8	Asian Vegetable Center	160
6	CN-1752-9	Asian Vegetable Center	192
7	Korojo	Hararghe	188
8	Becale-A	Hararghe	175
9	Becale-B	Hararghe	174
10	Korojo-2	Hararghe	111
11	Becale	Hararghe	188
12	Alemaya local-2	Hararghe	167
13	Alemaya Local-3	Hararghe	160
14	Koka-14	Central Ethiopia	142
15	Arbaminch	southern Ethiopia	196
16	Tis-8250-9	Nigeria Vegetable Center	188
17	Tis-8250-7	Nigeria Vegetable Center	143
18	Tis-9465-9	Nigeria Vegetable Center	175
19	Tis-9065-5	Nigeria Vegetable Center	120
20	Tis-82/0602-12	Nigeria Vegetable Center	188
21	Korojo-1	Hararghe	142
22	Bekale Type 1	Hararghe	185
23	Bekale type 2	Hararghe	164
24	Adu	Cuba	186
25	Berkome	Cuba	191

Experimental design and procedure

The experiment was conducted using Randomized Complete Block Design (RCBD) with three replications and with plot size of 33.6m with 1m and 0.3 m inter-row and intra-row spacing, respectively. Data was collected from the 10 plants that were grown in one central row. Young portion of 30 cm length of the vine cuttings planted where 2/3 of their length covered by soil. The accessions were planted on July/2014 as soon as the rain starts and the soil get sufficient moisture. All plots where receive the recommended cultural practices uniformly. Replanting was done to substitute the dead vine after one week of planting.

Harvesting was done after 90 % of the sweet potato leaves changed in to yellowish color. From each plot ten 10 plants were be considered for both storage root yield and yield related traits. In the field, the physical attributes was characterized immediately after harvest. From the total harvest, five sweet potato storage roots was randomly selected for laboratory analysis immediately after yield and yield related data recorded.

RESULT AND DISCUSSIONS

Analysis of variance

This indicates the existence of sufficient genetic variability among the accessions. In line with this study [7] revealed that yield and yield contributing characters such as length of vain, tuber number per plant, tuber weight per plant and tuber yield per plant varied significantly due to varietal difference. whereas number of branch per plant, days to bud sprouting, pH, dry matter content, peel content and specific gravity were no significant different for all accessions.

Estimates of range and means

The results of the present study on the estimates of range and mean for the characters studied are presented. Length of main vain exhibited a wide range of variation across the accessions the shortest were obtained from accession (CN1753-11) 46.86 cm and the tallest 145.67 cm.

For all characters under the study PCV value greater than GCV but the two values different in narrow indicating the variability due to genetic constituent of the genotypes was more than the variability exerted by environmental factor. Hence selection for desirable traits for variable characters would be effective for sweet potato improvement. The ranges for PCV was 6.72% in respect of days to maturity to 73.14% in case of marketable storage root yield and for that of GCV, it was 5.12% for days to physiological maturity to 66.72% in respect of average mass of storage root. Low PCV and GCV was obtained from days to bud sprouting (6.44%), number of branch per plant (6.53%), days to physiological maturity (5.12%) and storage root stalk length (9.31) indicating limited scope for improvement of this trait through selection. The result revealed that considerable phenotypic and genotypic variance among the genotypes for the trait. Large portion of phenotypic variance was accounted by genetic components. Generally, PCV and GCV estimates were observed to be high for marketable storage root yield, total storage root yield, average mass of storage root and root fresh weight indicating high genetic variability for effective selection.

Estimates of heritability (H2) in broad sense

All the traits considered in the study exhibited high heritability estimates indicating additive and non-additive genetic variances with lesser influence of the environment. Selection for such traits should fairly be easy due to closer correspondence between genotype and phenotype arising from relatively smaller contribution of environment to the phenotype. The high heritability value recorded for all the traits indicated the possibility of progress in selection process. Genotypic coefficient of variation along with heritability estimates would provide a heritability estimates were low for number of branch per plant (13.79), days to bud sprouting (13.85), ground cover (37.61) and storage root length (19.29) which leads imperfect scope for selection and improvements for this traits.

Estimates of expected genetic advance

High expected genetic advances were observed for marketable storage root yield, unmarketable storage root yield, total storage root yield, root fresh weight, average mass of storage root and length of main vain. Hence, selection for these characters is likely to be more effective, as high heritability values were associated with high genetic advance in the present study. Therefore, it is imperative that selection of germplasm lines based on phenotypic performance for these characters with low genetic advances would not be effective.

Genotypic correlation

The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for most of the characters indicating inherent association among most characters. Low phenotypic correlation could arise due to the modifying effect of environment on the association of characters at genetic level. The results of this study indicated that highly significant positive phenotypic associations were observed between total storage root yield t/ha and marketable storage root yield and root fresh weight. Among significant associations exhibited between pairs of characters at phenotypic level, highly significant positive correlation was observed between storage root girth and individual storage root weight. This suggested that improvement aimed at any of the character would automatically lead to improvement in the other.

Phenotypic correlation

Total storage root yield had significant phenotypic correlation with root fresh weight, average mass of storage root, marketable root number and unmarketable root number. The positive correlation was observed with most of above ground related traits such as length of main, days to bud sprouting, ground cover, vine inter node length, vine inter node diameter, mature leaf size and from root related traits such as marketable rot yield, root width and storage root length, average mass of storage root, marketable root number per plant and marketable root yield had positive correlation with storage root yield. As observed in total storage root yield (t/ha) had strong highly significant positive association with root fresh weight, average mass of storage root and significant positive correlation with marketable root number per plant with highly significant negative correlation of un marketable root number per plant.

CONCLUSION

Root and tuber crop in general and sweet potatoes in particular are very important crop to sustain food security in developing country like Ethiopia. Therefore, it is paramount important to increase production and productivity of this crop by appropriate variety selection to the specific environment and by adopting different agronomic practices. Variety development with desirable, heritable qualitative and quantitative trait is very important. This can be achieved by knowing of those traits that can be altered by environmental factors and heritable. For all characters under the study PCV value greater than GCV but the two values different in narrow indicating the variability due to genetic constituent of the genotypes was mare than the variability exerted by environmental factor. Hence selection for desirable traits for variable characters would be effective for sweet potato improvement. Similarly, high heritability estimates indicating additive and non-additive genetic variances with lesser influence of the environment. Selection for such traits should fairly be easy due to closer correspondence between genotype and phenotype arising from relatively smaller contribution of environment to the phenotype. Generally, PCV and GCV estimated were observed to be high for marketable storage root yield, total storage root yield, average mass of storage root and root fresh weight indicating high genetic variability for effective selection. If heritability of a character is very high greater than 80%, selection for such a character should be easy. This is because there would be a close correspondence between the genotype and phenotype due to a relatively small contribution of the environment to the phenotype. Since the finding are based on one locations and seasons is required to generate more reliable information on the estimation it's better to do across location and season.

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