

Full Length Research Paper

Characters association and path coefficient analysis of orange fleshed sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes evaluated in Hawassa, Ethiopia

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The experiment was conducted to assess associations between root yield and yield-related traits of orange-fleshed sweetpotato genotypes to identify traits that have maximum effect on root yield of sweetpotato to make possible selection. Twenty-four Orange Fleshed Sweetpotato genotypes were evaluated in 2017 main cropping season at Hawassa Agricultural Research Center using a Randomized Complete Block Design (RCBD) with three replications. Data were collected from 12 traits, and then subjected to analysis of variance (ANOVA), correlations and path coefficient analysis. The estimation of characters associated revealed that storage root yield was positively and significantly associated with roots number per plant, root length, root girth, harvest index at both genotypic and phenotypic levels. Some of the traits showed a highly significant ($p < 0.01$) positive genotypic and phenotypic correlations while the other traits showed significant negative correlations. The genotypic correlation coefficients were higher than phenotypic correlation coefficients in magnitude indicating fairly strong inherent association between the characters studied. Path analysis revealed that roots number per plant, root girth and harvest index had positive direct effects on storage root yield at both phenotypic and genotypic levels. Based on the results of current study, traits that showed a positive effect on storage root yield could be used as the best predictors of storage root yield in sweetpotato improvement program.

Key words: Character association, correlation coefficients, path coefficient, sweetpotato.

INTRODUCTION

Orange fleshed sweetpotato [*Ipomoea batatas* (L.) Lam.] is a rich source of β -carotene and has a large potential in fighting against vitamin A deficiency (VAD) in human diet in developing countries (Chassy et al., 2008; Burri, 2011). Previous reports by WHO (2009) and Tsegaye et al. (2010) indicated that VAD is a serious public health

problem happening mainly among children and women of childbearing age in Ethiopia. In this regard, orange-fleshed sweet potato (OFSP) is an invaluable crop for fighting against vitamin A deficiency in sub-Saharan Africa countries like Ethiopia (Tumwegamire et al., 2004; Low et al., 2009; Gurmu et al., 2015). Storage roots are

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commonly the edible part of sweetpotato. Since the storage root yield is a complex trait with low heritability, it requires the knowledge on the nature and magnitude of correlations between important traits to make possible direct or indirect selection for improvement of the crop (Gurmu et al., 2017). In sweetpotato, root flesh colour directly correlates with root β -carotene content, where root dry matter content negatively correlated with root β -carotene content (Gurmu et al., 2017). The authors also explained the importance of having knowledge on the number of traits to be evaluated and magnitude of their correlations for indirect selections. More to the point, correlation analysis provides information about the degree of relationship between important plant traits and is also a good index to predict yield response in relation to the change of a particular character. When higher numbers of variables are considered in correlation, the association becomes more complex.

Path coefficient analysis is a reliable statistical technique which provides means not to quantify the interrelationships of different yield components but also indicates whether the influence is directly reflected in the yield or takes some other pathway for ultimate effects (Dewey and Lu, 1959). Therefore, this research was conducted to demonstrate the association among various characters and identify traits that have maximum effect on root yield of orange fleshed sweetpotato genotypes.

MATERIALS AND METHODS

Description of the experimental site

The experiment was conducted during the 2017 under rain-fed condition at Hawassa Agricultural Research Center (HwARC). HwARC is located in Hawassa city (7°04'N, 38°31'E, 1700 m above sea level with the average annual rain fall of the area 1141 mm, minimum/maximum air temperature is 13.1/27.1°C respectively), the capital of Southern Nations, Nationalities, and Peoples' Regional State (SNNPRS), in the southern part of Ethiopia. The soil is volcanic in origin and is classified as Vitric Andosol which is suitable for sweetpotato production.

Experimental materials

Twenty four orange fleshed sweetpotato genotypes were used for the study, among which two released varieties in Ethiopia included as checks (Kulfo and Tula). The four genotypes are advanced lines from HwARC crosses and the rest are introduced varieties from Kenya, Uganda and Mozambique. The description of the genotypes is shown in Table 1.

Experimental design and field management

The experiment was arranged in Randomized Complete Block Design (RCBD) having three replications. There were three blocks each consisting 24 plots. A plot size was 7.2 m² with 3 m long and 2.4 m width. Each plot consisted four rows (ridges), with ten plants per a row. The spacing between rows and between plants within row was 60 and 30 cm, respectively. The spacing between blocks was 2 m. Ten holes per row and 40 per plot were prepared and one vine cutting (plant) of 30 cm length was planted in each hole of the

row (ridge). The trial was planted on 8 August, 2017. All plots received the recommended cultural practices uniformly and no fertilizer was applied. Replanting was done to substitute the dead vine after one week of planting. Hilling up was done after fourth week of planting and all plots were kept weed free by regular weeding and cultivation. Harvesting was done on 28 December, 2017 after sweetpotato leaves changed to yellowish color. Two central rows were used for data recording by excluding the two plants grown at both ends of the row and the two border rows.

Data collection

The data were recorded on the following parameters: vine length (cm), vine inter-nodal length (cm), mature leaf length (cm), vine girth (mm), petiole length (cm), ground coverage (%), number of storage roots per plant, storage root length (cm), storage root girth, aboveground fresh weight (t ha⁻¹), marketable yield (t ha⁻¹), unmarketable yield (t ha⁻¹), total storage root yield (t ha⁻¹), sweetpotato virus disease (SPVD), predominant skin colour, predominant flesh colour, β -carotene content, root dry matter content (RDMC), and harvest index (HI).

$$\text{Harvest Index} = \frac{\text{Economic Yield}}{\text{Biological Yield}} \times 100$$

$$\text{Yield per hectare in tones} = \frac{\text{Yield per net plot (kg)} \times 10,000}{\text{Net area of the plot (m}^2\text{)} \times 1000}$$

Data analysis

Correlation analysis

Phenotypic and genotypic correlations were computed following the method described by Singh and Chaudhary (1985) as:

$$r_g = \frac{C_{covx,y}}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}}$$

$$r_p = \frac{P_{covx,y}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

where r_p and r_g are phenotypic and genotypic correlation coefficients, respectively; $P_{covx,y}$ and $g_{covx,y}$ are phenotypic and genotypic covariance between variables x and y, respectively; σ^2_{px} and σ^2_{gx} are phenotypic and genotypic variances for variable x and y, respectively.

$$SE(r_p) = \sqrt{\frac{1-r^2_p}{n-2}}$$

where n is the number of genotypes tested, r^2_p is phenotypic correlation coefficient, SE (rp) = standard error of phenotypic correlation.

The calculated phenotypic correlation values were tested for its significance using t-test:

$$t = \frac{r_p}{SE(r_p)}$$

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where n is number of genotypes.

$$SE_{rgxy} = \sqrt{\frac{1-r^2_{gxy}}{h_2x}} \cdot h_2y$$

The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robinson and Comstock (1955) indicated as follows:

Table 1. List of genotypes used for the study.

No.	Genotypes	Source	Status	Year of release
1	Ukr/Eju-10	HwARC cross	Advanced line	Not yet released
2	Ukr/Eju-13	HwARC cross	Advanced line	Not yet released
3	Res/Tem-14	HwARC cross	Advanced line	Not yet released
4	Res/Tem-23	HwARC cross	Advanced line	Not yet released
5	Jewel	CIP-Kenya	Released abroad	1995
6	Carrot Dar	CIP-Kenya	Released abroad	1995
7	Maputha-1	CIP-Kenya	Released abroad	1995
8	Vita	CIP-Uganda	Released abroad	2007
9	Kabode	CIP-Uganda	Released abroad	2007
10	Naspot-12	CIP-Uganda	Released abroad	2013
11	Naspot-13	CIP-Uganda	Released abroad	2013
12	Tainung-15	CIP-Kenya	Released abroad	1995
13	Carrot C	CIP-Kenya	Released abroad	1995
14	Mayai	CIP-Kenya	Released abroad	1995
15	Kyoyabwerere	CIP-Kenya	Released abroad	1995
16	RW11-4743	CIP-Kenya	Released abroad	1995
17	Tomulabula	CIP-Kenya	Released abroad	1995
18	Wagabolige	CIP-Kenya	Released abroad	1995
19	Melinda	CIP-Mozambique	Released abroad	2011
20	Cacilia	CIP-Mozambique	Released abroad	2011
21	Gloria	CIP-Mozambique	Released abroad	2011
22	Jane	CIP-Mozambique	Released abroad	2011
23	Kulfo	Ethiopia	Released in Ethiopia	2005
24	Tula	Ethiopia	Released in Ethiopia	2005

HwARC = Hawassa Agricultural Research Center, CIP = International Potato Center.

$$t = \frac{rgxy}{SErgxy}$$

where h^2x = Heritability of trait x and h^2y = Heritability of trait y, $SErgxy$ = standard error of genotypic correlation for character x and y. All the analysis was done using SAS software version 9.0.

Path coefficient analysis

Path coefficient analysis provides an effective way of finding out direct and indirect sources of correlations and identifies the most reliable yield contributing traits. It is computed using the method suggested by Dewey and Lu (1959) using Microsoft Excel 2010. Thus, correlation coefficient of different characters with storage root yield was partitioned into direct and indirect effects adopting the following formula:

$$r_{iy} = r_{1ipi} + r_{2p2} + \dots + r_{1ipi} + \dots + r_{mipn}$$

where r_{iy} is correlation of i th character with storage root yield; r_{1ipi} is indirect effects of i th character on storage root yield through first character; r_{ni} is correlation between n th character and i th character; n is number of independent variables; P_i is direct effect of i th character on storage yield; P_n is direct effects of n th character on storage root yield.

Direct effect of different component characters on storage root yield was obtained by solving the following equations:

$$(r_{iy}) = (p_i) (r_{ij}); \text{ and } (p_i) = (r_{ij}) - 1(r_{1ipi})$$

where (P_i) is matrix of direct effect; (r_{ij}) is matrix of correlation coefficients among all the n th component characters; (r_{iy}) is matrix of correlation of all component characters with storage root yield; (r_{1ipi}) is indirect effect of i th character on storage root yield through first character.

RESULTS AND DISCUSSION

Genotypic and phenotypic correlations

Phenotypic and genotypic correlation coefficient between root yield and its 12 component traits in all possible combinations are presented in Table 2. Traits such as harvest index $r_p=0.82$, $r_g=0.83$, number of roots per plant $r_p=0.84$, $r_g=0.84$, marketable root yield $r_p=0.91$, $r_g=0.97$, unmarketable root yield $r_p=0.49$, $r_g=0.56$ showed a highly significant ($P<0.01$) and a significant ($P<0.05$) positive phenotypic and genotypic correlation was observed by root length $r_p=0.45$, $r_g=0.49$ while sweetpotato virus disease showed significant ($r_p=-0.33$ and $r_g=-0.34$) negative correlations. Root dry matter content, root beta-carotene content and root flesh colour exhibited non-significant correlations. In general, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients in magnitude, indicating fairly

Table 2. Genotypic (above diagonal) and phenotypic (below the diagonal) correlation coefficients among nine traits in 24 OFSP genotypes.

Trait	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	MRKY	UMRKY	TYLD
SPVD		-0.23 ^{ns}	-0.21 ^{ns}	-0.29*	-0.14 ^{ns}	-0.06 ^{ns}	0.30*	0.17 ^{ns}	-0.24*	-0.35*	-0.14 ^{ns}	-0.34*
RL	-0.20 ^{ns}		0.12 ^{ns}	0.36*	0.26*	0.61***	-0.03 ^{ns}	0.07 ^{ns}	0.52***	0.44**	0.40*	0.49**
RG	-0.20 ^{ns}	0.22 ^{ns}		0.02 ^{ns}	0.36*	-0.18 ^{ns}	-0.22 ^{ns}	0.09 ^{ns}	0.36*	0.48***	-0.05 ^{ns}	0.41*
AGFW	-0.25*	0.32*	0.04 ^{ns}		-0.45***	0.32*	-0.34*	-0.22 ^{ns}	0.04 ^{ns}	0.07 ^{ns}	0.08 ^{ns}	0.08 ^{ns}
HI	-0.16 ^{ns}	0.23 ^{ns}	0.31*	-0.43**		-0.14 ^{ns}	0.16 ^{ns}	0.25*	0.74***	0.80***	0.51***	0.83***
RDMC	-0.04 ^{ns}	0.48***	-0.14 ^{ns}	0.26*	-0.13 ^{ns}		-0.01 ^{ns}	-0.10 ^{ns}	0.07 ^{ns}	-0.02 ^{ns}	0.26*	0.05 ^{ns}
RBCC	0.24*	-0.02 ^{ns}	-0.16 ^{ns}	-0.29*	0.15 ^{ns}	-0.01 ^{ns}		0.78***	-0.13 ^{ns}	0.09 ^{ns}	-0.23 ^{ns}	0.02 ^{ns}
FC	0.14 ^{ns}	0.06 ^{ns}	0.06 ^{ns}	-0.09 ^{ns}	0.20 ^{ns}	-0.09 ^{ns}	0.75***		-0.02 ^{ns}	0.18 ^{ns}	-0.02 ^{ns}	0.15 ^{ns}
NRP	-0.24*	0.53***	0.33*	0.07 ^{ns}	0.59***	0.04 ^{ns}	-0.10 ^{ns}	0.00 ^{ns}		0.82***	0.47***	0.84***
MRKY	-0.32*	0.44***	0.36*	0.13 ^{ns}	0.76***	-0.03 ^{ns}	0.09 ^{ns}	0.18 ^{ns}	0.68***		0.34*	0.97***
UMRKY	-0.15 ^{ns}	0.20 ^{ns}	0.08 ^{ns}	0.02 ^{ns}	0.46***	0.20 ^{ns}	-0.19 ^{ns}	-0.03 ^{ns}	0.23 ^{ns}	0.21 ^{ns}		0.56***
TYLD	-0.33*	0.45***	0.34*	0.12 ^{ns}	0.82***	0.03 ^{ns}	0.02 ^{ns}	0.15 ^{ns}	0.67***	0.91***	0.49**	

*, ** and ***denote significant correlations at 0.05, 0.01 and 0.001 probability levels, respectively; ^{ns}Not significant, SPVD = Sweetpotato virus diseases, RL = Root length, RG = Root girth, AGFW= above ground fresh weight, HI = Harvest index, RDMC = Root dry matter content, RBCC = root beta carotene content, FC = Flesh colour, NRP = number of storage roots per plant, MRKY Marketable storage roots yield, UMRKY = Unmarketable storage roots yield, TYLD = Total storage root yield.

strong inherent association between the characters studied.

Total storage root yield had highly significant positive correlations with number of roots per plant, root length, root girth, harvest index, marketable root yield and unmarketable root yield, at both genotypic and phenotypic levels. The increase in positively correlated traits would increase the root yield in sweetpotato plant. The existence of the positive correlation between storage root yield and other traits suggest that the traits could be used as selection criteria for high storage root yield of sweetpotato (Gurmu et al., 2015, 2017; Gasura et al., 2008). Similar results have also been reported by Abdissa et al. (2012) who explained the positive and highly significant correlations among total storage root fresh weight and marketable tuberous root yield, unmarketable tuberous root yield and tuberous root number per plant, indicating the presence of a close relationship among these parameters in sweetpotato. Jha (2012) also reported the positive correlations of root yield per plant with biological yield per plant, harvest index and root diameter. The author suggested that selection for component traits may increase the root yield of sweetpotato. Also, in addition, Yohannes et al. (2010) reported that total storage root yield had significant and positive association with marketable storage root yield and average storage root weight of sweetpotato. The flesh colour and β -carotene content showed a strong positive correlation ($r=0.78$ and $r=0.75$), respectively, at both genotypic and phenotypic levels. Thus, the existence of a strong positive correlation between flesh colour and β -carotene content suggests that storage root flesh colour can be used as a selection means of sweetpotato genotypes for high β -carotene content, particularly, during early screening of large progenies (to

reduce handling of huge number of genotypes, economize space and other resources). The current results are in line with previous works that have been reported by various authors (Gurmu et al., 2017; Burgos et al., 2009; Vimala and Hariprakash, 2011).

Number of roots per plant had a strong positive association with root length, harvest index and marketable root yield, at genotypic and phenotypic levels. This indicates selection based on these traits would improve the total storage root, since these traits are the most important components of total storage root yield (Tadesse, 2006; Gurmu et al., 2015, 2017). Total storage root yield had negative correlation with SPVD, indicating the damaging effects of diseases severity on the total storage root yield. Similarly, Mekonnen et al. (2014) reported in their previous work a negative correlation between fresh root yield and SPVD with emphasis to the damaging effects of the disease on sweetpotato in Ethiopia. On the other hand, highly significant negative correlation was observed between harvest index and aboveground fresh weight (-0.43). This may signify that a genotype that possesses vigorous vegetative growth tends to produce less storage roots, which in turn imply the presence of competition between the shoots and roots for photosynthates (Tsegaye et al., 2006), a trait contributed to reasonable distribution structure of photosynthates that led to the high root yield of sweetpotato (Chen, 1965).

Genotypic path analysis of various traits on storage root yield

The path-coefficient analysis showed that harvest index and aboveground fresh weight had maximum positive

Table 3. Genotypic direct (bold diagonals) and indirect effects of yield contributing nine traits in 24 OFSP genotypes.

Traits	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	r _g
SPVD	-0.063	0.004	-0.013	-0.155	-0.133	-0.001	0.041	-0.012	-0.020	-0.34*
RL	0.014	-0.180	0.007	0.196	0.249	0.013	-0.004	-0.005	0.043	0.49**
RG	0.014	-0.002	0.060	0.011	0.348	-0.004	-0.031	-0.006	0.029	0.41*
AGFW	0.018	-0.007	0.001	0.542	-0.437	0.007	-0.047	0.015	0.003	0.08
HI	0.009	-0.005	0.021	-0.243	0.975	-0.003	0.023	-0.017	0.060	0.83***
RDMC	0.004	-0.011	-0.011	0.171	-0.136	0.502	-0.002	0.007	0.006	0.05
RBCC	-0.019	0.001	-0.013	-0.183	0.159	0.000	0.140	-0.650	-0.011	0.08
FC	-0.011	-0.001	0.006	-0.121	0.242	-0.002	0.610	-0.069	-0.001	0.15
NRP	0.015	-0.010	0.022	0.022	0.624	0.002	-0.019	0.001	0.591	0.84***

SPVD = Sweetpotato virus diseases, RL = root length, RG = root girth, AGFW= above ground fresh weight, HI = harvest index, RDMC = root dry matter content, RBCC = root beta carotene content, FC = flesh colour, NRP = number of storage roots per plant, rg=genotypic correlation.

direct effects of 0.975 and 0.542, respectively on total storage root yield (Table 2). Harvest index exhibited a negative indirect effect through aboveground fresh weight (-0.243). Thus, the effect of harvest index on total storage root yield was not only due to its direct positive effect but also due to its negative indirect effect by influencing other characters such as aboveground biomass (Tsegaye et al., 2006). These two traits (harvest index and aboveground fresh weight) were also significantly and negatively correlated ($r_g = -0.43$). Similar results have been reported by Gurmu et al. (2017) in their previous study. Traits such as number of roots per plant and root dry matter content exerted positive direct effects on total storage yield with values of 0.591 and 0.502, respectively, at genotypic level. Number of roots per plant also exerted a high positive indirect effect ($r = 0.624$) through harvest index on total storage root yield, because harvest index was the ratio of storage root yield per total plant biomass. Thus, this implies that the higher storage root number and greater proportion of assimilate translocation to the storage root contributed to an increase in the fresh weight and subsequent biomass production (Borhan et al., 2016).

The highly positive indirect effect of number of roots per plant through HI contributed more to its highly significant positive correlation with total storage root yield. RBCC exerted negligible positive direct effect (0.140) on total storage root yield. This trait had highly positive correlation with root flesh color ($r = 0.78$). The existence of a strong positive correlation between flesh colour and Gurmu et al. (2017) β -carotene content in sweetpotato was previously reported by other authors (Burgos et al., 2009; Vimala and Hariprakash, 2011). Gurmu et al. (2017) reported the relationship between flesh colour and β -carotene content in sweetpotato genotypes and observed a high correlation of $r = 0.76$, which is similar to the results of the current study between flesh colour and $r = 0.61$. Hence, root flesh colour can be used as selection criterion for high β -carotene content in sweetpotato genotypes. Root dry matter content was another trait which exerted

positive direct effect (0.202) on total storage root yield (Gurmu et al., 2017). Similarly, root length, which exhibited highly significant correlation with total root yield, showed negative direct effect (-0.180) on total storage root yield. Conversely, flesh color, which has no correlation with total storage root yield, exerted negative direct effect (-0.069) on total storage root yield (Table 3). Traits that have negative correlations or no correlations with yield might exert a positive direct effect on yield (Gurmu et al., 2017). The negative correlation observed between SPVD and total storage root yield showed that this trait exerted negative direct effect (-0.063) on total storage yield; implying when SPVD severity increases, the total storage yield tends to decrease. This finding is in agreement with the work of Mekonnen et al. (2014) who reported a negative correlation between storage root yield and SPVD which was expected as SPVD is a damaging disease complex of sweetpotato in Ethiopia.

Phenotypic path analysis of various traits on storage root yield

Similar to the results observed at genotypic level, harvest index showed the maximum positive direct effect (0.94) on total storage root yield at phenotypic level (Table 4). This trait also exerted high negative indirect effect through aboveground fresh weight (-0.256). However, this negative indirect effect was compensated by the highest positive direct effect, ensuring high positive correlation between harvest index and total storage root yield (Tsegaye et al., 2006). Similarly, aboveground fresh weight yield and number of roots per plant also exhibited relatively the highest positive direct effect (0.795, 0.691), respectively, on total storage root yield. Even though, aboveground fresh weight had no correlation coefficient with total yield, it influenced total storage yield indirectly through other character. Thus, aboveground fresh weight and number of roots per plant could be used as indirect selection means for total storage root yield in sweetpotato.

Table 4. Phenotypic direct (bold diagonals) and indirect effects of yield contributing nine traits in 24 OFSP genotypes

Trait	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	r _p
SPVD	-0.026	-0.005	0.000	-0.149	-0.171	0.000	0.025	-0.012	0.003	-0.33*
RL	0.005	-0.023	0.000	0.190	0.246	-0.002	-0.002	-0.005	-0.006	0.45***
RG	0.005	0.005	0.001	0.024	0.331	0.001	-0.017	-0.005	-0.004	0.34*
AGFW	0.006	0.008	0.000	0.795	-0.459	-0.001	-0.031	0.008	-0.001	0.12 ^{ns}
HI	0.004	0.005	0.000	-0.256	0.94	0.000	0.016	-0.018	-0.007	0.82***
RDMC	0.001	0.011	0.000	0.155	-0.139	0.201	-0.001	0.008	0.000	0.03 ^{ns}
RBCC	-0.006	0.000	0.000	-0.173	0.160	0.000	0.106	-0.066	0.001	0.02 ^{ns}
FC	-0.004	0.001	0.000	-0.054	0.214	0.000	0.080	-0.089	0.000	0.15 ^{ns}
NRP	0.006	0.012	0.000	0.042	0.630	0.000	-0.011	0.000	0.691	0.67***

SPVD = Sweetpotato virus diseases, RL = root length, RG = root girth, AGFW= above ground fresh weight, HI = harvest index, RDMC = root dry matter content, RBCC = root beta carotene content, FC = flesh colour, NRP = number of storage roots per plant, r_p= phenotypic correlation.

Root dry matter content, root beta carotene and root girth also exerted slightly positive direct effect on total storage root yield, with path coefficients of 0.201, 0.106 and 0.001, respectively (Table 4). This is partially in agreement with the report by Gurmu et al. (2017). SPVD, root length and flesh colour showed negative direct effect of -0.026, -0.023 and -0.089, respectively, on total storage root yield. In the current study, at phenotypic level, most of traits showed similar trends of direct and indirect contribution to the total storage root yield as indicated at genotypic level, except the differences in the extent of the contribution (Tables 3 and 4).

Conclusion

This study showed that the presence of extensive genetic variation among sweetpotato genotypes for all traits tested. The existence of the positive correlation between storage root yield and other traits suggests that the traits could be used as selection criteria for high storage root yield of sweetpotato. Also, a negative correlation between storage root yield and SPVD severity at both genotypic and phenotypic levels indicated the damaging effects of diseases severity on the storage root yield of sweetpotato. The path analysis revealed that root number per plant, root girth and harvest index had direct positive effect and indirect positive effect through influencing other traits on storage root yield at both genotypic and phenotypic levels. These traits could be used as indirect selection means in sweetpotato storage root yield improvement. Therefore, the traits that showed high positive correlation and direct effects on storage root yield can be used as a tool to make possible selection in sweetpotato improvement.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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