Advances in Crop Science and Technology

Mekonnen, and Gurmu, Adv Crop Sci Tech 2021, 9:11

Research Article **Open Access**

Screening of Sweet Potato Genotypes for Adaptation to Highland Environments in Ethiopia

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Received date: December 09, 2021; **Accepted date:** December 23, 2021; **Published date:** December 30, 2021

Citation: Mekonnen B, Gurmu F (2021) Screening of Sweet Potato Genotypes for Adaptation to Highland Environments in Ethiopia. Adv Crop Sci Tech 9: 488.

Abstract

Sweetpotato is considered as a lowland crop and the potential of the crop has not been fully exploited in the highland areas. The objective of the current study was to screen released and elite sweetpotato genotypes in highland areas in order to identify best genotypes for release. The screening work was conducted at Gedeb district at an altitude of 2350 meters above sea level during the main rainy season in 2019. The experiment consisted of 110 new sweetpotato genotypes from diverse origins and three recently released check varieties. An augmented block design was used in order to accommodate the large number of genotypes. The analysis of variance indicated the presence of significant differences ($p<0.01$) among the new entries for root yield, number of roots per plant and reaction to Sweetpotato Virus Disease (SPVD). The root yield of the new entries ranged from 1.43 to 56.20 t ha^{-1} while that of the checks varied from 20.51 to 28.71 t ha^{-1}. High root yield that ranged from 31-56 t ha^{-1} was recorded from 14 genotypes. SPVD severity scores varied from mild symptoms to severe with severity scores ranging from 1 to 4. Most of the evaluated genotypes showed low SPVD severity scores implying the resistance/tolerance of the genotypes. Based on the traits concerned, more than 50 genotypes are identified and selected for further multi-stage evaluations and variety development for the highland environments in Ethiopia and other East African countries with similar agro-ecologies.

Keywords: Augmented design; Highland; Root yield; Screening; Sweetpotato

Introduction

Sweetpotato [*Ipomoea batatas* (L) Lam] is an important food security crop grown in diverse agro ecologies globally. Sweetpotato fulfills a number of basic roles in the global food system where it is mainly used for human consumption (IFPRI, 2014). According to a report of FAO (2017), African countries accounted for about 21.2% of the world sweetpotato production in 2014. In Ethiopia, sweetpotato is among very valuable root crops and mainly grown in the eastern, southern and south western parts of the country. Since the inception of sweetpotato research in Ethiopia, about 28 varieties have been officially released for production. The varieties have high root yield, high dry matter content, resistance to Sweetpotato Virus Disease (SPVD), and the orange fleshed varieties have high better beta-carotene (pro-vitamin A) content. Moreover, various agronomic recommendations and seed system establishment works have been made in collaboration with different stakeholders. Sweetpotato is considered as a lowland crop because of its adaptation to the tropics and warm temperate regions of the world. Accordingly, in Ethiopia, the crop is best suited to low to mid-altitudes with an elevation of up to 1800 Meter above Sea Level (MASL). In some areas, the production of the crop goes up to an altitude of over 2200 (MASL).

However, so far, most of the variety evaluation activities have been conducted in low to mid-altitudes and the potential of the crop has not been fully exploited in the highland areas. In addition, there is a frequent request from various communities living in the highland areas for sweetpotato varieties that are adapted to highland areas. The production of sweetpotato in the highland areas will give opportunities for the densely populated communities to use sweetpotato as a food and nutrition security crop and for the household income generation. Therefore, based on the demand from various farming communities and stakeholders, the screening of sweetpotato genotypes for highland adaptation has been conducted at Gedeb district, Gedeo zone of the Southern Region in Ethiopia.

Materials and Methods

One hundred and ten sweetpotato genotypes (Table 1) were evaluated in highland areas specifically known as Gubeta at an altitude of 2350 masl. The study materials were obtained from different backgrounds such as advanced lines (developed from polycross breeding), introduced varieties (released abroad) and most varieties that have been released in Ethiopia [1]. The field experiment was conducted using augmented block design with un-replicated entries and replicated check varieties that occurred once in every block in the experiment. The experimental area was divided in to10 blocks each consisted of 14 rows in such a way that each row in each block was treated as a single plot. Each genotype was represented by a plot size of 3 m^2 i.e. 3 m long and 1 m width [2]. The spacing between rows and plants was 1 m and 0.3 m, respectively. Ten holes per row spacing are prepared and vine cuttings of 30 cm long were used for planting the trial. Three recently released varieties, namely. Alamura (Ukr/Eju-10), Dilla (Ukr/Eju-13) and Kabode were included in the study as checks. The three check varieties were planted at random on rows in a way that the same check variety appeared in every block only once [3]. The remaining 11 rows in each block were assigned to the new entries (genotypes). All plots received the recommended cultural practices uniformly and no fertilizer was applied. Hilling- up was done after fourth weeks of planting and all plots were kept weed free with regular hand weeding and cultivation.

Data were recorded on SPVD severity using a scale of 1 to 5, where 1=no visible symptoms, 2=mild symptoms (a few local lesions on a few leaves), 3=moderate symptoms (mosaic symptoms on leaves), 4=severe symptoms (mosaic symptoms with plants showing stunted growth) and 5=very severe symptoms of purpling/yellowing or mosaic on leaves, severe leaf distortion, reduced leaf size and severe stunting. Root Flesh Colour (FC) was estimated based on sweetpotato descriptors developed by Huaman. Data on root yield and number of roots per plant was taken at harvest from the entire row and the yield was converted and expressed in ton per hectare [4].

Statistical analysis

The collected data were subjected to analysis following the procedures developed for augmented design. The analysis of variance was done using SPAD (Statistical package for Augmented Design) software developed by IASRI, New Delhi. A Critical Difference (CD) was employed to compare means among control varieties, among new entries and new entries vs. control varieties at 5% probability levels based on augmented design [5-8].

No	Genotypes	FC	Status	No	Genotypes	FC	Status
1	CN1448-49-28-20	O	Advanced line	57	MUSG014001-3-11	O	Advanced line
2	MUSG014019-7-4	W	Advanced line	58	MUSG014001-3-42	O	Advanced line
3	MUSG014001-3-2	W	Advanced line	59	Tio Jeo-10	O	Advanced line
4	MUSG014065-21-	W	Advanced line	60	MGSG1006-7-2	W	Advanced line
5	MUSG014001-3-2	W	Advanced line	61	CORDNER-15-4	O	Advanced line
6	CN1448-49-28-8	W	Advanced line	62	MUSG014052-51-2	O	Advanced line
7	105413-4-7	W	Advanced line	63	MUSG014001-3-26	O	Advanced line
8	Tomurabuka	W	Released abroad	64	MUSG014001-3-48	O	Advanced line
9	CORDNER15-9	O	Advanced line	65	MUSG014052-51-5	O	Advanced line
10	CN1448-49-28-17	O	Advanced line	68	MUSG014052-51-2	O	Advanced line
11	MUSG014019-7-4	O	Advanced line	69	MUSG014001-3-13	O	Advanced line
12	CN1448-49-26-7	O	Advanced line	70	CORDNER15-9	O	Advanced line
13	MUSG014065-21-1	O	Advanced line	71	MUSG014001-3-10	O	Advanced line
14	Tio Jeo-2	O	Advanced line	72	CORDNER-15-9	O	Advanced line
15	Awassa-83	W	Released in Ethiopia	73	MUSG014012-26-1	O	Advanced line
16	MUSG014001-3-2	W	Advanced line	74	Tio Jeo-6	O	Advanced line
17	13NC9350A-9-8	O	Advanced line	75	MUSG014046-20-6	O	Advanced line
18	RW11-4743	O	Released abroad	76	Vita	O	Released abroad
19	NASPOT-13	O	Released abroad	77	CN1448-49-26-6	O	Advanced line
20	MUSG014019-7-1	O	Advanced line	78	MUSG014012-26-1	O	Advanced line

21	107031-18-2	O	Advanced line	79	MUSG014019-7-10	O	Advanced line
2	MUSG014065-21-3	W	Advanced line	80	MUSG014019-7-23		Advanced line
23	MUSG014065-21-1	W	Advanced line	81	MUSG014052-51-3	O	Advanced line
24	Kulfo	O	Released in Ethiopia	82	MUSG014001-3-26	O	Advanced line
25	CN1448-49-26-3	W	Advanced line	83	MUSG014052-51-3	O	Advanced line
26	Mayayi	O	Released abroad	84	MUSG014019-7-4	O	Advanced line
27	Kyoyabwerer	O	Released abroad	85	MUSG014001-3-37	W	Advanced line
28	MUSG014001-3-49	O	Advanced line	86	6	W	Advanced line
29	NASPOT-8	O	Released abroad	87	MGSG1006-7-4	W	Advanced line
30	MUSG014044-7-14	W	Advanced line	88	477	W	Advanced line
31	MUSG014052-51-3	W	Advanced line	89	MUSG014012-26-1	W	Advanced line
32	MUSG014001-3-13	O	Advanced line	90	564	W	Advanced line
34	MUSG014001-3-35	O	Advanced line	91	285	W	Advanced line
35	CN1448-49-28-9	O	Advanced line	92	MUSG014019-7-46	O	Advanced line
36	MUSG014052-51-2	O	Advanced line	93	MUSG014046-20-2	O	Advanced line
37	MUSG014019-7-50	O	Advanced line	94	661	W	Advanced line
38	MUSG014012-26-3	O	Advanced line	95	Berkume	W	Released in Ethiopia
39	MUSG014052-51-3	O	Advanced line	96	MUSG014019-7-22	O	Advanced line
40	MUSG014052-51-2	O	Advanced line	97	MGSG1006-7-4	W	Advanced line
41	MUSG014019-7-57	O	Advanced line	98	Hawassa-09	W	Released in Ethiopia
42	MUSG014019-7-56	O	Advanced line	99	MUSG110033-6-1	O	Advanced line
43	MUSG014052-51-1	O	Advanced line	100	MGSG1006-7-7	W	Advanced lin
44	MUSG014052-51-1	O	Advanced line	101	535	W	Advanced line
45	MUSG014001-3-41	O	Advanced line	102	Kyoyabwerer	O	Released abroad
46	MUSG014019-7-24	O	Advanced line	103	MUSG014065-21-2	P	Advanced line

47	MUSG014052-51-4	O	Advanced line	104	Tio-Jeo-22	O	Advanced line
48	MUSG014052-51-2	O	Advanced line	105	NASPOT-12	O	Released abroad
49	CN1448-49-28-10	O	Advanced line	106	MUSG014012-26-2	O	Advanced line
50	Amelia	O	Released abroad	107	MUSG014001-3-49	O	Advanced line
51	MUSG014001-3-13	O	Advanced line	108	MUSG014001-3-57	O	Advanced line
52	MUSG014019-7-36	O	Advanced line	109	MUSG014052-51-2	O	Advanced line
53	MUSG014019-7-22	O	Advanced line	110	MUSG014012-26-2	O	Advanced line
54	Tola	W	Released in Ethiopia	111	Alamura (check)	O	Released in Ethiopia
55	MUSG014019-7-40	O	Advanced line	112	Dilla (check)	O	Released in Ethiopia
56	CORDNER-15-8	O	Advanced line	113	Kabode (check)	O	Released in Ethiopia

Table 1. List of sweetpotato genotypes used for the study.

Results and Discussion

Performance of sweet potato genotypes for root yield and its component trait at the highland area

The result of the analysis of variance indicated the presence of a highly significant difference ($p<0.001$) among new entries, among check varieties, and new entries vs. check varieties for root yield and number of roots per plant (Table 2) [9]. Among the evaluated 110 sweetpotato genotypes, about 25 genotypes gave root yield that is more than the average yield (24.7 t ha^{-1}) of the three checks. Thirty nine genotypes produced root yields 10-20 t ha^{-1} while twenty genotypes produced 21-30 t ha^{-1}. Root yields that ranged from 31-40 t ha^{-1} was recorded from 12 genotypes [10]. Two genotypes designated as G33 and G47 produced the highest root yields of 53.49, 56.20 t ha^{-1}, respectively. Two released varieties namely, Hawassa-09 and Berkume produced a root yield of more than 40 t ha^{-1}. The lowest root yield (<10 t ha^{-1}) was obtained from 35 genotypes (Table 3; Figure 1). Root yield is an important trait for the subsistence farmers as well as the large scale sweetpotato producers for home consumption and as raw materials for industrial use. Breeding for higher root yield requires that breeders take in to consideration all yield components which positively affect the root yield in sweetpotato [11-15].

Mean squares						
Character	**Block (df=9)**	**Genotype (df=112)**	**Error (df=18)**	**Among control varieties (df=2)**	**Among new entries (df=109)**	**New entries vs. Control (df=1)**
NRPP	1.18	2.7	0.76	2.04	2.2	57.80
SPVD	0.73	1.76	0.47	0.95	1.95	20.70
RYLD	7.33	129.80	2.71	168.26	119.02	1228.52

Table 2. Mean squares for three traits of sweetpotato genotypes based on adjusted mean values.

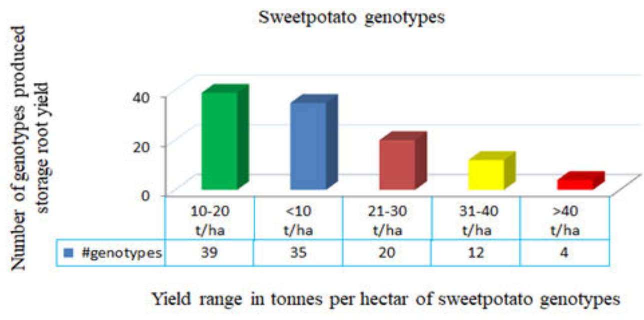

Figure 1. Graph shows mean root yield of sweet potato evaluated at Gubeta (2350 masl).

The analysis of variance indicated that there is a highly significant difference among genotypes vs. checks (p<0.01) and among the tested genotypes (p<0.05) for number of roots per plant [16]. A non-significant difference was observed between the check varieties that were included in the study (Table 2). Number of root per plant is a direct contributor for root yield in sweetpotato and it is considered as one of the primary traits of interest in sweetpotato improvement program [17]. However, the size of the roots is very important since under (less than 100 g) and oversized (more than 500 g) roots are not preferred by the consumer and considered as unmarketable. Genotypes with high percentage of small number of roots per plant (less than 100 g) should not be promoted to further evaluation [18]. In this study, genotypes that produced a large number of small-sized (unmarketable) roots per plant were considered as non-adaptable to the highland environment (Table 2).

The highest mean number of roots per plant was obtained from genotypes coded as G27, G33 and G72 (7.4, 7.2 and 7.0), respectively while the least number of roots per plant was recorded from G9, G90, G92 and G100, with values of 0.3, 0.3, 0.8 and 0.5 in that order (Table 3). The variability among genotypes for root yield and its component trait (number of roots per plant) might be attributed to genetic and environmental factors. Vinaj and Babu indicated that variability for most of the yield components in sweetpotato is attributable to genetic and environmental factors [19]. Especially altitude highly influences genotypes' performance for root yield and its component traits. As altitude increases, the performance of the crop is highly affected resulting in poor yields. But the presence of wider genetic variability in the traits of interest provides better chances to improve the crop for highland adaptation through selection.

The results of the current study suggested that new genotypes can be selected based on root yield and component traits for further multi-location evaluation and variety development for the highland environment. The current yields obtained under the highland condition are comparable with the yields that are obtained from the major sweetpotato producing areas in Ethiopia, such as Hawassa and Wolaita areas [20].

Genotype code	Genotype name	Character		
		SPVD (1-5)	NRPP (No.)	RYLD (t ha-1)
G47	MUSG014052-51-38	0.4	6.2	56.2
G33	MUSG014044-7-9	1.4	7	53.49
G95	Berkume	1.4	4.3	40.91
G98	Hawassa- 09	1.4	3.2	40.75
G32	MUSG014001-3-13	1.4	5.8	39.74
G72	CORDNER-15-9	0.6	7.2	38.88
G23	MUSG014065-21-13	1.4	6.5	37.66
G43	MUSG014052-51-13	4.4	5.9	37.39
G68	MUSG014052-51-21	0.6	6.9	37.22
G27	Kyoyabwerer	1.4	7.4	35.85
G93	MUSG014046-20-2	3.4	5.9	35.33
G105	NASPOT-12	1.4	6.6	34.6
G21	107031-18-2	1.6	5.8	32.47
G76	Vita	0.6	6	32.4
G66	CN1448-49-26-9	1.4	6.9	32.25
G65	MUSG014052-51-5	1.4	4.2	32.08
G26	Mayayi	1.6	5	30.08

G70	CORDNER-15-15	0.6	4.8	29.12
G60	MUGSG1006-7-2	1.4	5.4	28.75
G58	MUSG014001-3-42	3.4	2.9	28.15
G22	MUSG014065-21-3	1.6	4.8	27.94
G54	Tola	0.4	4.8	26.62
G17	13NC9350A-9-8	3.6	5.8	26.22
G41	MUSG014019-7-57	1.4	4.9	26.12
G59	To Jeo-10	2.4	4.9	25.14
G57	MUSG014001-3-11	2.4	3	24.34
G74	Tio Jeo-6	0.6	3	23.88
G48	MUSG014052-51-25	0.4	5.9	23.76
G29	NASPOT-8	1.4	3.9	23.41
G83	MUSG014052-51-36	0.7	4.9	23.05
G39	MUSG014052-51-3	2.4	3.9	23
G81	MUSG014052-51-35	0.7	4.1	22.01
G88	477	1.7	3.2	22.01
G101	535	3.4	5.3	21.82
G25	CN1448-49-26-3	1.4	4.4	21.58
G1	CN1448-49-28-20	0.7	5.3	21.1
G11	MUSG014019-7-46	1.7	2.6	20.92
G96	MUSG014019-7-22	2.4	3.7	20.51
G50	Amelia	0.4	3	20.28
G77	Cn1448-49-26-6	0.6	4.2	19.88
G86	6	0.7	1.6	19.72
G42	MUSG014019-7-56	1.4	2.5	19.6
G90	564	1.4	0.3	19.45
G52	MUSG014019-7-36	0.4	2	18.84
G24	Kulfo	1.4	2.1	18.08
G55	MUSG014019-7-40	0.4	2	16.62
G71	MUSG014001-3-10	0.6	4.2	16.55
G104	Tio Jeo-22	1.4	2	16.55
G63	MUSG014001-3-26	3.4	1.1	16.25
G51	MUSG014001-3-4	0.4	2	15.95
G6	CN1448-49-28-8	0.7	2.3	15.92
G20	MUSG014019-7-10	1.6	1	15.38
G38	MUSG014012-26-32	1.4	1.9	15.01

G100	MGSG1006-7-7	1.4	0.5	13.49
G99	MUSG110033-6-1	1.4	2.9	13.15
G73	MUSG014012-26-13	0.6	6.7	13.05
G84	MUSG01019-7-4	0.7	3.9	12.94
G46	MUSG014019-7-24	0.4	1.5	12.62
G49	CN1448-49-28-10	0.4	1	12.62
G18	RW11-4743	1.6	1	12.61
G9	CORDNER-15-14	0.7	0.3	12.58
G56	CORDNER-15-8	1.4	1.6	12.44
G92	MUSG014019-7-46	1.4	0.8	12.41
G82	MUSG014001-3-21	2.7	3.1	12.38
G19	NASOT-13	1.6	1.8	12.05
G102	MUSG014001-3-17	4.4	2.5	11.9
G53	MUSG014019-7-22	0.4	2	11.62
G16	MUSG014001-3-28	3.6	2.8	11.34
G80	MUSG014019-7-23	0.7	1	11.27
G75	MUSG014046-20-8	0.6	4.5	11.22
G67	CORDNER-15-23	0.6	3.4	11.03
G40	MUSG014052-51-25	1.4	2.3	11
G8	Tomurabuka	0.7	1.8	10.92
G10	CN1448-49-28-17	0.7	2.3	10.36
G37	MUSG014019-7-50	1.4	1.9	10.01
G34	MUSG014001-3-35	2.4	2.1	9.83
G85	MUSG014001-3-37	0.7	1.9	9.47
G108	MUSG014001-3-2	1.4	3.1	9.38
G30	MUSG014044-7-14	4.4	1.3	8.82
G15	Hawassa-83	1.6	2.1	8.72
G36	MUSG014052-51-23	1.4	2.5	8.35
G45	MUSG014001-3-41	0.4	1.1	7.73
G5	MUSG014001-3-27	3.7	2.5	7.58
G110	MUSG014001-3-13	3.4	2.1	7.58
G91	285	1.4	1.7	7.41
G97	MUSG1006-7-4	1.7	3.2	7.41
G78	MUSG014012-26-18	0.7	2.1	7.38
G107	MUSG014001-3-49	1.4	1.5	7.38
G28	MUSG014001-3-9	3.4	1.9	7.34

Citation: Mekonnen B, Gurmu F (2021) Screening of Sweet Potato Genotypes for Adaptation to Highland Environments in Ethiopia. Adv Crop Sci Tech 9: e488.

G7	105413-4-7	0.7	1.2	7.25
G35	CN1448-49-28-9	1.4	2.9	7.24
G61	CORDNER-15-4	1.4	2.3	6.99
G44	MUSG014052-51-13	3.4	2.9	6.44
G31	MUSG014052-52-31	1.4	2.1	6.41
G62	MUSG014052-51-23	2.4	1.2	6.25
G79	MUSG014019-7-10	0.7	1.4	6.19
G69	MUSG014001-3-13	2.6	5.6	6.11
G109	MUSG014001-3-1	1.4	1.3	5.98
G12	CN1448-49-26-7	2.6	2.9	5.38
G103	MUSG014064-21-21	1.4	3.1	5.16
G64	NUSG014001-3-48	1.4	2	5.14
G94	661	2.4	1.9	4.5
G89	MUSG014012-26-10	1.4	3	4.08
G106	MUSG014012-26-21	1.6	2	3.81
G14	TioJeo	1.6	1.5	3.72
G3	Musg014001-3-28	2.7	3.3	3.58
G4	MUSG014065-21-8	0.7	1.3	3.42
G87	MGSG1006-7-4	0.7	2	1.97
G2	MUSG014019-7-45	3.7	1.4	1.33
G13	MUSG014065-21-14	1.6	1	0.38
Overall mean		1.6	3.2	17.3
	Check varieties			
Kabode		1.1	4.7	28.71
Alamura		1.3	4.5	24.83
Dilla		1.4	3.8	20.51
Overall mean		1.3	4.3	24.7
Critical difference (CD) at 5% level of significance				
CD for genotypes in the different blocks	2.35	2.98	5.67	
CD for genotypes in the same block	2.03	2.58	4.89	
CD for genotypes vs. Checks	1.7	2.16	4.09	
Mean	1.44	3.13	20.01	
CV (%)	47.5	27.9	18.7	
R2	91.6	95.9	99.7	

Table 3. Adjusted mean root yield (tha^{-1}), number of roots per plant and reaction to SPVD for thesweetpotato genotypes evaluated at Gedeb district in 2019 during the main rainy season.

Reaction of the genotypes to SPVD

Analysis of variance revealed the presence of a highly significant difference among test genotypes and between test genotypes and controls ($p<0.05$) for reaction to SPVD. However, there was no significant difference among the three check varieties for this trait (Table 2). SPVD symptoms scores varied from mild symptoms to severe with severity score ranged from 1 to 4. Most of the evaluated genotypes showed low scores (<2.0) for SPVD severity (Table 2), indicating the resistance/tolerance of the genotypes to the disease [21]. Genotypes that were coded as G43, G102, G3, G2, G28, G44, G16, G63, G5, G110, G17, G58, and G101showed high SPVD scores that were above 3.0 rating scales (Table 2) indicating the susceptibility of those genotypes to SPVD [22]. According to various reports, SPVD is the most devastating disease causing reduction in plant growth and storage root yields in sweet potato. Mukasa reported that mild and severe strains of sweet potato viruses have been detected in plants expressing mild and severe symptoms. In general, genotypes with low SPVD scores, having better root yield and flesh colour, are considered and promoted for further evaluations in next breeding stages [23-26].

Evaluation of the storage root flesh colour intensities of the genotypes

In terms of root flesh colour, the 110 genotypes included in the study possessed varying flesh colour intensities that ranged from white to deep orange flesh colour. Genotypes with dark orange and intermediate orange flesh colour are both considered as orange. Accordingly, the majority (71%) of the tested genotypes possessed orange flesh colour, out of which 30% were selected as the best ones based on various traits [27]. The rest genotypes (29%) had white flesh colour where 14% were selected as the best genotypes for further evaluations (Figure 2). In Ethiopia and other East African countries, the white fleshed varieties are preferred by most farmers due to their high dry matter contents [28]. However, the white fleshed sweetpotato varieties have no β- carotene (a pre-cursor of vitamin A). Vitamin A plays a significant role in metabolic functions, eyesight, regular growth and development, and the immune system. The orange flesh colour in sweetpotato indicates the level of β- carotene in the storage roots. That means, there is a strong positive correlation between the orange flesh colour and β-carotene contents in sweetpotato. Therefore, storage root flesh colour can be used as a selection index of sweetpotato genotypes for high β- carotene content, particularly during early screening of large number of progenies.

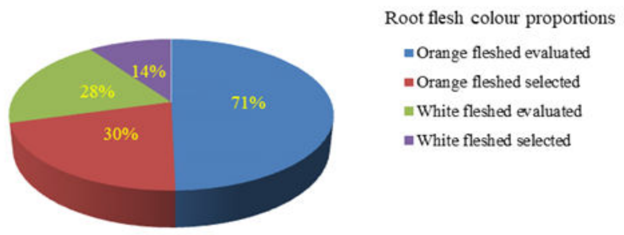

Figure 2. A graph showing proportion of root flesh colour of the evaluated genotypes.

Conclusion

Evaluation and selection of sweet potato genotypes adapted to highland environment is a crucial step in variety development especially for meeting food security, reducing poverty and diversifying nutrition in the highland farming communities.

In this study, most of the evaluated genotypes produced high root yield and showed low reaction to SPVD severity in the highland conditions. Based on traits such as high root yield, low reaction to SPVD and root flesh colour intensity, 50 genotypes are identified for further multi-stage evaluations and variety development for the highland environments in Ethiopia and other East African countries with similar agro-ecologies.

Acknowledgements

The authors would like to express their gratitude to the South Agricultural Research Institute (SARI) and the Ethiopian Institute of Agricultural Research (EIAR) for their financial support. The SweetGAINS project of CIP, funded by the Bill and Melinda Gates Foundation, is especially acknowledged for the financial support to run the field works.

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