

# Preliminary Study on Evaluation of Sweet Potato Genotypes for Resistance to Sweet Potato Virus Disease (SPVD)

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# ABSTRACT

Host plant resistance in sweet potato, under a long-term management approach, is one of the most effective, economical, and environmentally benign management approaches for sweet potato virus diseases (SPVD). In the current study, different sweet potato genotypes were evaluated for resistance to the SPDV and also with higher yield potential under field conditions. The experiment was conducted from July – November 2018 at the University for Development Studies (UDS) experimental field. Thirty-two sweet potato genotypes, including five, already released varieties (also served as checks) were used. The genotypes (treatments) were arranged in a Randomized *Complete Block Design (RCBD) with three plications. The results showed that three of the checks* (Apomuden, Bohye, Tu-Purple) and PG17207-N1, PG17257-N1, PG17305-and N had significantly higher virus susceptibility levels as compared to the remaining genotypes. Thirteen (13) genotypes showed no visible symptom of the virus, fifteen (15) genotypes were moderately resistant to the disease whiles the remaining four (4) were slightly susceptible to the disease. The results further revealed that PG17584-N1, PG17257-N1 and PG17149-N2 produced the highest root yield while the least was observed for PG17205-N. PG17584-N1, PG17257-N1. Furthermore, PG17149-N2 combines higher root yield with resistance to the SPVD. They can therefore be used as resistant sources for further breeding interventions.

Keywords: Genotypes, Resistance, Sweet potato, Virus incidence, Yield

## **INTRODUCTION**

Sweet potato (*Ipomoea batatas* L.) is mostly cultivated for its storage roots with highquality carbohydrates and other nutrients. Also, the nutrient-rich foliage also serves as vegetable and animal feed across many communities known for its cultivation (Nguyen *et al.*, 2021; Padmaja *et al.*, 2012; Otoo *et al.*, 2001). In Ghana, it is mostly produced by peasant farmers, usually in the Northern Ghana, Central, and Volta regions (Bidzakin *et al.*, 2014). In most cases, sweet potato survives under difficult conditions and withstands unfavourable weather challenges. This makes it easy to be cultivated by many resource-poor smallholder farmers. However, other biotic and abiotic factors, yield loss and storage pests and disease pose a big threat to Ghana's crop production (Sowley *et al.*, 2015).

Among the biotic factors, viruses, fungal, and nematode, and insect pests attack are the most devastating yield-limiting factors in sweet potato production. These hindrances prevail both in the field and post-harvest (Abrham et al., 2021; Ngailo et al., 2013; Clark et al., 2012; Fuglie, 2007). Among the diseases, SPVD has been reported as the most important sweet potato disease in most of the tropical regions in Africa, and perhaps across the globe (Mbewe et al., 2021; Mukasa et al., 2006). SPVD can cause over 90 % yield loss (in terms of both root and foliage) among susceptible genotypes if not managed (Jones, 2021; Ngailo et al., 2013; Gutierrez et al., 2003). SPVD is caused by a dual infection and synergistic relationship between sweet potato feathery mottle potyvirus (SPFMV) and sweet potato chlorotic stunt crinivirus (SPCSV) (Mbewe et al., 2021; Mukasa et al., 2006; Karyeija et al., 2000). SPFMV is a member of potyviridae family. SPFMV alone on the plant does not have a serious effect and usually has just little to no symptoms on the crop. Their impact usually results in minimal or negligible yield loss (Clark & Hoy, 2006).

According to Kokkinos and Clark (2006), SPFMV alone's effect in plants is similarly However, the effect increases low. dramatically in a joint infection of the SPFMV and SPCSV (Mukasa et al., 2006; Kokkinos & Clark, 2004; Gutierrez et al., 2003; Karyeija et al., 2000). This increases the severity of the disease and subsequently leads to higher yield losses (Jones, 2021; Ngailo et al., 2013). Sweet potato feathery mottle virus is common in most sweet potato production regions (Abdulrahman et al 2022; Ngailo et al., 2013).

In Ghana, the virus incidence is high in the southern part of the country where the rainfall pattern is bi-modal as compared to the Northern part of the country where the rainfall pattern is uni-modal (Putri *et al.*, 2016).

Diseased plants become severely stunted and the leaves become small and narrow, often with a distorted edge and also puckering, vein-clearing, and mottling on some severe occasions (Ngailo *et al.*, 2013). Planting diseased vine cuttings or storage roots are the greatest collective sources of sweet potato viral diseases. In as much as this could be threatening, vine cuttings from mature crops seem to be the easiest way of propagating the crop (Valverde *et al.*, 2007). This leads to a higher rate of transmission of the virus diseases through infected propagules to newly planted fields.

Disease control measures such as good farm sanitation, cultural practices, and proper control of vector populations to retard or prevent damage, have been postulated (Abdulrahman et al., 2022). Presently, no practical treatment to control the SPVD has been reported. Nevertheless, the use of clean and healthy planting materials that are free of the virus has been reported as an effective. economical, and environmentally friendly approach to managing viral diseases in many crops (Abdulrahman et al., 2022; Adikini et al., 2015; Clark et al., 2012). Breeding for SPVD resistance could therefore be the surest way of mitigating the impact of the disease (Abdulrahman et al., 2022; Ewell, 2002). This was evidenced by a yield boost up of 30 % and 60 % as reported by Gibson et al. (2004) and Clark & Hoy (2006), respectively. As an objective, this study seeks to evaluate resistance to sweet potato virus diseases and root and biomass productivity among some sweet potato populations.

## MATERIALS AND METHODS

# Experimental site

The experiment was conducted at the University for Development Studies Nyankpala, Northern region, Ghana ( $9^0$  42' N latitude and  $0^0$  92' W longitude) The area experiences a unimodal rainfall amount of about 1000-1100 mm unevenly distributed

between April and October as reported by Owusu *et al.* (2013).

#### Source of planting material

Thirty-two virus-free sweet potato genotypes (vines) were obtained from the CSIR-Savanna Agriculture Research Institute (CSIR-SARI). Among these, twenty-seven (PGA16026-1, PG17035-N1, PG17584-N1, PG17265-N1, PG17149-N2, PG17259-N1, PG17362-N1, PG17257-N2, PG17412-N2, PG17354-N1, PG17409-N6, PG17257-N1, PG17294-N1, PG17192-N6, G17146-N1, PG17136-N1, PG17140-N2, PG17206-N1, PG17206-N5, PG17226-N1, PG17172-N2, PG17208-N2, PG17207-N1, PG17171-N1, PG17212-N3, PG17305-N1, and PG17205-N1) were advance breeding lines, while the remaining five (Apomuden, Bohye, Ligri, Tu-Purple, and CIP442162) were already released varieties in Ghana (Ghana Variety Release Catalogue, 2019).

## Land preparation and planting

Sweet potato vines (about 30 cm in length) were planted on ridges with a planting distance of 30 x 30 cm. The genotypes (treatments) were arranged in a Randomized Complete Block Design (RCBD) and were replicated three times.

The vines were planted vertically by inserting half to two-thirds of their total length into the soil. The part of the vine left above ground contained at least one node.

Weed control was done manually when necessary, using a hoe. Earthing-up was done during weeding to seal soil cracks in ridges to prevent root tubers that are forming from being exposed.

## **Data collection**

Disease assessment

**Disease severity** 

Visual assessment of SPVD symptoms was done at 6 and 8 weeks after planting (WAP), respectively. The severity of the disease was assessed using color and size deviation of the leaf and vines (purple, mosaic, vein clearing (Gutierrez *et al.*, 2003). Virus severity was assessed using a modified 9-point scale according to Abidin *et al.* (2013), such that;

1= No visible symptom

2= Visible but indistinct virus symptoms

3= Visible but < 5% of plants per experimental unit

4= Visible symptoms between 6 and 15% of plants per experimental unit

5= Visible symptoms between 16 and 33% of plants experimental unit

6= Visible in more than 1/3 but less than 2/3 (34 - 66%)

7= Visible in up to 99% of per experimental unit.

8= Visible in all plants.

9= Causes stunting and death in plants.

# **Plant vigor**

Visual assessment was used to assess plant vigor in the presence of disease. Some of the indicators of this parameter include: Shoot growth (the presence of many actively growing shoots is a good indication of excess vigor), length of internodes (long or short), and canopy gaps.

The vigorous growth was scored using a modified 9-point scale according to Abidin *et al.* (2013), where;

1= Underdeveloped vines,

2= Feeble vines and stems, elongated internodes distances,

3= Feeble to medium-strong vines, medium-thick stems, and elongated internodes distances,

4= medium-strong and thick stems with fair internode distances,

5= medium-strong and thick vines with elongated internodes distances,

6= medium-strong and thick stems with fair internode distances,

7= well-developed stems with short internode distances,

8= strong vines, thicker stems with shorter internode distance,

9= very strong and thicker stems, and shorter internode distances.

Agronomic parameters such as vine length (6 and 8 WAP), total root tuber yield and dry biomass yield were also assessed.

## Statistical analysis

Data enumerated were subjected to analysis of variance (ANOVA) using Genstat statistical package (12<sup>th</sup> edition) Treatment means were separated using Least Significant Differences (LSD) at 5%.

## RESULTS

#### SPVD severity and plant vigor

Disease severity varied significantly among genotypes at both 6 and 8 WAP (P < 0.05). Disease severity scores in this study ranged between 1.0 and 4.5. Bohye (which was used as control) had the highest disease severity scores on both assessment occasions (4 and 4.5 for 6 and 8 WAP, respectively). Thirteen genotypes (Ligri, PG17136-N1, PG17146-N1, PG17149-N2, PG17192-N6, PG17206-N1, PG17206-N5, PG17212-N3, PG17226-N1, PG17257-N2, PG17294-N1, PG17305-N1, PG17412-N2) did not show any visible symptom of the disease. However, Ligri and PG17035-N1 had a disease severity score of 1.5 at 8 WAP (Fig. 1). Genotypes with no symptoms on both assessment virus occasions could be said to have some significant levels of resistance to the disease. In general, the disease severity score among genotypes was higher at 8 WAP as compared to 6 WAP.

Genotypes were comparable to each other with regards to disease severity at both 6 and 8 WAP (P > 0.05). Even though there was an improvement in plant vigor at 8 WAP as compared to that of 6 WAP, the least plant vigor for the two assessment occasions is 5.5 with just two genotypes (PG171466-N1 and PG17362-N1) having plant vigor scores of 8. This means that an average genotype in this experiment had a medium-strong vine with thick stems and medium internode distances. However, at 8 WAP, plant vigor among genotypes rose above 8.0. This means that at 8 WAP, most genotypes had strong vines, and thicker stems with shorter internode distances (Fig 2). On this account, the thirteen (13) genotypes that had no symptoms of the disease were classified to be resistant to the disease. Fifteen (15) genotypes with a score above 1.0 but equal to or less than 2.5 have been classified as moderately resistant to the disease. The remaining genotypes, based on their severity scores (above 3.0) and considered plant vigor are slightly susceptible to the disease. This result corroborates with that of Putri et al. (2016), who reported a higher disease incidence and severity among genotypes in Ghana. Similarly, Gruneberg et al. (2009) also reported a higher SPVD pressure among sweet potato cultivars that are susceptible to the disease. Furthermore, the rise in disease severity and severity at 8 WAP could be attributed to an increase in the virus population due to the constant multiplication of the virus.



Figure 1: Virus severity of the various genotypes at 6WAP and 10WAP



Figure 2: Vine Vigor of the various genotypes at both 6WAP and 10WAP

#### Vine length

Genotypes in this study exhibited significant variations in terms of vine length (P < 0.05). Apart from PG17207-N1 which had a vine length of 83.4 cm, all the other genotypes had a vine length above 85 cm (Fig. 3). Among the genotypes, PG17192-N6, PG17136-N1, PG17146-N1 had the longest vine length of 165.7, 164.5 and 163.5 cm which was

significantly different from the rest of the genotypes. The longer vine lengths observed for PG17192-N6, PG17136-N1, PG17146-N1 could be a result of their resistance to the SPVD. This is in concordance with a study by Gibson *et al.* (2014), who reported a decrease in the general growth and development among sweet potato cultivars that are susceptible to SPVD.



Figure 3: Mean vine length of the various genotypes

#### Root and biomass yield

There were significant differences (P <0.001) among treatments with regards to root yield. The highest root yield was observed for PG17584-N1 (31.4 t/ha) whilst the lowest was observed for PG17205-N1 (3.53 t/ha). Most genotypes in this study had a root yield between 6.0 and 7.0 t/ha. In general, most genotypes with lower disease severity scores had higher root yields as compared to those genotypes with higher incidence and severity levels of the disease (Fig. 4) Genotypes in this study did not show any variation in terms of foliage yield (P > 0.05). The highest biomass yield was observed for PG17584-N1 (68.42 t/ha) whilst the lowest was observed for Bohye (4.5 t/ha). However, about 86 % of the genotypes in the current study had a biomass yield of at least 7 t/ha. (Fig. 5). Also, most high-yielding genotypes in this study exhibited some considerable levels of resistance to SPVD. This could mean that disease incidence and severity had a negative influence on the yield of the susceptible genotypes. This finding corroborates with Gutierrez et al. (2003) who also reported about 90 % root yields among sweet potato genotypes that were resistant to the SPVD. The difference in yield as observed between the resistant and susceptible genotypes can be attributed to the effect of the virus on the susceptible genotypes. The current result is also in agreement with the reports of Stephan *et al.* (2013) who also reported a noticeable variation among sweet potato varieties in terms of virus resistance and its influence on the quantity and quality of root and biomass yields among sweet potato varieties.

#### **Correlation analysis**

Both disease and agronomic parameters in this study related variably to each other. There were positive correlations among virus scores on all the assessment occasions. However, there was a negative correlation between virus scores and all the agronomic parameters namely, plant vigor, vine length, biomass yield and root yield. This means that as the disease severity rises, plant vigor, vine length, biomass yield and root yield reduce. Plant vigor in all the assessment occasions correlated positively with vine length, biomass yield and root yield. This means that an increase in plant vigor insights plants growth and development, as seen in vine length, biomass yield and root yield. Similarly, vine length also correlated positively with biomass and root yields.

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Likewise, biomass yield also correlated positively with root yield (Table 1). This could mean that root yield increases with a rise in biomass yield. The findings of the current study corroborate with Jones (2021) and Ngailo *et al.* (2013). Perhaps, a rise in the vegetative development of sweet potato has virus in Nigeria.

increased the photosynthetic ability of plants, leading to a higher production of photosynthates that could be stored in the roots. A similar finding was reported by Abdulrahman *et al.* (2022) who screened some sweet potato cultivars for resistance to the feathery mottle



Figure 4: Root yield performance of the various genotypes



Figure 5: Foliage yield of the various genotypes

	VS 6WAP	VS 8WAP	PV 6WAP	PV 8WAP	VL	Biomass	Root yield
VS 6WAP	-						
VS 8WAP	0.9578***	-					
PV 6WAP	-0.2122	-0.221	-				
PV 8WAP	-0.0744	-0.0952***	0.7969***	-			
VL	-0.6208**	-0.6307**	0.4997*	0.3507*	-		
Biomass	-0.3537*	-0.3818*	0.2081	0.2366	0.2534	-	
Root yield	-0.3427*	-0.3056*	0.3325*	0.3223*	0.3484*	0.474*	-

**Table 1:** Correlation analysis between virus scores (VS) at 6, and 8 WAP, plant vigor (PV) at 6, and 8 WAP, vine length (VL), biomass yield, and root yield

\*=significant at 0.05, \*\*=significant at 0.01, \*\*\*=significant at 0.001

# CONCLUSION

In the current study, genotypes reacted variably in terms of resistance or otherwise susceptibility to SPVD. Thirteen (13) genotypes were classified as resistant to the disease, fifteen (15) were classified as moderately resistant, whilst the remaining was classified as susceptible to the disease. genotypes; PG17584-N1, Three (3) PG17257-N1 and PG17149-N2 combine SPVD resistance with high root and biomass yields. Resistant genotypes from this study may serve as relevant breeding materials in future breeding interventions. However, a multilocational experiment should be conducted to assess the stability of the resistant genotypes across many locations and perhaps, ecological zones. Furthermore, an experiment on the influence of the date of planting on the incidence and severity of SPVD should be further conducted with these genotypes.

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